



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 178609**

**TO: Jeffrey Parkin**  
**Location: rem/3D39/3C18**  
**Art Unit: 1648**  
**Friday, February 17, 2006**  
**Case Serial Number: 09/669187**

**From: Toby Port**  
**Location: Biotech-Chem Library**  
**REM-1A59**  
**Phone: 571-272-2523**  
  
**toby.port@uspto.gov**

### **Search Notes**

**Examiner Parkin,**

**See attached results.**

**If you have any questions about this search feel free to contact me at any time.**

**Thank you for using STIC search services!**

**Toby Port**  
**X22523**

THIS PAGE BLANK (USFO)



STIC-Biotech/ChemLib

178609

mg

From: Parkin, Jeffrey  
Sent: Friday, February 03, 2006 6:25 PM  
To: STIC-Biotech/ChemLib  
Subject: U.S. Serial No. 09/669,187

Aloha!

Please search **SEQ ID NOS.: 73, 80, 81, 148, and 906** from U.S. Serial No. **09/669,187** v. all relevant databases, including interference. Please limit search results to oligonucleotides less than 50 nt in length, if possible. Place results on both paper and electronic format (i.e., disk, e-mail, etc.). Thanks!

Jeffrey S. Parkin, Ph.D.  
Primary Examiner  
Art Unit 1648  
REM 3D39  
2-0908

3C18

RECEIVED  
FEB - 6 2006  
STIC

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:51:58 ; Search time 479.835 Seconds  
(without alignments)  
2369.293 Million cell updates/sec

Title: US-09-669-187A-73

Perfect score: 20

Sequence: 1 ttttgggttttgggtttt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.in.\*

3: gb.env.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pr.\*

9: gb.ro.\*

10: gb.sts.\*

11: gb.sy.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.htg.\*

15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	100.0	20	6	AX103881 Sequence
2	20	100.0	20	6	AX546934 Sequence
3	20	100.0	28	6	CS077910 Sequence
4	20	100.0	28	6	CS077991 Sequence
5	20	100.0	36	2	OFREP2
6	20	100.0	39	6	AR074313 Sequence
7	20	100.0	39	6	AX032675 Sequence
8	20	100.0	44	6	AR104530 Sequence
9	20	100.0	44	6	AR175791 Sequence
10	20	100.0	44	6	E37018
11	20	100.0	44	6	AR390695 Sequence
12	20	100.0	44	6	AR393309 Sequence
13	20	100.0	44	6	AR592667 Sequence
14	20	100.0	44	6	AX810603 Sequence
15	20	100.0	44	6	BD011269 Human tel
16	20	100.0	46	6	AR104529 Sequence
17	20	100.0	46	6	AR175790 Sequence
18	20	100.0	46	6	E37017 Human telom

19	20	100.0	46	6	AR390694	AR390694 Sequence
20	20	100.0	46	6	AR393308	AR393308 Sequence
21	20	100.0	46	6	AR592666	AR592666 Sequence
22	20	100.0	46	6	AX810602	AX810602 Sequence
23	20	100.0	46	6	BD011268	BD011268 Human tel
24	20	100.0	48	6	AR104525	AR104525 Sequence
25	20	100.0	48	6	AR104528	AR104528 Sequence
26	20	100.0	48	6	AR175786	AR175786 Sequence
27	20	100.0	48	6	AR175789	AR175789 Sequence
28	20	100.0	48	6	E37014	E37014 Human telom
29	20	100.0	48	6	AR390691	AR390691 Sequence
30	20	100.0	48	6	AR393305	AR393305 Sequence
31	20	100.0	48	6	AR592662	AR592662 Sequence
32	20	100.0	48	6	AR592665	AR592665 Sequence
33	20	100.0	48	6	AX810599	AX810599 Sequence
34	20	100.0	48	6	BD011265	BD011265 Human tel
35	20	100.0	50	6	AR104527	AR104527 Sequence
36	20	100.0	50	6	AR175788	AR175788 Sequence
37	20	100.0	50	6	E37016	E37016 Human telom
38	20	100.0	50	6	AR390693	AR390693 Sequence
39	20	100.0	50	6	AR393307	AR393307 Sequence
40	20	100.0	50	6	AR592664	AR592664 Sequence
41	20	100.0	50	6	AX810601	AX810601 Sequence
42	20	100.0	50	6	BD011267	BD011267 Human tel
43	18	90.0	50	6	AR104527	AR104527 Sequence
44	18	90.0	50	6	AR175788	AR175788 Sequence
45	18	90.0	50	6	E37016	E37016 Human telom
46	18	90.0	50	6	AR390693	AR390693 Sequence
47	18	90.0	50	6	AR393307	AR393307 Sequence
48	18	90.0	50	6	AR592664	AR592664 Sequence
49	18	90.0	50	6	AX810601	AX810601 Sequence
50	18	90.0	50	6	BD011267	BD011267 Human tel
51	16.8	84.0	39	2	OPACJTBELC	L02847 Oxytricha f
52	16.8	84.0	44	6	AR104530	AR104530 Sequence
53	16.8	84.0	44	6	AR175791	AR175791 Sequence
54	16.8	84.0	44	6	E37018	E37018 Human telom
55	16.8	84.0	44	6	AR390695	AR390695 Sequence
56	16.8	84.0	44	6	AR393309	AR393309 Sequence
57	16.8	84.0	44	6	AR592667	AR592667 Sequence
58	16.8	84.0	44	6	AX810603	AX810603 Sequence
59	16.8	84.0	44	6	BD011269	BD011269 Human tel
60	16.8	84.0	46	6	AR104529	AR104529 Sequence
61	16.8	84.0	46	6	AR175790	AR175790 Sequence
62	16.8	84.0	46	6	E37017	E37017 Human telom
63	16.8	84.0	46	6	AR390694	AR390694 Sequence
64	16.8	84.0	46	6	AR393308	AR393308 Sequence
65	16.8	84.0	46	6	AR592666	AR592666 Sequence
66	16.8	84.0	46	6	AX810602	AX810602 Sequence
67	16.8	84.0	46	6	BD011268	BD011268 Human tel
68	16.8	84.0	48	6	AR104525	AR104525 Sequence
69	16.8	84.0	48	6	AR104528	AR104528 Sequence
70	16.8	84.0	48	6	AR175786	AR175786 Sequence
71	16.8	84.0	48	6	AR175789	AR175789 Sequence
72	16.8	84.0	48	6	E37014	E37014 Human telom
73	16.8	84.0	48	6	AR390691	AR390691 Sequence
74	16.8	84.0	48	6	AR393305	AR393305 Sequence
75	16.8	84.0	48	6	AR592662	AR592662 Sequence
76	16.8	84.0	48	6	AR592665	AR592665 Sequence
77	16.8	84.0	48	6	AX810599	AX810599 Sequence
78	16.8	84.0	48	6	BD011265	BD011265 Human tel
79	16	80.0	16	6	AR104544	AR104544 Sequence
80	16	80.0	16	6	AR175805	AR175805 Sequence
81	16	80.0	16	6	E36807	E36807 Human telom
82	16	80.0	16	6	AR390484	AR390484 Sequence
83	16	80.0	16	6	AR393098	AR393098 Sequence
84	16	80.0	16	6	AR592679	AR592679 Sequence
85	16	80.0	16	6	AX810149	AX810149 Sequence
86	16	80.0	16	6	BD011058	BD011058 Human tel
87	15	80.0	20	2	OFREP1	V01082 Oxytricha f
88	15.2	76.0	20	6	CS013559	CS013559 Sequence
89	15.2	76.0	22	6	CS113618	CS113618 Sequence
90	14.8	74.0	24	6	AR207616	AR207616 Sequence
91	14.8	74.0	24	6	AX104500	AX104500 Sequence

92	14.8	74.0	24	6	AX104502	Sequence	165	13.2	66.0	29	6	CS125435	Sequence
93	14.8	74.0	24	6	AX104691	Sequence	166	13.2	66.0	29	6	AX928232	Sequence
94	14.8	74.0	24	6	AX137294	Sequence	167	13.2	66.0	30	6	AR000058	Sequence
95	14.8	74.0	24	6	AX355707	Sequence	168	13.2	66.0	30	6	AR064881	Sequence
96	14.8	74.0	24	6	AX547553	Sequence	c 169	13.2	66.0	41	6	CQ869331	Sequence
97	14.8	74.0	24	6	AX547555	Sequence	170	13.2	66.0	30	6	CQ817934	Sequence
98	14.8	74.0	24	6	AX547744	Sequence	171	13.2	66.0	43	6	AX058564	Sequence
99	14.8	74.0	24	6	AX593918	Sequence	172	13.2	66.0	49	6	AX058563	Sequence
100	14.8	74.0	24	6	AX961611	Sequence	c 173	13.2	66.0	50	6	I42216	Sequence
101	14.8	74.0	24	6	BD014843	Universal	c 174	13.2	66.0	50	6	BD014161	Probe for
102	14.8	74.0	24	6	CS131752	Sequence	175	12.8	64.0	18	6	AR297501	Sequence
c 103	14.8	74.0	24	6	CS131752	Sequence	176	12.8	64.0	18	6	AX599218	Sequence
c 104	14.8	74.0	46	6	AR207615	Sequence	177	12.8	64.0	18	6	AX599352	Sequence
c 105	14.8	74.0	46	6	AX137293	Sequence	178	12.8	64.0	18	6	AX599695	Sequence
c 106	14.8	74.0	23	6	BD014842	Universal	179	12.8	64.0	18	6	AX599696	Sequence
c 107	14.2	71.0	23	6	E35795	Process for	180	12.8	64.0	18	6	AX599792	Sequence
c 108	14.2	71.0	26	6	AR104518	Sequence	181	12.8	64.0	18	6	AX767670	Sequence
c 109	14.2	71.0	26	6	AR104543	Sequence	182	12.8	64.0	18	6	AX796126	Sequence
c 110	14.2	71.0	26	6	AR175779	Sequence	183	12.8	64.0	18	6	AX796226	Sequence
c 111	14.2	71.0	26	6	AR175804	Sequence	c 184	12.8	64.0	20	6	AR236874	Sequence
c 112	14.2	71.0	26	6	E37007	Human telom	c 185	12.8	64.0	21	6	CQ799734	Sequence
c 113	14.2	71.0	26	6	AR390684	Sequence	c 186	12.8	64.0	21	6	AR296682	Sequence
c 114	14.2	71.0	26	6	AR393298	Sequence	187	12.8	64.0	24	6	CQ903961	Sequence
c 115	14.2	71.0	26	6	AR592655	Sequence	188	12.8	64.0	24	6	AX104112	Sequence
c 116	14.2	71.0	26	6	AR592678	Sequence	189	12.8	64.0	24	6	AX104166	Sequence
c 117	14.2	71.0	26	6	AX810592	Sequence	190	12.8	64.0	24	6	AX104243	Sequence
c 118	14.2	71.0	29	6	BD011258	Human tel	191	12.8	64.0	24	6	AX105106	Sequence
c 119	14.2	71.0	32	6	AX394124	Sequence	192	12.8	64.0	24	6	AX355699	Sequence
c 120	14.2	71.0	35	6	E06305	Primer. 9/1	193	12.8	64.0	24	6	AX355819	Sequence
c 121	14.2	71.0	35	6	E06501	Primer. 9/1	194	12.8	64.0	24	6	AX355820	Sequence
c 122	14	70.0	15	6	AR095959	Sequence	195	12.8	64.0	24	6	AX547165	Sequence
c 123	14	70.0	15	6	AR104531	Sequence	196	12.8	64.0	24	6	AX547219	Sequence
c 124	14	70.0	15	6	AR104533	Sequence	197	12.8	64.0	24	6	AX547296	Sequence
c 125	14	70.0	15	6	AR175792	Sequence	198	12.8	64.0	24	6	AX593909	Sequence
c 126	14	70.0	15	6	AR175794	Sequence	199	12.8	64.0	24	6	AX593920	Sequence
c 127	14	70.0	15	6	E36806	Human telom	c 200	12.8	64.0	24	6	AX593921	Sequence
c 128	14	70.0	15	6	AR359628	Sequence	c 201	12.8	64.0	28	6	CQ894850	Sequence
c 129	14	70.0	15	6	AR390483	Sequence	c 202	12.8	64.0	31	6	BD247607	Streptoco
c 130	14	70.0	15	6	AR393097	Sequence	c 203	12.8	64.0	31	6	AR198761	Sequence
c 131	14	70.0	15	6	AR592668	Sequence	c 204	12.6	63.0	19	6	AX599175	Sequence
c 132	14	70.0	15	6	AR592669	Sequence	c 205	12.6	63.0	21	6	CS059446	Sequence
c 133	14	70.0	15	6	AX033371	Sequence	c 206	12.6	63.0	22	6	AR296307	Sequence
c 134	14	70.0	15	6	AX033372	Sequence	207	12.6	63.0	22	6	CQ807573	Sequence
c 135	14	70.0	15	6	AX810148	Sequence	208	12.6	63.0	22	6	AX116710	Sequence
c 136	14	70.0	15	6	BD011057	Human tel	209	12.6	63.0	22	6	AX511797	Sequence
c 137	14	70.0	20	6	AX339139	Sequence	210	12.6	63.0	23	6	CS048929	Sequence
c 138	13.8	69.0	19	6	AR444879	Sequence	211	12.6	63.0	23	6	CS048932	Sequence
c 139	13.8	69.0	49	6	AX772455	Sequence	c 212	12.6	63.0	24	6	CS013792	Sequence
140	13.8	69.0	50	6	AR356126	Sequence	c 213	12.6	63.0	24	6	AX114887	Sequence
141	13.8	69.0	50	6	AR537682	Sequence	c 214	12.6	63.0	29	6	AR142922	Sequence
142	13.6	68.0	21	6	AR074334	Sequence	215	12.6	63.0	30	6	CQ857114	Sequence
143	13.6	68.0	21	6	I21708	Sequence 4	216	12.6	63.0	30	6	AX793377	Sequence
144	13.6	68.0	21	6	AX032696	Sequence	217	12.6	63.0	40	6	AR083586	Sequence
145	13.6	68.0	26	6	I26260	Sequence 7	218	12.6	63.0	40	6	AR160411	Sequence
146	13.6	68.0	29	6	AX104113	Sequence	219	12.6	63.0	40	6	AR216833	Sequence
147	13.6	68.0	29	6	AX355103	Sequence	220	12.6	63.0	40	6	AR369636	Sequence
148	13.6	68.0	29	6	AX547166	Sequence	221	12.6	63.0	40	6	BD008982	SpSa poly
149	13.6	68.0	32	6	AX104237	Sequence	222	12.6	63.0	40	6	BD009195	Novel Sps
150	13.6	68.0	32	6	AX355706	Sequence	223	12.6	63.0	40	15	AX838493	Arabidops
151	13.6	68.0	32	6	AX547290	Sequence	c 224	12.6	63.0	40	15	AX838543	Arabidops
c 152	13.6	68.0	40	6	AX394946	Sequence	c 225	12.6	63.0	50	6	CQ003524	Sequence
153	13.6	68.0	43	6	AX058571	Sequence	c 226	12.4	62.0	18	6	AR060409	Sequence
154	13.6	68.0	47	6	AR289107	Sequence	c 227	12.4	62.0	18	6	AR094563	Sequence
155	13.6	68.0	47	6	AR290741	Sequence	c 228	12.4	62.0	18	6	AR094564	Sequence
c 156	13.6	68.0	50	6	CQ003525	Sequence	c 229	12.4	62.0	18	6	AR128967	Sequence
c 157	13.4	67.0	20	6	AR032105	Sequence	230	12.4	62.0	19	6	AX817169	Sequence
c 158	13.4	67.0	21	6	CQ873830	Sequence	231	12.4	62.0	19	6	AX817184	Sequence
c 159	13.4	67.0	30	6	AX394125	Sequence	232	12.4	62.0	19	6	AX824393	Sequence
c 160	13.4	67.0	32	6	AR287340	Sequence	233	12.4	62.0	20	6	BD090050	A method
c 161	13.2	66.0	25	6	CQ857416	Sequence	234	12.4	62.0	21	6	E33097	Tetrahydroc
162	13.2	66.0	25	6	CQ894348	Sequence	c 235	12.4	62.0	21	6	AR299170	Sequence
163	13.2	66.0	25	6	AX786820	Sequence	236	12.4	62.0	22	6	CQ807361	Sequence
164	13.2	66.0	26	6	AB2168	Sequence 3	237	12.4	62.0	22	6	AX795983	Sequence



JOURNAL	Patent: WO 2005035579-A 28 21-APR-2005;	
FEATURES	University of Louisville Research Foundation (US)	
source	Location/Qualifiers	
	1. .28	
	/organism="synthetic construct"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:32630"	
	/note="Description of Artificial Sequence: Synthetic polynucleotide sequence"	
ORIGIN		
Query Match	100.0%; Score 20; DB 6; Length 28;	
Best Local Similarity	100.0%; Pred. No. 1.9e+02;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TTTTGGGGTTTGGGGTTTT 20	
Db		
	5 TTTTGGGGTTTGGGGTTTT 24	
RESULT 4		
LOCUS	CS097991 28 bp DNA linear PAT 03-JUN-2005	
DEFINITION	Sequence 29 from Patent WO2005037323.	
ACCESSION	CS097991	
VERSION	CS097991.1 GI:66954236	
KEYWORDS	synthetic construct	
SOURCE	synthetic construct	
ORGANISM	other sequences; artificial sequences.	
REFERENCE	1	
AUTHORS	Bates,P.J., Girvan,A.C. and Barve,S.S.	
TITLE	Method for inhibiting nf-kappa b signaling and use to treat or prevent human disease	
JOURNAL	Patent: WO 2005037323-A 29 28-APR-2005;	
FEATURES	University of Louisville Research Foundation, Inc. (US)	
source	Location/Qualifiers	
	1. .28	
	/organism="synthetic construct"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:32630"	
	/note="Description of Artificial Sequence: Synthetic polynucleotide sequence"	
ORIGIN		
Query Match	100.0%; Score 20; DB 6; Length 28;	
Best Local Similarity	100.0%; Pred. No. 1.9e+02;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TTTTGGGGTTTGGGGTTTT 20	
Db		
	5 TTTTGGGGTTTGGGGTTTT 24	
RESULT 5		
OFREP2	Oxytricha fallax right end of linear DNA fragments in macronucleus.	
LOCUS	36 bp DNA linear INV 06-JUL-1989	
DEFINITION	Oxytricha fallax	
ACCESSION	V01083	
VERSION	V01083.1 GI:9755	
KEYWORDS	repetitive sequence.	
SOURCE	Oxytricha fallax	
ORGANISM	Oxytricha fallax	
REFERENCE	Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia; Stichotrichida; Oxytrichidae; Oxytricha.	
AUTHORS	1 (bases 1 to 36)	
TITLE	Dawson,D. and Herrick,G.	
JOURNAL	Macronuclear DNA sequences of Oxytricha fallax homologous to the macronuclear inverted terminal repeat	
PUBLISHED	Nucleic Acids Res. 10 (9), 2911-2924 (1982)	
FEATURES	7099969 Location/Qualifiers	
source	1. .36	

---

ORIGIN		
Query Match	100.0%; Score 20; DB 2; Length 36;	
Best Local Similarity	100.0%; Pred. No. 1.9e+02;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TTTTGGGGTTTGGGGTTTT 20	
Db		
	5 TTTTGGGGTTTGGGGTTTT 24	
RESULT 6		
LOCUS	AR074313 39 bp DNA linear PAT 28-AUG-2000	
DEFINITION	Sequence 121 from patent US 5952490.	
ACCESSION	AR074313	
VERSION	AR074313.1 GI:10001068	
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 39)	
AUTHORS	Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y., Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and Imbach,J.Louis.	
TITLE	Oligonucleotides having a conserved G4 core sequence	
JOURNAL	Patent: US 5952490-A 121 14-SEP-1999;	
FEATURES	Location/Qualifiers	
source	1. .39	
	/organism="unknown"	
	/mol_type="unassigned DNA"	
ORIGIN		
Query Match	100.0%; Score 20; DB 6; Length 39;	
Best Local Similarity	100.0%; Pred. No. 1.8e+02;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TTTTGGGGTTTGGGGTTTT 20	
Db		
	8 TTTTGGGGTTTGGGGTTTT 27	
RESULT 7		
AX032675	AX032675 39 bp DNA linear PAT 20-SEP-2000	
LOCUS	Sequence 121 from Patent EP1016715.	
DEFINITION	AX032675	
ACCESSION	AX032675	
VERSION	AX032675.1 GI:10279613	
KEYWORDS	unidentified	
SOURCE	unidentified	
ORGANISM	unclassified sequences.	
REFERENCE	1	
AUTHORS	Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J., Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and Wyatt,J.R.	
TITLE	Oligonucleotides having a conserved g4 core sequence	
JOURNAL	Patent: EP 1016715-A 121 05-JUL-2000;	
FEATURES	ISIS PHARMACEUTICALS INC (US)	
source	Location/Qualifiers	
	1. .39	
	/organism="unidentified"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:32644"	
ORIGIN		
Query Match	100.0%; Score 20; DB 6; Length 39;	
Best Local Similarity	100.0%; Pred. No. 1.8e+02;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

```

Qy 1 TTTTGGGGTTTGGGGTTTT 20
Db 8 TTTTGGGGTTTGGGGTTTT 27

RESULT 8
LOCUS AR104530 linear PAT 14-FEB-2001
DEFINITION Sequence 42 from patent US 6093809.
ACCESSION AR104530
VERSION AR104530.1 GI:12817238
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Cecch, T.R. and Lingner, J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 42 25-JUL-2000;
FEATURES
source
1..44
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20
Db 25 TTTTGGGGTTTGGGGTTTT 44

RESULT 9
LOCUS AR175791 linear PAT 17-DEC-2001
DEFINITION Sequence 42 from patent US 6309867.
ACCESSION AR175791
VERSION AR175791.1 GI:17917090
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Cecch, T.R. and Nakamura, T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 42 30-OCT-2001;
FEATURES
source
1..44
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20
Db 25 TTTTGGGGTTTGGGGTTTT 44

RESULT 10
LOCUS E37018 linear PAT 18-JUN-2001
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E37018
VERSION E37018.1 GI:13022981
KEYWORDS JP 1999253177-A/226.
SOURCE unidentified
ORGANISM unclassified.

```

---

```

REFERENCE 1 (bases 1 to 44)
AUTHORS Thomas, R.S., Jochimu, R., Toru, N., Karen, B.C., Greg, B.M.,
Calvin, B.H. and William, H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 1999253177-A 226 21-SEP-1999;
JERON CORP, UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
PN JP 1999253177-A/226
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,643, 18-APR-1997 US 08/844,419, PR
25-APR-1997 US 08/846,017, 06-MAY-1997 US 08/851,843, PR
09-MAY-1997 US 08/854,050, 14-AUG-1997 US 08/911,312, PR
14-AUG-1997 US 08/912,951, 14-AUG-1997 US 08/915,503 PI THOMAS
R SECHI, JOCHIMU RINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B
MORIN.
PI CALVIN B HAREI, WILLIAM H ANDREWS
PC C12N15/09, A61K31/70, A61K38/55, A61K39/395, A61K48/00,
PC C12Q1/02,
PC C12Q1/48, C12Q1/68, G01N33/15, G01N33/48, G01N33/50//C07K14/47, PC
C07K16/40,
PC C12N1/19, C12N1/21, C12N5/10, C12N9/12, C12P21/08, (C12N1/19, PC
C12R1:84),
PC (C12N1/21, C12R1:19), (C12N9/12, C12R1:19), (C12N9/12, C12R1:84),
PC (C12N9/12, C12R1:91), C12N15/00, A61K37/64, C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..44
Location/Qualifiers
1..44
/organism="Unidentified".
FEATURES
source
1..44
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20
Db 25 TTTTGGGGTTTGGGGTTTT 44

RESULT 11
LOCUS AR390695 44 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 568 from patent US 6610839.
ACCESSION AR390695
VERSION AR390695.1 GI:40112629
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Morin, G.B. and Andrews, W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 568 26-AUG-2003;
GERON Corporation, Menlo Park, CA
FEATURES
source
1..44
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20

```

```
Db      25 TTTTGGGGTTTGGGGTTTT 44

RESULT 12
LOCUS   AR393309
DEFINITION Sequence 568 from patent US 6617110.
ACCESSION AR393309
VERSION  AR393309.1 GI:40118689
KEYWORDS
SOURCE  Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS  Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
          Harley,C.B. and Andrews,W.H.
TITLE    Cells immortalized with telomerase reverse transcriptase for use in
          drug screening
JOURNAL  Patent: US 6617110-A 568 09-SEP-2003;
          Geron Corporation and University Technology Corporation; Menlo
          Park, CA
FEATURES             Location/Qualifiers
   source             1..44
                     /organism="unknown"
                     /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 TTTTGGGGTTTGGGGTTTT 20
    |||||
Db   25 TTTTGGGGTTTGGGGTTTT 44

RESULT 13
LOCUS   AR592667
DEFINITION Sequence 42 from patent US 6808880.
ACCESSION AR592667
VERSION  AR592667.1 GI:56641387
KEYWORDS
SOURCE  Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 44)
AUTHORS  Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
          Harley,C. and Andrews,W.H.
TITLE    Method for detecting polynucleotides encoding telomerase
JOURNAL  Patent: US 6808880-A 42 26-OCT-2004;
          Geron Corporation and Regents of the University of Colorado; Menlo
          Park, CA
FEATURES             Location/Qualifiers
   source             1..44
                     /organism="unknown"
                     /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 TTTTGGGGTTTGGGGTTTT 20
    |||||
Db   25 TTTTGGGGTTTGGGGTTTT 44

RESULT 14
LOCUS   AX810603
DEFINITION Sequence 568 from Patent EP1333094.
ACCESSION AX810603
VERSION  AX810603.1 GI:38524092
KEYWORDS
SOURCE  Unidentified
ORGANISM Unidentified
REFERENCE 1
AUTHORS  Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
          Harley,C.B. and Andrews,W.H.
TITLE    Human telomerase catalytic subunit
JOURNAL  Patent: EP 1333094-A 568 06-AUG-2003;
          Geron Corporation (US); University Technology Corporation (US)
FEATURES             Location/Qualifiers
   source             1..44
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 TTTTGGGGTTTGGGGTTTT 20
    |||||
Db   25 TTTTGGGGTTTGGGGTTTT 44

RESULT 15
LOCUS   BD011269
DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011269
VERSION  BD011269.1 GI:18639642
KEYWORDS
SOURCE  Unidentified
ORGANISM Unidentified
REFERENCE 1 (bases 1 to 44)
AUTHORS  Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
          Harley,C.B. and Andrews,W.H.
TITLE    Human telomerase catalytic subunit
JOURNAL  Patent: JP 2001081042-A 226 27-MAR-2001;
          GERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT  OS Unidentified
          PN JP 2001081042-A/226
          PD 27-MAR-2001
          PF 27-JUL-2000 JP 2000227474
          PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
          25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
          09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
          14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
          R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
          MORIN,
          PI CALVIN B HARLEY,WILLIAM H ANDREWS
          PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
          PC C07K5/10,
          PC C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12, PC
          C12N15/09,
          PC C12Q1/02,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
          G01N33/53,
          PC G01N33/566,G01N33/573//C12P21/08,A61K37/02,C12N15/00 CC
          Strandedness: Single;
          CC Topology: Linear;
          FH Key Location/Qualifiers
          FT source 1..44
          FT /organism='Unidentified'.
          FT Location/Qualifiers
          1..44
          /organism="unidentified"
          /mol_type="genomic DNA"
          /db_xref="taxon:32644"

ORIGIN
```



Query Match 100.0%; Score 20; DB 6; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
DB 25 TTTTGGGTTTGGGGTTTT 44

RESULT 16  
AR104529  
LOCUS AR104529 46 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 41 from patent US 6093809.  
ACCESSION AR104529  
VERSION AR104529.1 GI:12817237  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 46)  
AUTHORS Cech,T.R. and Lingner,J.  
TITLE Telomerase  
JOURNAL Patent: US 6093809-A 41 25-JUL-2000;  
FEATURES  
source Location/Qualifiers  
1..46  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
DB 27 TTTTGGGTTTGGGGTTTT 46

RESULT 17  
AR175790  
LOCUS AR175790 46 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 41 from patent US 6309867.  
ACCESSION AR175790  
VERSION AR175790.1 GI:17917089  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 46)  
AUTHORS Cech,T.R. and Nakamura,T.  
TITLE Telomerase  
JOURNAL Patent: US 6309867-A 41 30-OCT-2001;  
FEATURES  
source Location/Qualifiers  
1..46  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
DB 27 TTTTGGGTTTGGGGTTTT 46

RESULT 18  
E37017  
LOCUS E37017 46 bp DNA linear PAT 18-JUN-2001  
DEFINITION Human telomerase catalytic subunit promoter.  
ACCESSION E37017  
VERSION E37017.1 GI:13022980

KEYWORDS JP 1999253177-A/225.  
SOURCE unidentified  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 46)  
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M., Calvin,B.H. and William,H.A.  
TITLE Human telomerase catalytic subunit promoter  
JOURNAL Patent: JP 1999253177-A 225 21-SEP-1999;  
COMMENT JERON CORP. UNIVERSITY TECHNOLOGY CORP  
OS Unidentified  
PN JP 1999253177-A/225  
PD 21-SEP-1999  
PF 15-OCT-1998 JP 1998320169  
PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR 25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR 09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR 14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503, PI THOMAS R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B MORIN,  
PI CALVIN B HAREI,WILLIAM H ANDREWS  
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,  
PC C12Q1/02,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC C07K16/40,  
PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC C12R1:84),  
PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84), PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC  
Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..46  
Location/Qualifiers  
/organism="Unidentified".  
1..46  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

FEATURES  
source Location/Qualifiers  
1..46  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
DB 27 TTTTGGGTTTGGGGTTTT 46

RESULT 19  
AR390694  
LOCUS AR390694 46 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 567 from patent US 6610839.  
ACCESSION AR390694  
VERSION AR390694.1 GI:40112628  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 46)  
AUTHORS Morin,G.B. and Andrews,W.H.  
TITLE Promoter for telomerase reverse transcriptase  
JOURNAL Patent: US 6610839-A 567 26-AUG-2003;  
Geron Corporation, Menlo Park, CA  
FEATURES  
source Location/Qualifiers  
1..46  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

```
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   |||||
Db 27 TTTTGGGTTTGGGGTTTT 46

RESULT 20
AR393308
LOCUS AR393308 46 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 567 from patent US 6617110.
ACCESSION AR393308
VERSION AR393308.1 GI:40118687
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
         Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in
        drug screening
JOURNAL Patent: US 6617110-A 567 09-SEP-2003;
        Geron Corporation and University Technology Corporation; Menlo
        Park, CA
FEATURES
    source
        Location/Qualifiers
            1..46
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   |||||
Db 27 TTTTGGGTTTGGGGTTTT 46

RESULT 21
AR592666
LOCUS AR592666 46 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 41 from patent US 6808880.
ACCESSION AR592666
VERSION AR592666.1 GI:56641386
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
         Harley,C. and Andrews,W.H.
TITLE Method for detecting polynucleotides encoding telomerase
JOURNAL Patent: US 6808880-A 41 26-OCT-2004;
        Geron Corporation and Regents of the University of Colorado; Menlo
        Park, CA
FEATURES
    source
        Location/Qualifiers
            1..46
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   |||||
Db 27 TTTTGGGTTTGGGGTTTT 46

, RESULT 22
```

```
AX810602
LOCUS AX810602 46 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 567 from Patent EPI333094.
ACCESSION AX810602
VERSION AX810602.1 GI:38524091
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
         Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: EP 1333094-A 567 06-AUG-2003;
        Geron Corporation (US) ; University Technology Corporation (US)
FEATURES
    source
        Location/Qualifiers
            1..46
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   |||||
Db 27 TTTTGGGTTTGGGGTTTT 46

RESULT 23
BD011268
LOCUS BD011268 46 bp DNA linear PAT 31-JAN-2002
DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011268
VERSION BD011268.1 GI:18639641
KEYWORDS JP 2001081042-A/225.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 46)
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
         Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 225 27-MAR-2001;
        GERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
        PN JP 2001081042-A/225
        PD 27-MAR-2001
        PF 27-JUL-2000 JP 2000227474
        PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
        25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
        09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
        14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
        R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI
        MORIN,
        PI CALVIN B HARLEY,WILLIAM H ANDREWS
        PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
        PC C07K5/10,
        PC C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12, PC
        C12N15/09,
        PC C12Q1/02,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
        G01N33/53
        PC G01N33/566,G01N33/573//C12P21/08,A61K37/02,C12N15/00 CC
        Strandedness: Single;
        CC Topology: Linear;
        FH Key Location/Qualifiers
        FT source 1..46
        FT /organism='Unidentified'.
        FT Location/Qualifiers
            1..46
                /organism="unidentified"
```

```
ORIGIN
  Query Match      100.0%; Score 20; DB 6; Length 46;
  Best Local Similarity 100.0%; Pred. No. 1.8e+02;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 1 TTTTGGGTTTTCGGGTTTT 20
     |||||
  Db 27 TTTTGGGTTTTCGGGTTTT 46

RESULT 24
AR104525
LOCUS AR104525 48 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 37 from patent US 6093809.
ACCESSION AR104525
VERSION AR104525.1 GI:12817233
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 37 25-JUL-2000;
FEATURES
  source
    1..48
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
  Query Match      100.0%; Score 20; DB 6; Length 48;
  Best Local Similarity 100.0%; Pred. No. 1.8e+02;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 1 TTTTGGGTTTTCGGGTTTT 20
     |||||
  Db 29 TTTTGGGTTTTCGGGTTTT 48

RESULT 25
AR104528
LOCUS AR104528 48 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 40 from patent US 6093809.
ACCESSION AR104528
VERSION AR104528.1 GI:12817236
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 40 25-JUL-2000;
FEATURES
  source
    1..48
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
  Query Match      100.0%; Score 20; DB 6; Length 48;
  Best Local Similarity 100.0%; Pred. No. 1.8e+02;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 1 TTTTGGGTTTTCGGGTTTT 20
     |||||
  Db 29 TTTTGGGTTTTCGGGTTTT 48

RESULT 26
AR175786
LOCUS AR175786 48 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 37 from patent US 6309867.
ACCESSION AR175786
VERSION AR175786.1 GI:17917085
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 37 30-OCT-2001;
FEATURES
  source
    1..48
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
  Query Match      100.0%; Score 20; DB 6; Length 48;
  Best Local Similarity 100.0%; Pred. No. 1.8e+02;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 1 TTTTGGGTTTTCGGGTTTT 20
     |||||
  Db 29 TTTTGGGTTTTCGGGTTTT 48

RESULT 27
AR175789
LOCUS AR175789 48 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 40 from patent US 6309867.
ACCESSION AR175789
VERSION AR175789.1 GI:17917088
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 48)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 40 30-OCT-2001;
FEATURES
  source
    1..48
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
  Query Match      100.0%; Score 20; DB 6; Length 48;
  Best Local Similarity 100.0%; Pred. No. 1.8e+02;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 1 TTTTGGGTTTTCGGGTTTT 20
     |||||
  Db 29 TTTTGGGTTTTCGGGTTTT 48

RESULT 28
E37014
LOCUS E37014 48 bp DNA linear PAT 18-JUN-2001
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E37014
VERSION E37014.1 GI:13022977
KEYWORDS JP 199253177-A/222.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 48)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
  Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 199253177-A 222 21-SEP-1999;
  JERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
```

PN JP 19992531177-A/222  
PD 21-SEP-1999  
PF 15-OCT-1998 JP 1998320169  
PR 01-OCT-1996 US 08/724.643,18-APR-1997 US 08/844.419, PR  
25-APR-1997 US 08/846.017,06-MAY-1997 US 08/851.843, PR  
09-MAY-1997 US 08/854.050,14-AUG-1997 US 08/911.312, PR  
14-AUG-1997 US 08/912.951,14-AUG-1997 US 08/915.503 PI THOMAS  
R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B  
MORIN,  
PI CALVIN B HAREI,WILLIAM H ANDREWS  
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K48/00,  
PC C12Q1/02,  
PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC  
C07K16/40,  
PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,C12N1/19, PC  
C12R1:84),  
PC (C12N1/21,C12R1:19), (C12N9/12,C12R1:19), (C12N9/12,C12R1:84),  
PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC  
Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..48  
FT /organism='Unidentified'.  
FT Location/Qualifiers  
1..48  
/organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

FEATURES  
source  
1..48  
/organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 29  
LOCUS AR390691 48 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 564 from patent US 6610839.  
ACCESSION AR390691  
VERSION AR390691.1 GI:40112625  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Morin,G.B. and Andrews,W.H.  
TITLE Promoter for telomerase reverse transcriptase  
JOURNAL Patent: US 6610839-A 564 26-AUG-2003;  
Geron Corporation; Menlo Park, CA  
FEATURES  
source 1..48  
/organism='unknown'  
/mol\_type='genomic DNA'

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 30  
LOCUS AR393305 48 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 564 from patent US 6617110.

ACCESSION AR393305  
VERSION AR393305.1 GI:40118681  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,  
Harley,C.B. and Andrews,W.H.  
TITLE Cells immortalized with telomerase reverse transcriptase for use in  
drug screening  
JOURNAL Patent: US 6617110-A 564 09-SEP-2003;  
Geron Corporation and University Technology Corporation; Menlo  
Park, CA  
FEATURES  
source 1..48  
/organism='unknown'  
/mol\_type='genomic DNA'  
ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 31  
LOCUS AR592662 48 bp DNA linear PAT 15-DEC-2004  
DEFINITION Sequence 37 from patent US 6808880.  
ACCESSION AR592662  
VERSION AR592662.1 GI:56641382  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,  
Harley,C. and Andrews,W.H.  
TITLE Method for detecting polynucleotides encoding telomerase  
JOURNAL Patent: US 6808880-A 37 26-OCT-2004;  
Geron Corporation and Regents of the University of Colorado; Menlo  
Park, CA  
FEATURES  
source 1..48  
/organism='unknown'  
/mol\_type='unassigned DNA'  
ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 32  
LOCUS AR592665 48 bp DNA linear PAT 15-DEC-2004  
DEFINITION Sequence 40 from patent US 6808880.  
ACCESSION AR592665  
VERSION AR592665.1 GI:56641385  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,

TITLE Harley, C. and Andrews, W.H.  
JOURNAL Method for detecting polynucleotides encoding telomerase  
Patent: US 680880-A 40 26-OCT-2004;  
Geron Corporation and Regents of the University of Colorado; Menlo  
Park, CA

FEATURES Location/Qualifiers  
source 1..48  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGTTTGGGGTTTT 48

## RESULT 33

AX810599 48 bp DNA linear PAT 25-NOV-2003  
LOCUS  
DEFINITION Sequence 564 from Patent EP1333094.  
ACCESSION AX810599  
VERSION AX810599.1 GI:38524088

KEYWORDS unidentifed  
SOURCE unclassified sequences.  
ORGANISM

## REFERENCE

AUTHORS Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B.,  
Harley, C.B. and Andrews, W.H.

TITLE Human telomerase catalytic subunit  
JOURNAL Patent: EP 1333094-A 564 06-AUG-2003;  
Geron Corporation (US); University Technology Corporation (US)

## FEATURES

source 1..48  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGTTTGGGGTTTT 48

## RESULT 34

BD011265 48 bp DNA linear PAT 31-JAN-2002  
LOCUS  
DEFINITION Human telomerase catalytic subunit.  
ACCESSION BD011265  
VERSION BD011265.1 GI:18639638

KEYWORDS JP 2001081042-A/222.  
SOURCE unidentifed  
ORGANISM unclassified.

## REFERENCE

AUTHORS Sechi, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Mori, G.B.,  
Harley, C.B. and Andrews, W.H.

TITLE Human telomerase catalytic subunit  
JOURNAL Patent: JP 2001081042-A 222 27-MAR-2001;  
GERON CORP, UNIVERSITY TECHNOLOGY CORP

## COMMENT

OS Unidentified  
PN JP 2001081042-A/222  
PD 27-MAR-2001  
PF 27-JUL-2000 JP 2000227474  
PR 01-OCT-1996 US 08/724643, 18-APR-1997 US 08/844419 PR

25-APR-1997 US 08/846017, 06-MAY-1997 US 08/851843 PR  
09-AUG-1997 US 08/854050, 14-AUG-1997 US 08/911312 PR  
14-AUG-1997 US 08/912951, 14-AUG-1997 US 08/915503 PI THOMAS  
R SECHI, JOACHIM LINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B  
MORIN,

PI CALVIN B HARLEY, WILLIAM H ANDREWS  
PC A61K39/00, A61K31/7088, A61K39/00, A61K48/00, A61P35/00, A61P43/00,  
PC C07K5/10,  
PC C07K5/107, C07K5/117, C07K7/06, C07K7/08, C07K16/40, C12N9/12, PC  
C12N15/09,

PC C12Q1/02, C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC  
G01N33/53,  
PC G01N33/566, G01N33/573//C12P21/08, A61K37/02, C12N15/00 CC

Strandedness: Single;  
CC Topology: Linear;

FT Key Location/Qualifiers

FT source 1..48

FT /organism="Unidentified".

FT Location/Qualifiers

source 1..48

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGTTTGGGGTTTT 48

## RESULT 35

AR104527 50 bp DNA linear PAT 14-FEB-2001  
LOCUS  
DEFINITION Sequence 39 from patent US 6093809.  
ACCESSION AR104527  
VERSION AR104527.1 GI:12817235

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 50)

AUTHORS Cech, T.R. and Lingner, J.

TITLE Telomerase

JOURNAL Patent: US 6093809-A 39 25-JUL-2000;

FEATURES Location/Qualifiers

source 1..50

/organism="unknown"

/mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 31 TTTTGGGTTTGGGGTTTT 50

## RESULT 36

AR175788 50 bp DNA linear PAT 17-DEC-2001  
LOCUS  
DEFINITION Sequence 39 from patent US 6309867.  
ACCESSION AR175788  
VERSION AR175788.1 GI:17917087

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

```
REFERENCE 1 (bases 1 to 50)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 39 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 31 TTTTGGGGTTTGGGGTTTT 50

RESULT 37
E37016 50 bp DNA linear PAT 18-JUN-2001
LOCUS Human telomerase catalytic subunit promoter.
DEFINITION E37016
ACCESSION E37016
VERSION E37016.1 GI:13022979
KEYWORDS JP 199253177-A/224.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 199253177-A 224 21-SEP-1999;
COMMENT JERON CORP./UNIVERSITY TECHNOLOGY CORP
OS Unidentified
PN JP 199253177-A/224
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503 PI THOMAS
R SECHI,JOCHIMU RINGER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
MORIN,
PI CALVIN B HAREI,WILLIAM H ANDREWS
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
PC C12Q1/02,
PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
C07K16/40,
PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,C12N1/19, PC
C12R1/84),
PC (C12N1/21,C12R1:19), (C12N9/12,C12R1:19), (C12N9/12,C12R1:84),
PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..50
FT /organism='Unidentified'.
FEATURES source
1..50
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 31 TTTTGGGGTTTGGGGTTTT 50

REFERENCE 1 (bases 1 to 50)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 39 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 31 TTTTGGGGTTTGGGGTTTT 50

RESULT 38
AR390693 50 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 566 from patent US 6610839.
DEFINITION AR390693
ACCESSION AR390693
VERSION AR390693.1 GI:40112627
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Morin,G.B. and Andrews,W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 566 26-AUG-2003;
COMMENT Geron Corporation; Menlo Park, CA
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 31 TTTTGGGGTTTGGGGTTTT 50

RESULT 39
AR393307 50 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 566 from patent US 6617110.
DEFINITION AR393307
ACCESSION AR393307
VERSION AR393307.1 GI:40118685
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in
drug screening
JOURNAL Patent: US 6617110-A 566 09-SEP-2003;
COMMENT Geron Corporation and University Technology Corporation; Menlo
Park, CA
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 31 TTTTGGGGTTTGGGGTTTT 50

RESULT 40
AR592664 50 bp DNA linear PAT 15-DEC-2004
LOCUS Sequence 39 from patent US 680880.
DEFINITION AR592664
ACCESSION AR592664
VERSION AR592664.1 GI:56641384
KEYWORDS
SOURCE Unknown.
```

```
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
TITLE Method for detecting polynucleotides encoding telomerase
JOURNAL Patent: US 6808880-A 39 26-OCT-2004;
Geron Corporation and Regents of the University of Colorado; Menlo
Park, CA
FEATURES
source Location/Qualifiers
1..50
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTGGGGTTTGGGGTTT 20
|||||
Db 31 TTTTGGGGTTTGGGGTTT 50
|||||
RESULT 41
AX810601 50 bp DNA linear PAT 25-NOV-2003
LOCUS Sequence 566 from Patent EP1333094.
DEFINITION AX810601
ACCESSION AX810601
VERSION AX810601.1 GI:38524090
KEYWORDS
SOURCE unclassified
ORGANISM unclassified
unclassified sequences.
REFERENCE 1
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
TITLE Human telomerase catalytic subunit
JOURNAL Patent: EP 1333094-A 566 06-AUG-2003;
Geron Corporation (US) ; University Technology Corporation (US)
FEATURES
source Location/Qualifiers
1..50
/mol_type="unclassified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTGGGGTTTGGGGTTT 20
|||||
Db 31 TTTTGGGGTTTGGGGTTT 50
|||||
RESULT 42
BD011267 50 bp DNA linear PAT 31-JAN-2002
LOCUS Human telomerase catalytic subunit.
DEFINITION BD011267
ACCESSION BD011267
VERSION BD011267.1 GI:18639640
KEYWORDS JP 2001081042-A/224.
SOURCE unclassified
ORGANISM unclassified
unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 224 27-MAR-2001;
GERON CORP.,UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
```

---

```
PN JP 2001081042-A/224
PD 27-MAR-2001
PF 27-JUL-2000 JP 2000227474
PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
03-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN,PI GREG B
MORIN,
PI CALVIN B HARLEY,WILLIAM H ANDREWS
PC A61K39/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
PC C07K5/10,
PC C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12,PC
C12N15/09,
PC C12Q1/02,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,PC
G01N33/53,
PC G01N33/566,G01N33/573//C12P21/08,A61K37/02,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..50
FT /organism='Unidentified'.
FT /organism='Unidentified'.
FT /organism='Unidentified'.
FEATURES
source Location/Qualifiers
1..50
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTGGGGTTTGGGGTTT 20
|||||
Db 31 TTTTGGGGTTTGGGGTTT 50
|||||
RESULT 43
AR104527/c 50 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 39 from patent US 6093809.
DEFINITION AR104527
ACCESSION AR104527
VERSION AR104527.1 GI:12817235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 39 25-JUL-2000;
FEATURES
source Location/Qualifiers
1..50
/mol_type="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTTGGGGTTTGGGGTTT 18
|||||
Db 18 TTTTGGGGTTTGGGGTTT 1
|||||
RESULT 44
AR175788/c 50 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 39 from patent US 630867.
DEFINITION AR175788
ACCESSION AR175788
VERSION AR175788.1 GI:17917087
```

```

KEYWORDS      .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 50)
AUTHORS        Cech,T.R. and Nakamura,T.
TITLE          Telomerase
JOURNAL        Patent: US 6309867-A 39 30-OCT-2001;
FEATURES       Location/Qualifiers
               source
               1..50
               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
Query Match      90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTT 18
   |||||
Db 18 TTTTGGGTTTGGGGTT 1

RESULT 46
LOCUS      AR390693/c
DEFINITION Sequence 566 from patent US 6610839.
ACCESSION  AR390693
VERSION     AR390693.1 GI:40112627
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 50)
AUTHORS    Morin,G.B. and Andrews,W.H.
TITLE      Promoter for telomerase reverse transcriptase
JOURNAL    Patent: US 6610839-A 566 26-AUG-2003;
           Geron Corporation; Menlo Park, CA
FEATURES   Location/Qualifiers
           source
           1..50
           /organism="unknown"
           /mol_type="genomic DNA"

ORIGIN
Query Match      90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTT 18
   |||||
Db 18 TTTTGGGTTTGGGGTT 1

RESULT 47
LOCUS      AR393307/c
DEFINITION Sequence 566 from patent US 6617110.
ACCESSION  AR393307
VERSION     AR393307.1 GI:40118685
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 50)
AUTHORS    Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
           Harley,C.B. and Andrews,W.H.
TITLE      Cells immortalized with telomerase reverse transcriptase for use in
           drug screening
JOURNAL    Patent: US 6617110-A 566 09-SEP-2003;
           Geron Corporation and University Technology Corporation; Menlo
           Park, CA
FEATURES   Location/Qualifiers
           source
           1..50
           /organism="unknown"
           /mol_type="genomic DNA"

ORIGIN
Query Match      90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTT 18
   |||||
Db 18 TTTTGGGTTTGGGGTT 1

RESULT 48
LOCUS      AR592664/c
DEFINITION Sequence 39 from patent US 6808880.

```



```
ACCESSION AR592664
VERSION AR592664.1 GI:56641384
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Cecchi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
          Harley,C. and Andrews,W.H.
TITLE Method for detecting polynucleotides encoding telomerase
JOURNAL Patent: US 680880-A 39 26-OCT-2004;
          Geron Corporation and Regents of the University of Colorado; Menlo
          Park, CA
FEATURES             Location/Qualifiers
     source           1..50
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
Query Match          90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGGGGTTTGGGGTT 18
   |||||
Db 18 TTTTGGGGTTTGGGGTT 1
   |||||
RESULT 49
AX810601/c          50 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 566 from Patent EP1333094.
ACCESSION AX810601
VERSION AX810601.1 GI:38524090
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
          unclassified sequences.
REFERENCE 1
AUTHORS Cecchi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
          Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: EP 1333094-A 566 06-AUG-2003;
          Geron Corporation (US) ; University Technology Corporation (US)
FEATURES             Location/Qualifiers
     source           1..50
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN
Query Match          90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGGGGTTTGGGGTT 18
   |||||
Db 18 TTTTGGGGTTTGGGGTT 1
   |||||
RESULT 50
BD011267/c          50 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011267
VERSION BD011267.1 GI:18639640
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
          unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Cecchi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
          Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 224 27-MAR-2001;
          GERON CORP.UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
        PN JP 2001081042-A/224
        PD 27-MAR-2001
        PF 27-JUL-2000 JP 2000227474
        PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
        PR 25-APR-1997 US 08/846017,06-MAY-1997 US 08/851843 PR
        PR 09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
        PR 14-AUG-1997 US 08/912951,14-AUG-1997 US 08/915503 PI THOMAS
        PR R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN,PI GREG B
        MORIN,
        PI CALVIN B HARLEY,WILLIAM H ANDREWS
        PC A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
        PC C07K5/10,
        PC C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12, PC
        C12N15/09,C12Q1/02,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
        G01N33/53,
        PC G01N33/566,G01N33/573//C12P21/08,A61K37/02,C12N15/00 CC
        Strandedness: Single;
        CC Topology: Linear;
        FH Key Location/Qualifiers
        FT source 1..50
        FT /organism='Unidentified'.
        FT /Location/Qualifiers
        source 1..50
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"
ORIGIN
Query Match          90.0%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGGGGTTTGGGGTT 18
   |||||
Db 18 TTTTGGGGTTTGGGGTT 1
   |||||
Search completed: February 15, 2006, 18:55:18
Job time : 490.835 secs
```

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:25:23 ; Search time 150.744 Seconds  
(without alignments)  
884.241 Million cell updates/sec

Title: US-09-669-187A-73

Perfect score: 20

Sequence: 1 ttttggggttttggggtttt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 segs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

N Geneseq\_21.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	4	Aaf98948 Immunosti
2	20	100.0	20	6	Abs77589 Angiogene
3	20	100.0	20	9	Acd99381 Immunosti
4	20	100.0	20	9	Adb36450 Immunosti
5	20	100.0	20	12	Adg76003 Non-CpG D
6	20	100.0	20	13	Adu89389 Allergic
7	20	100.0	28	10	Adm64883 Non-antis
8	20	100.0	28	10	Adj94159 Oligonuc
9	20	100.0	28	12	Adi28732 Guanosine
10	20	100.0	28	14	Adv53924 Non-antis
11	20	100.0	28	14	Adz58647 Inflammat
12	20	100.0	28	14	Adz25617 G-quadrat
13	20	100.0	32	3	Aaz57146 Exemplary
14	20	100.0	39	2	Aaq61979 Oxytricha
15	20	100.0	44	2	Aav17009 Telomeras
16	20	100.0	46	2	Aav17008 Telomeras
17	20	100.0	48	2	Aav17007 Telomeras
18	20	100.0	48	2	Aav17004 Telomeras
19	20	100.0	50	2	Aav17006 Telomeras

20	18.4	92.0	29	12	ADf69702	Adf69702 Human HLT
21	18.4	92.0	29	14	ADV09385	Adv09385 Human HLT
22	18.4	92.0	29	14	ADV09348	Adv09348 Human HLT
23	18	90.0	29	14	AAT28342	Aat28342 Multi-G O
24	18	90.0	18	2	AAV17006	Aav17006 Telomeras
25	17.4	87.0	50	2	AAQ44008	Aaq44008 Target se
26	16.8	84.0	26	2	AAQ44992	Aaq44992 Sequence
27	16.8	84.0	28	2	AAQ36268	Aaq36268 APP4par,
28	16.8	84.0	28	2	AAQ36269	Aaq36269 APP4anti,
29	16.8	84.0	28	2	AAQ36269	Aaq36269 APP4anti,
30	16.8	84.0	44	2	AAV17009	Aav17009 Telomeras
31	16.8	84.0	46	2	AAV17008	Aav17008 Telomeras
32	16.8	84.0	48	2	AAV17007	Aav17007 Telomeras
33	16.8	84.0	48	2	AAV17004	Aav17004 Telomeras
34	16.8	84.0	50	6	ABZ05743	Abz05743 Human leu
35	16	80.0	20	3	AAA39694	Aaa39694 S. lemnae
36	15.4	77.0	30	3	AAA39699	Aaa39699 S. lemnae
37	15.4	77.0	19	14	ADV45884	Adv45884 Human CpG
38	15.2	76.0	43	10	ACF58129	Acf58129 HLTf non-
39	15.2	76.0	20	14	ADM84828	Adm84828 MAP3K9 ma
40	15.2	76.0	22	14	AEA51773	Aea51773 Prostate
41	15.2	76.0	31	10	ADJ94146	Adj94146 Oligonuc
42	15.2	76.0	36	10	ADJ94145	Adj94145 Oligonuc
43	14.8	74.0	50	6	ABZ01038	Abz01038 Human leu
44	14.8	74.0	24	4	AAF99500	Aaf99500 Immunosti
45	14.8	74.0	24	4	AAF99678	Aaf99678 Immunosti
46	14.8	74.0	24	4	AAF99498	Aaf99498 Immunosti
47	14.8	74.0	24	5	AAF61386	Aaf61386 Strand di
48	14.8	74.0	24	6	ABS78208	Abs78208 Angiogene
49	14.8	74.0	24	6	ABS78399	Abs78399 Angiogene
50	14.8	74.0	24	6	ABS78210	Abs78210 Angiogene
51	14.8	74.0	24	6	ABL39306	Ab139306 Immunosti
52	14.8	74.0	24	9	ACD99979	Acd99979 Immunosti
53	14.8	74.0	24	9	ACH03219	Ach03219 Immunosti
54	14.8	74.0	24	9	ACD99981	Acd99981 Immunosti
55	14.8	74.0	24	9	ADB37000	Adb37000 Immunosti
56	14.8	74.0	24	9	ADB37180	Adb37180 Immunosti
57	14.8	74.0	24	9	ADB37002	Adb37002 Immunosti
58	14.8	74.0	24	10	ADB82243	Adb82243 Nucleic a
59	14.8	74.0	24	10	ADJ94158	Adj94158 Oligonuc
60	14.8	74.0	24	12	ADG75905	Adg75905 Immunosti
61	14.8	74.0	24	12	ADG76026	Adg76026 Non-CpG D
62	14.8	74.0	24	12	ADG76008	Adg76008 Non-CpG D
63	14.8	74.0	24	12	ADG76016	Adg76016 Non-CpG D
64	14.8	74.0	24	13	ADU90199	Adu90199 Allergic
65	14.8	74.0	24	13	ADU90008	Adu90008 Allergic
66	14.8	74.0	24	13	ADU90010	Adu90010 Allergic
67	14.8	74.0	40	14	AEA61446	Aea61446 Primer Gw
68	14.8	74.0	46	5	AAF61385	Aaf61385 Strand di
69	14.8	74.0	46	10	ADE82242	Ade82242 Nucleic a
70	14.8	74.0	47	10	AAI99716	Aai99716 DNA fragm
71	14.4	72.0	17	14	ADV45134	Adv45134 Human CpG
72	14.4	72.0	20	12	ADE52685	Ades2685 dnaform35
73	14.4	72.0	23	14	ADV46099	Adv46099 Human CpG
74	14.4	72.0	23	14	ADV46329	Adv46329 Human CpG
75	14.4	72.0	50	6	ABZ05474	Abz05474 Human leu
76	14.2	71.0	23	3	AAA70710	Aaa70710 Rat inter
77	14.2	71.0	26	2	AAV16997	Aav16997 Telomeras
78	14.2	71.0	29	3	Aaz47434	Aaz47434 PCR prime
79	14.2	71.0	32	6	ABK47161	Abk47161 Mouse Ots
80	14.2	71.0	32	12	ADQ90579	Adq90579 PCR prime
81	14.2	71.0	35	2	AAQ32580	Aaq32580 HCV anti
82	14.2	71.0	36	14	ADY78133	Ady78133 Human p53
83	14.2	71.0	38	14	ABE91280	Aeb91280 Reverse p
84	14.2	71.0	41	6	ABL58642	Ab158642 Human tra
85	14.2	71.0	50	6	ABZ04226	Abz04226 Human leu
86	14.2	71.0	50	6	ABZ07614	Abz07614 Human leu
87	14.2	71.0	50	12	ADP10110	Adp10110 50-mer ol
88	14	70.0	18	6	ABQ65362	Abq65362 Human gen
89	14	70.0	18	6	ABK34150	Abk34150 Human OAT
90	14	70.0	18	6	ABK28088	Abk28088 Human OAT
91	14	70.0	18	8	ADA20547	Ada20547 Prostate
92	14	70.0	18	8	ADA84350	Ada84350 Human OAT

C	93	14	70.0	20	6	AAS63371	Aas63371 OAT gene,	166	13.2	66.0	30	2	AAV07783	Aav07783 HBV.104 a
C	94	14	70.0	50	6	ABZ05334	Abz05334 Human leu	167	13.2	66.0	30	2	AAV83012	Aav83012 Amplifier
C	95	13.8	69.0	20	10	ADG33702	Adg33702 Human PCR	C 168	13.2	66.0	30	13	ADR68159	Adr68159 Template
C	96	13.8	69.0	20	14	ADM44915	Adm44915 Human tax	169	13.2	66.0	33	6	ABL41262	AbL41262 Human cyt
C	97	13.8	69.0	24	12	ADF69700	Adf69700 Human HLT	170	13.2	66.0	36	6	ABK28860	Abk28860 HPV captu
C	98	13.8	69.0	24	14	ADV09346	Adv09346 Human HLT	171	13.2	66.0	37	14	ABE91284	Abe91284 Reverse p
C	99	13.8	69.0	24	14	ADV09383	Adv09383 Human HLT	172	13.2	66.0	38	2	AAQ05016	Aaq05016 Sequence
C	100	13.8	69.0	42	14	ABE91286	Abe91286 Reverse p	173	13.2	66.0	38	2	AAQ05015	Aaq05015 Sequence
C	101	13.8	69.0	48	12	ADG39672	Adg39672 Oligonuc	174	13.2	66.0	38	2	AAQ36338	Aaq36338 HSVORL1a
C	102	13.8	69.0	50	2	AAV76555	Aav76555 Staphyloc	175	13.2	66.0	38	2	AAQ36337	Aaq36337 HSVORL1p
C	103	13.8	69.0	50	14	AEA15553	Aea15553 Three-way	176	13.2	66.0	38	2	AAQ36341	Aaq36341 HSVORL2a
C	104	13.8	68.0	20	12	ADK76357	Adk76357 Chimeric	177	13.2	66.0	39	2	AAQ36340	Aaq36340 HSVORL2p
C	105	13.6	68.0	21	2	AAQ61989	Aaq61989 HIV repli	178	13.2	66.0	39	6	AAL44900	Aal44900 Triplex f
C	106	13.6	68.0	21	2	AAQ35001	Aaq35001 HIV inhib	179	13.2	66.0	41	12	ADO61382	Ado61382 Camelid b
C	107	13.6	68.0	25	12	ADO80263	Ado80263 Arabidops	180	13.2	66.0	43	4	ABL56750	AbL56750 Sequence
C	108	13.6	68.0	25	12	ADQ77382	Adq77382 PCR prime	181	13.2	66.0	49	4	ABL56749	AbL56749 Sequence
C	109	13.6	68.0	25	13	ADR11810	Adr11810 ABCG2-M I	C 182	13.2	66.0	50	2	AAQ06696	Aaq06696 HBV.1LA2
C	110	13.6	68.0	25	13	ADR11811	Adr11811 ABCG2-U I	C 183	13.2	66.0	50	2	AAQ12918	Aaq12918 Template
C	111	13.6	68.0	27	9	ACD91394	Acd91394 Adjuvant-	C 184	13.2	66.0	50	2	AAT74366	Aat74366 Template
C	112	13.6	68.0	27	14	ADX87232	Adx87232 HIV treat	185	13	65.0	13	5	ABC90426	Abc90426 Oligonuc
C	113	13.6	68.0	28	14	ADV98895	Adv98895 Human CD3	186	13	65.0	13	5	ABC80374	Abc80374 Oligonuc
C	114	13.6	68.0	29	4	AAF99178	Aaf99178 Immunosti	C 187	13	65.0	13	5	ABC80375	Abc80375 Oligonuc
C	115	13.6	68.0	29	6	ABS77821	Abs77821 Angiogene	C 188	13	65.0	13	5	ABF88480	Abf88480 Oligonuc
C	116	13.6	68.0	29	6	ABL38761	AbL38761 Immunosti	C 189	13	65.0	13	5	ABF88480	Abf88480 Oligonuc
C	117	13.6	68.0	29	9	ACD99609	Acd99609 Immunosti	C 190	13	65.0	13	5	ABF88481	Abf88481 Oligonuc
C	118	13.6	68.0	29	9	ADB36680	Adb36680 Immunosti	191	12.8	64.0	18	3	AAZ74880	Aaz74880 Human bia
C	119	13.6	68.0	29	13	ADU89621	Adu89621 Allergic	192	12.8	64.0	18	8	ABZ10895	Abz10895 Haematopo
C	120	13.6	68.0	32	2	AAQ43976	Aaq43976 Triple he	193	12.8	64.0	18	8	ABZ10418	Abz10418 Haematopo
C	121	13.6	68.0	32	4	AAF99300	Aaf99300 Immunosti	194	12.8	64.0	18	8	ABZ10896	Abz10896 Haematopo
C	122	13.6	68.0	32	6	ABS77945	Abs77945 Angiogene	195	12.8	64.0	18	8	ABZ10992	Abz10992 Haematopo
C	123	13.6	68.0	32	6	ABL39305	AbL39305 Immunosti	196	12.8	64.0	18	8	ABZ10552	Abz10552 Haematopo
C	124	13.6	68.0	32	9	ACD99725	Acd99725 Immunosti	197	12.8	64.0	18	10	ADC70079	Adc70079 Primer ol
C	125	13.6	68.0	32	9	ADB36802	Adb36802 Immunosti	198	12.8	64.0	18	10	ADC69980	Adc69980 Primer ol
C	126	13.6	68.0	32	10	ADD25667	Add25667 Binding d	199	12.8	64.0	18	10	ADE84322	Ade84322 Human lym
C	127	13.6	68.0	32	10	ADD89955	Add89955 CpG oligo	C 200	12.8	64.0	18	10	ADE43560	Ade43560 Human IDE
C	128	13.6	68.0	32	12	ADJ56900	Adj56900 CpG oligo	C 201	12.8	64.0	18	12	ADH54038	Adh54038 Human neu
C	129	13.6	68.0	32	13	ADU89745	Adu89745 Allergic	C 202	12.8	64.0	18	14	ABE43074	Abe43074 Human glu
C	130	13.6	68.0	32	14	ADY21485	Ady21485 Llana IgG	C 203	12.8	64.0	19	14	AEA42647	Aea42647 Human WNT
C	131	13.6	68.0	40	6	AAAL46471	AaL46471 M catarrh	C 204	12.8	64.0	19	14	AEA42810	Aea42810 Human WNT
C	132	13.6	68.0	42	2	AAZ57303	Aaz57303 Ret D-roh	205	12.8	64.0	20	2	AAQ44023	Aaq44023 Triplex f
C	133	13.6	68.0	42	5	AAF75059	Aaf75059 Primer #4	206	12.8	64.0	20	2	AAQ44020	Aaq44020 Triplex f
C	134	13.6	68.0	42	10	ADG62896	Adg62896 Human TR1	C 207	12.8	64.0	20	2	AAQ44019	Aaq44019 Target se
C	135	13.6	68.0	42	13	ADT89685	Adt89685 Human mat	208	12.8	64.0	20	2	AAQ44018	Aaq44018 Target se
C	136	13.6	68.0	43	4	ABL56757	AbL56757 Nucleotid	C 209	12.8	64.0	20	2	AAQ44024	Aaq44024 Triplex f
C	137	13.6	68.0	47	3	AAZ68129	Aaz68129 Human map	C 210	12.8	64.0	20	6	ABS65467	Abs65467 Human Pro
C	138	13.6	68.0	47	3	AAZ66495	Aaz66495 Human map	C 211	12.8	64.0	20	11	ABD28214	Abd28214 R19956-de
C	139	13.6	68.0	50	4	AAAL28957	AaL28957 Human SNP	C 212	12.8	64.0	20	11	ABD28214	Abd28214 R19956-de
C	140	13.4	67.0	20	2	AAQ14701	Aaq14701 Oligonuc	213	12.8	64.0	20	13	ADR23443	Adr23443 GSTPl oli
C	141	13.4	67.0	20	2	AAQ97995	Aaq97995 Peptide n	214	12.8	64.0	21	3	AAZ74061	Aaz74061 Human bla
C	142	13.4	67.0	21	13	ADR83347	Adr83347 Human pol	215	12.8	64.0	21	4	AAF30784	Aaf30784 CHRM2 gen
C	143	13.4	67.0	21	12	ADG75991	Adg75991 Immunosti	C 216	12.8	64.0	21	12	ADN35703	Adn35703 Human NSC
C	144	13.4	67.0	30	6	ABK47162	Abk47162 Mouse Ots	217	12.8	64.0	21	12	ADP11105	Adp11105 Set 1 rig
C	145	13.4	67.0	30	12	ADQ90580	Adq90580 PCR prime	C 218	12.8	64.0	22	14	ADV45579	Adv45579 Human CpG
C	146	13.4	67.0	32	3	AAZ88100	Aaz88100 RRE-dl co	C 219	12.8	64.0	22	14	ADV45349	Adv45349 Human CpG
C	147	13.4	67.0	32	3	AAZ88114	Aaz88114 Vector pr	220	12.8	64.0	24	4	AAF98734	Aaf98734 Human IFN
C	148	13.4	67.0	36	9	ADA19169	Ada19169 Rat Kohji	221	12.8	64.0	24	4	AAF99230	Aaf99230 Immunosti
C	149	13.4	67.0	37	14	AE91283	Ae91283 Reverse p	222	12.8	64.0	24	4	AAF99177	Aaf99177 Immunosti
C	150	13.4	67.0	38	14	AE91281	Ae91281 Reverse p	223	12.8	64.0	24	4	AAF99306	Aaf99306 Immunosti
C	151	13.4	67.0	41	14	AE91289	Ae91289 Reverse p	224	12.8	64.0	24	6	ABS77951	Abs77951 Angiogene
C	152	13.4	67.0	50	13	ADU24818	Adu24818 Retroelem	225	12.8	64.0	24	6	ABS77820	Abs77820 Angiogene
C	153	13.4	67.0	50	13	ADU22285	Adu22285 Human tra	226	12.8	64.0	24	6	ABS77874	Abs77874 Angiogene
C	154	13.2	66.0	18	12	ADG76053	Adg76053 Non-CpG D	227	12.8	64.0	24	6	ABL39298	AbL39298 Immunosti
C	155	13.2	66.0	19	2	AAQ09332	Aaq09332 Human bia	228	12.8	64.0	24	6	ABL39410	AbL39410 Immunosti
C	156	13.2	66.0	21	2	AAZ24688	Aaz24688 Llana IgG	229	12.8	64.0	24	6	ABL39411	AbL39411 Immunosti
C	157	13.2	66.0	24	11	ADJ59808	Adj59808 Arabidops	230	12.8	64.0	24	6	ABV73960	Abv73960 CpG-like
C	158	13.2	66.0	24	14	ADY81848	Ady81848 Thale-crc	231	12.8	64.0	24	6	ABV73971	Abv73971 GpI oligo
C	159	13.2	66.0	25	12	ADJ92615	Adj92615 Expressio	232	12.8	64.0	24	8	ABV73972	Abv73972 2pC oligo
C	160	13.2	66.0	25	13	ADR41943	Adr41943 Versatile	233	12.8	64.0	24	6	ABV73972	Abv73972 2pC oligo
C	161	13.2	66.0	25	14	ADX70261	Adx70261 Versatile	234	12.8	64.0	24	9	ACD99731	Acd99731 Immunosti
C	162	13.2	66.0	26	2	AAV81225	Aav81225 Llana hc-	235	12.8	64.0	24	9	ADB36732	Adb36732 Immunosti
C	163	13.2	66.0	29	10	ADDI4976	Addi4976 Calcitonin	236	12.8	64.0	24	9	ADB36679	Adb36679 Immunosti
C	164	13.2	66.0	29	14	AEA81016	Aea81016 Human ERB	237	12.8	64.0	24	9	ADB36808	Adb36808 Immunosti
C	165	13.2	66.0	30	2	AAQ45786	Aaq45786 HBV ampli	238	12.8	64.0	24	10	ADG62671	Adg62671 Methylate

239	12.8	64.0	24	11	ADL59790	Adl59790 Arabidops
240	12.8	64.0	24	12	ADG76022	Adg76022 Non-CpG D
241	12.8	64.0	24	13	ADU23253	Adu23253 Toll-like
242	12.8	64.0	24	13	ADU89751	Adu89751 Allergic
243	12.8	64.0	24	13	ADU89620	Adu89620 Allergic
244	12.8	64.0	24	13	ADU89674	Adu89674 Allergic
245	12.8	64.0	24	14	ADY81830	Ady81830 Thale-cra
246	12.8	64.0	25	12	ADQ77972	Adq77972 PCR prime
247	12.8	64.0	25	12	ADQ77980	Adq77980 PCR prime
248	12.8	64.0	25	12	ADQ77971	Adq77971 PCR prime
249	12.8	64.0	25	12	ADQ78075	Adq78075 PCR prime
250	12.8	64.0	25	12	ADQ77974	Adq77974 PCR prime
251	12.8	64.0	25	12	ADQ77976	Adq77976 PCR prime
252	12.8	64.0	25	12	ADQ78077	Adq78077 PCR prime
253	12.8	64.0	25	12	ADQ77978	Adq77978 PCR prime
254	12.8	64.0	25	12	ADQ77969	Adq77969 PCR prime
255	12.8	64.0	25	12	ADQ78078	Adq78078 PCR prime
256	12.8	64.0	26	2	AAQ44006	Aaq44006 Target se
257	12.8	64.0	26	2	AAQ44010	Aaq44010 Target se
258	12.8	64.0	28	13	ADT88370	Adt88370 ParG prim
259	12.8	64.0	31	2	AAQ44765	Aaq44765 Steroid h
260	12.8	64.0	31	2	AAQ44765	Aaq44765 Steroid h
261	12.8	64.0	31	3	AAA49331	Aaa49331 Primer us
262	12.8	64.0	35	11	ADO77990	Ado77990 Chimeric
263	12.8	64.0	35	11	ADO77989	Ado77989 Chimeric
264	12.8	64.0	37	6	ACN19904	Acn19904 WNV Zinz
265	12.8	64.0	41	12	ADK17690	Adk17690 Cytochrom
266	12.8	64.0	41	14	AE991290	Aeb91290 Reverse p
267	12.8	64.0	45	2	AAE74449	Aat67449 H. pylori
268	12.8	64.0	46	2	AAE74508	Aat67449 H. pylori
269	12.8	64.0	50	6	ABZ05136	Abz05136 Human leu
270	12.6	63.0	13	5	ABH09453	Abh09453 Oligonuc
271	12.6	63.0	13	5	ABH09452	Abh09452 Oligonuc
272	12.6	63.0	19	8	ABZ10375	Abz10375 Haematopo
273	12.6	63.0	20	12	ADJ25248	Adj25248 Human end
274	12.6	63.0	20	12	ADJ25340	Adj25340 Human end
275	12.6	63.0	20	12	ADK74370	Adk74370 Chimeric
276	12.6	63.0	20	12	ADK76005	Adk76005 Chimeric
277	12.6	63.0	20	12	ADK73634	Adk73634 Chimeric
278	12.6	63.0	20	12	ADK76773	Adk76773 Chimeric
279	12.6	63.0	20	12	ADK79971	Adk79971 Chimeric
280	12.6	63.0	20	12	ADK81477	Adk81477 Chimeric
281	12.6	63.0	21	3	AAZ73686	Aaz73686 Human bia
282	12.6	63.0	21	14	ADY94237	Ady94237 Sequenci
283	12.6	63.0	22	4	AAH39037	Aah39037 SNP speci
284	12.6	63.0	22	6	ABS59605	Abs59605 Real-time
285	12.6	63.0	22	12	ADL56894	Adl56894 Human NOV
286	12.6	63.0	22	12	ADO39278	Ado39278 Human NOV
287	12.6	63.0	22	13	ADS90007	Ads90007 Human PCR
288	12.6	63.0	23	9	ADA13696	Ada13696 Short int
289	12.6	63.0	23	10	ADG29769	Adg29769 EGFR-targ
290	12.6	63.0	23	11	ADL80060	Adl80060 Human HBR
291	12.6	63.0	23	11	ADM55565	Adm55565 Human Y C
292	12.6	63.0	23	11	ADM55562	Adm55562 Human Y C
293	12.6	63.0	23	12	ADQ78147	Adq78147 PCR prime
294	12.6	63.0	23	12	ADQ78164	Adq78164 PCR prime
295	12.6	63.0	23	12	ADG78188	Adg78188 RASSF1A g
296	12.6	63.0	23	13	ADG78213	Adg78213 RASSF1A g
297	12.6	63.0	23	13	ADG59095	Adg59095 Human liv
298	12.6	63.0	23	14	ADV46309	Adv46309 Human Cpg
299	12.6	63.0	24	2	AAV09446	Aav09446 Cpg-conta
300	12.6	63.0	24	2	AAV09582	Aav09582 MSP ampli

ALIGNMENTS

RESULT 1

ADP98948  
ID AAF98948 standard; DNA; 20 BP.

XX AAF98948;

AC

XX

DT	12-JUN-2001	(first entry)
XX	Immunostimulatory nucleic acid #64.	
DE	Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;	
XX	immunostimulatory; tumour; viral infection; bacterial infection;	
KW	fungal infection; parasitic infection; cancer; asthma;	
KW	infectious disease; allergy; immune deficiency; phosphorothioate; ss.	
XX	Synthetic.	
XX	WO200122972-A2.	
PN	05-APR-2001.	
XX	25-SEP-2000; 2000WO-US026383.	
PD	25-SEP-1999; 99US-0156113P.	
XX	27-SEP-1999; 99US-0156135P.	
PF	23-AUG-2000; 2000US-0227436P.	
XX	(IOWA ) UNIV IOWA RES FOUND.	
PA	(COLB-) COLEY PHARM GMBH.	
XX	Krieg AM, Schetter C, Vollmer J;	
PI	WPI; 2001-273485/28.	
XX	Vaccinating against tumors, infectious diseases, allergies and asthma	
PT	using immunostimulatory Py-rich and TG nucleic acids.	
XX	Disclosure; Page 39; 338pp; English.	
PS	The present invention relates to a method for stimulating an immune	
XX	response. The method comprises administering an immunostimulatory nucleic	
CC	acid to a non-rodent subject in sufficient quantity to stimulate an	
CC	immune response. The present sequence is one such immunostimulatory	
CC	nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich	
CC	(py-rich) or thymidine (T) rich. The method is used to vaccinate subjects	
CC	against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae	
CC	and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,	
CC	haemophilus, campylobacter, clostridium, Escherichia coli and/or	
CC	staphylococcus), fungal antigens and/or parasitic antigens. The method is	
CC	also useful for preventing cancer, asthma, infectious disease, allergy or	
CC	immune deficiency. The present sequence can also be used to redirect a	
CC	Th2 to a Th1 immune response and to activate immune cells. Note: the	
CC	present sequence may have a phosphorothioate backbone	
XX	Sequence 20 BP; 0 A; 0 C; 8 G; 12 T; 0 U; 0 Other;	
SQ	Query Match 100.0%; Score 20; DB 4; Length 20;	
	Best Local Similarity 100.0%; Pred. No. 52;	
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 TTTTGGGTTTGGGGTTT 20	
Db	1 TTTTGGGTTTGGGGTTT 20	
RESULT 2		
ABS77589	ABS77589 standard; DNA; 20 BP.	
ID	ABS77589;	
XX	ABS77589;	
XX	13-DEC-2002 (first entry)	
DT	Angiogenesis inhibitory oligonucleotide #73.	
DE	Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;	
XX	tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;	
KW	diabetic retinopathy; retinopathy of prematurity; macular degeneration;	
KW	corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;	

KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX Synthetic.  
XX WO200253141-A2.  
XX 11-JUL-2002.  
XX 14-DEC-2001; 2001WO-US048458.  
XX 14-DEC-2000; 2000US-0255534P.  
XX (COLE-) COLLEY PHARM GROUP INC.  
PA Bratzler RL;  
XX WPI; 2002-566690/60.  
XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.  
XX Claim 2; Page 20; 276pp; English.  
XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX SQ Sequence 20 BP; 0 A; 0 C; 8 G; 12 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 1 TTTTGGGTTTGGGGTTTT 20  
RESULT 3  
ACD99381  
ID ACD99381 standard; DNA; 20 BP.  
XX  
XX ACD99381;  
AC ACD99381;  
DT 25-SEP-2003 (first entry)  
DE Immunostimulatory nucleic acid #67.  
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX Synthetic.  
OS  
XX US2003050268-A1.  
PN 13-MAR-2003.  
PD  
XX

PF 29-MAR-2002; 2002US-00112653.  
XX 29-MAR-2001; 2001US-0279642P.  
XX (KRIE/) KRIEG A M.  
PA (BERG/) BERG D J.  
XX Krieg AM, Berg DJ;  
XX WPI; 2003-521815/49.  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX Disclosure; Page 10; 229pp; English.  
XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX SQ Sequence 20 BP; 0 A; 0 C; 8 G; 12 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 1 TTTTGGGTTTGGGGTTTT 20  
RESULT 4  
ADB36450  
ID ADB36450 standard; DNA; 20 BP.  
XX  
XX ADB36450;  
XX 04-DEC-2003 (first entry)  
XX Immunostimulatory nucleic acid #64.  
DE  
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX Synthetic.  
XX US2003087848-A1.  
PN  
XX 08-MAY-2003.  
PD  
XX 02-FEB-2001; 2001US-00776479.  
PF  
XX 03-FEB-2000; 2000US-0179991P.  
PR  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
DR  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX  
XX Disclosure; Page 6; 221pp; English.  
XX



RESULT 7  
 AAD64883  
 ID AAD64883 standard; DNA; 28 BP.  
 XX  
 XX AAD64883;  
 AC  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Non-antisense oligonucleotide, GRO J1.  
 XX  
 XX Neoplastic; malignancy; lung carcinoma; ss.  
 KW  
 XX Unidentified.  
 OS  
 XX US2003194754-A1.  
 FN  
 XX 16-OCT-2003.  
 PD  
 XX 08-APR-2002; 2002US-00118854.  
 PF  
 XX 08-APR-2002; 2002US-00118854.  
 PR  
 XX (MILL/) MILLER D M.  
 PA (BATE/) BATES P J.  
 PA (TREN/) TRENT J O.  
 PA (AUXK/) XU X.  
 XX  
 XX Miller DM, Bates PJ, Trent JO, Xu X;  
 FI WPI; 2003-875400/81.  
 DR  
 XX Determining neoplastic state of cell, involves detecting presence of  
 PT plasma membrane nucleotide in cell or quantifying amount of plasma  
 PT membrane nucleolin in cell.  
 PT  
 XX Claim 11; SEQ ID NO 28; Opp; English.  
 PS  
 XX The present invention relates to method for determining neoplastic state  
 CC of a cell, involves detecting the presence of plasma membrane nucleotide  
 CC in the cell or quantifying the amount of plasma membrane nucleolin in the  
 CC cell. The invention is useful for diagnosing pre-malignant cells,  
 CC malignant cells and lung small cell carcinoma. The present sequence is a  
 CC non-antisense oligonucleotide  
 CC  
 XX Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 10; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTTGGGGTTTGGGGTTTT 20  
 Db 5 TTTTGGGGTTTGGGGTTTT 24  
 RESULT 8  
 ADJ94159  
 ID ADJ94159 standard; DNA; 28 BP.  
 XX  
 XX ADJ94159;  
 AC  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Oligonucleotide of the invention #26.  
 XX  
 KW ds; linear polynucleotide; cation; telomere repeat.  
 XX  
 OS Unidentified.  
 XX  
 XX JP2003169676-A.  
 PN  
 XX 17-JUN-2003.  
 PD

XX  
 PF 05-DEC-2001; 2001JP-00371975.  
 XX  
 PR 05-DEC-2001; 2001JP-00371975.  
 XX  
 PA (TAKE/) TAKENAKA S.  
 PA (TUMK-) TUM KENKYUSHO KK.  
 XX  
 XX WPI; 2003-639772/61.  
 DR  
 XX Quantitative method of cation for clinical laboratory test, involves  
 PT adding linear polynucleotide containing telomere repeat sequence with  
 PT donor and acceptor at edge portions, to solution containing cation.  
 PT  
 XX Disclosure; Page 29; 8pp; Japanese.  
 PS  
 XX The invention relates to a novel quantitative method for adding linear  
 CC polynucleotide to solution containing a cation. The linear polynucleotide  
 CC contains telomere repeat sequence with donor at one edge portion and  
 CC acceptor at another edge portion. The optical detection is performed  
 CC using this linear polynucleotide. The method of the invention is useful  
 CC in medical fields such as clinical laboratory test and fields with cation  
 CC fixed assay. The present sequence is used in the exemplification of the  
 CC invention.  
 CC  
 XX Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 10; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTTGGGGTTTGGGGTTTT 20  
 Db 5 TTTTGGGGTTTGGGGTTTT 24  
 RESULT 9  
 ADI28732  
 ID ADI28732 standard; DNA; 28 BP.  
 XX  
 AC ADI28732;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE Guanosine-rich oligonucleotide GRO J, used in apoptosis detection.  
 XX  
 KW Apoptosis; nucleolin; AIDS; cancer; neurodegenerative disease;  
 KW autoimmune disease; infection; diagnosis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004003554-A1.  
 XX  
 PD 08-JAN-2004.  
 XX  
 XX 26-JUN-2003; 2003WO-US020167.  
 PF  
 XX 26-JUN-2002; 2002US-0392143P.  
 PR  
 XX (UYLO-) UNIV LOUISVILLE RES FOUND INC.  
 PA (BATE/) BATES P J.  
 PA (MIYY/) MI Y.  
 XX  
 XX Bates PJ, Mi Y;  
 PI  
 XX WPI; 2004-083166/08.  
 DR  
 XX Detecting apoptosis comprises preparing a sample from which cells have  
 PT been removed and detecting at least one of nucleolin and PARP-I in the  
 PT sample.  
 PT  
 XX Claim 9; SEQ ID NO 28; 66pp; English.  
 XX  
 XX



CC The present sequence is that of guanosine-rich oligonucleotide GRO J,  
 CC which can be used in the method of the invention. The method is for the  
 CC detection of apoptosis. It involves preparing a sample from which cells  
 CC have been removed, and detecting nucleolin and/or poly(ADP-ribose)  
 CC polymerase (PARP-1) in the sample, where the sample is blood, serum,  
 CC plasma, tissue, tissue culture medium or sputum. Detection of nucleolin  
 CC involves detection of a complex between nucleolin and a nucleolin binding  
 CC molecule, preferably an anti-nucleolin antibody or a GRO, such as GRO J,  
 CC which is characterised as a good plasma membrane nucleolin-binding GRO.  
 CC The method allows detection of excessive apoptosis in a subject suspected  
 CC of having AIDS, a neurodegenerative disease, an ischaemic injury, an  
 CC autoimmune disease, a tumour, a cancer (especially endocervical  
 CC adenocarcinoma, prostatic carcinoma, breast cancer, leukaemia and non-  
 CC small cell lung carcinoma), a viral infection, an acute inflammatory  
 CC condition or sepsis (all claimed).

XX Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTTCGGGTTTT 20  
 DB 5 TTTTGGGTTTTCGGGTTTT 24

#### RESULT 10

ADY53924

ID ADY53924 standard; DNA; 28 BP.

XX AC ADY53924;

XX 19-MAY-2005 (first entry)

DE Non-antisense GRO nucleolin-binding oligonucleotide GRO29A.

XX Diagnosis; therapy; tumor; cancer; neoplasm; cytostatic; nucleolin; ss;  
 KW guanine-rich oligonucleotide; gene silencing; RNA interference; melanoma;  
 KW lymphoma; sarcoma; glioma; leukemia; hepatocellular carcinoma.

XX Synthetic.

XX US2005053607-A1.

XX 10-MAR-2005.

XX 09-OCT-2003; 2003US-00683480.

XX 08-APR-2002; 2002US-00118854.

PA (BATE/) BATES P J.

PA (MILL/) MILLER D M.

PA (TREN/) TRENT J O.

PA (XUXX/) XU X.

XX Bates PJ, Miller DM, Trent JO, Xu X;

XX WPI; 2005-213006/22.

PT Treating cancer in a subject comprises administering to the subject a  
 PT therapeutically effective amount of an anti-nucleolin agent and a  
 PT carrier.

XX Disclosure; SEQ ID NO 28; 32pp; English.

CC The invention relates to treating cancer in a subject comprises  
 CC administering to the subject a therapeutically effective amount of an  
 CC anti-nucleolin agent and a carrier. Also included is a pharmaceutical  
 CC composition comprising a nucleolin antibody or an inhibitory RNA against  
 CC nucleolin, and a carrier. The method and antibodies, RNA and composition  
 CC are useful for treating cancer, such as melanoma, lymphoma, plasmacytoma,  
 CC sarcoma, glioma, thymoma, leukemia, hepatoma, or breast, prostate, colon,

CC liver, esophageal, brain, lung, ovary, or cervical cancer. The present  
 CC sequence is a GRO (guanine-rich oligonucleotide) which binds to nucleolin  
 CC (thereby inhibiting cancer cell growth).

XX Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTTCGGGTTTT 20  
 DB 5 TTTTGGGTTTTCGGGTTTT 24

#### RESULT 11

ADZ58647

ID ADZ58647 standard; DNA; 28 BP.

XX AC ADZ58647;

XX 14-JUL-2005 (first entry)

DE Inflammation treatment-related GRO J oligonucleotide SeqID29.

XX Inflammation; antiinflammatory; analgesic; gynecological; hepatotropic;  
 KW neuroprotective; nootropic; antiarthritic; antirheumatic;  
 KW gastrointestinal-Gen.; antiulcer; gene therapy; dysmenorrhea;  
 KW alcoholic hepatitis; pancreatitis; Alzheimers disease;  
 KW rheumatoid arthritis; asthma; gastrointestinal disease; psoriasis;  
 KW atherosclerosis; Crohns disease; ulcerative colitis; GRO J; ss.

XX Unidentified.

XX WO2005037323-A2.

XX 28-APR-2005.

XX 08-OCT-2004; 2004WO-US033185.

XX 10-OCT-2003; 2003US-0510466P.

XX (UYLO-) UNIV LOUISVILLE RES FOUND INC.

XX Bates PJ, Girvan AC, Barve SS;

XX WPI; 2005-315628/32.

XX Treating inflammation, e.g. acute or chronic inflammation such as  
 PT rheumatoid arthritis, asthma, psoriasis, and atherosclerosis, in a  
 PT patient comprises administering to the patient a composition comprising a  
 GRO.

XX Claim 2; SEQ ID NO 29; 60pp; English.

XX This invention relates to a novel method for treating inflammation in a  
 CC patient which comprises administering to the patient a composition  
 CC comprising a GRO (guanosine-rich oligonucleotide). The invention may be  
 CC useful for the development of compounds with an antiinflammatory,  
 CC analgesic, gynecological, hepatotropic, neuroprotective, nootropic,  
 CC antiarthritic, antiinematic, gastrointestinal-Gen. or antiulcer activity  
 CC whilst the disclosed sequence may prove useful for gene therapy. The  
 CC methods are useful for treating inflammation associated with an acute  
 CC inflammatory condition. The acute inflammatory condition is selected from  
 CC primary dysmenorrhea, acute alcoholic liver disease and acute  
 CC pancreatitis. The inflammation may also be of Alzheimer's disease or  
 CC associated with a chronic inflammatory disease. The chronic inflammatory  
 CC disease is selected from rheumatoid arthritis, asthma, gastrointestinal  
 CC tract disease, psoriasis, atherosclerosis, Crohns disease, ulcerative  
 CC colitis alcohol, chronic alcoholic liver disease, non-alcoholic  
 CC steatohepatitis and chronic pancreatitis. The present sequence is that of  
 CC the oligonucleotide GRO J which was used during the development of the  
 CC novel method of the invention.

```

XX SQ Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 5 TTTTGGGGTTTGGGGTTTT 24

RESULT 12
AD225617
ID AD225617 standard; DNA; 28 BP.
XX AC AD225617;
XX DT 14-JUL-2005 (first entry)
DE G-quadruplex-forming carbazole-binding DNA Oxy28, SEQ ID NO:11.
XX KW Telomere; stabilizer; telomerase inhibitor; cancer; neoplasm; cytostatic;
XX KW ss.
XX OS Unidentified.
XX PN US2005090671-A1.
XX PD 28-APR-2005.
XX PF 22-OCT-2003; 2003US-00690984.
XX PR 22-OCT-2003; 2003US-00690984.
XX PA (CHAN/) CHANG T.
XX PA (CHAN/) CHANG C.
XX PA (WUJ/) WU J.
XX PI Chang T, Chang C, Wu J;
XX DR WPI; 2005-331984/34.
XX PT New carbazole compound stabilizing G-quadruplex of telomere, useful to
XX PT treat telomerase-related disease e.g. cancer.
XX PS Example 9; SEQ ID NO 11; 12pp; English.
XX CC The invention relates to novel carbazole compounds which thermally
XX CC stabilize the intramolecular G-quadruplex structure of human telomeres.
XX CC The folding of telomeric DNA into G-quadruplexes inhibits telomerase, the
XX CC enzyme present in over 85% of tumor cells which adds nucleotides to
XX CC telomeres, preventing them from reducing in length during cell division.
XX CC The carbazole compounds of the invention may be used to treat telomere-
XX CC related disease, e.g., cancer. Sequences AD225610-AD225619 represent DNA
XX CC sequences capable of duplex or quadruplex formation which were
XX CC demonstrated to be bound by a carbazole compound of the invention. The
XX CC present sequence represents a G-quadruplex-forming DNA capable of being
XX CC bound by a carbazole compound. Note: The specification states that this
XX CC sequence forms a G-quadruplex structure; however, further details on how
XX CC the structure is formed has not been provided.
XX SQ Sequence 28 BP; 0 A; 0 C; 16 G; 12 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 5 TTTTGGGGTTTGGGGTTTT 24

us-09-669-187a-73.szlm50.rng

RESULT 13
AA257146
ID AA257146 standard; DNA; 32 BP.
XX AC AA257146;
XX DT 24-MAR-2000 (first entry)
XX DE Exemplary quadruplex nucleic acid SEQ ID NO:9.
XX KW Quadruplex DNA; antibody; binding; detection; isolation; purification;
XX KW ss.
XX OS Synthetic.
XX PN US6001657-A.
XX PD 14-DEC-1999.
XX PF 11-OCT-1996; 96US-00729598.
XX PR 12-OCT-1995; 95US-0005242P.
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX PA (JACK-) JACKSON LAB.
XX PI Roberts JF, Pelsue SC, Hardin CC, Brown BA;
XX DR WPI; 2000-096139/08.
XX PT Quadruplex nucleic acid and antibody binding assay useful for detecting
XX PT and purifying antibodies and nucleic acids from a biological sample.
XX PS Disclosure; Col 3; 11pp; English.
XX CC A method has been developed for binding quadruplex nucleic acids. The
XX CC method comprises contacting a quadruplex nucleic acid with a monoclonal
XX CC antibody that selectively binds to quadruplex nucleic acid to form an
XX CC antibody-quadruplex nucleic acid complex. The method can be used for
XX CC detecting antibodies that bind to quadruplex nucleic acids and to collect
XX CC antibodies that bind to quadruplex nucleic acids. The method is also
XX CC suitable for detecting, isolating and purifying quadruplex nucleic acids.
XX CC The detecting step can be carried out on a biological sample such as
XX CC cerebrospinal fluid, tissues samples, blood samples or other sample
XX CC suspected of containing quadruplex nucleic acids. The method can be used
XX CC for the purification of quadruplex nucleic acids from solutions and to
XX CC purify aptamers from combinatorial libraries or heterogeneous solutions,
XX CC in particular to purify or detect DNA aptamers that specifically bind the
XX CC thrombin molecule critical in the thrombin-catalysed, fibrin-clot
XX CC formation cascade of blood platelets. The antibodies can then be used to
XX CC detect levels of a known therapeutic aptamer in a patient and monitor
XX CC clearance and dosage levels in a treatment protocol involving the
XX CC aptamer. The present sequence represents an oligonucleotide used in the
XX CC exemplification of the present invention
XX SQ Sequence 32 BP; 0 A; 0 C; 16 G; 16 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 1 TTTTGGGGTTTGGGGTTTT 20

RESULT 14
AAQ61979
ID AAQ61979 standard; DNA; 39 BP.
XX AC AAQ61979;
XX DT 25-MAR-2003 (revised)
```

DT 04-NOV-1994 (first entry)  
 XX Oxytricha telomeric sequence.  
 XX  
 XX Inhibition; replication; herpes simplex virus; HSV; HIV; aging; length;  
 KW human cytomegalovirus; influenza virus; inflammation; telomere  
 KW neurological disorders; phospholipase A2 activity; hyperproliferation;  
 KW malignancy; cardiovascular disease; snake bite; malignancy; retard; ss.  
 XX  
 XX Oxytricha sp.  
 XX WO9408053-A1.  
 XX 14-APR-1994.  
 XX  
 XX 29-SEP-1993; 93WO-US009297.  
 XX  
 XX 29-SEP-1992; 92US-00954185.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;  
 PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;  
 XX  
 XX WPI; 1994-135613/16.  
 XX  
 XX New modified oligo-nucleotide contg guanine quartet - inhibits activity  
 PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length  
 PT of chromosomes.  
 XX  
 XX Example 7; Page 36; 144pp; English.  
 XX  
 XX This sequence represents a guanine rich sequence derived from the  
 CC Oxytricha telomeric region. This sequence forms an unusual structure  
 CC termed a G quartet. The formation of this structure is monovalent cation  
 CC dependant and is disrupted by high temperature. Sequences which share the  
 CC guanine rich nature of this telomeric sequence may be used to inhibit  
 CC human type II phospholipase A2 activity. Oligonucleotides such as these  
 CC may also be used for inhibiting activity of HSV, HIV, human  
 CC cytomegalovirus or influenza virus, or for treating inflammatory and  
 CC neurological disorders caused by phospholipase A2 activity in cases of  
 CC hyperproliferation, malignancy, cardiovascular disease and snake bite.  
 CC They may also be used for inhibiting division of malignant cells by  
 CC modulating telomere length, which may also retard aging. (Updated on 25-  
 CC MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 39 BP; 0 A; 0 C; 20 G; 16 T; 0 U; 3 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 2; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTTGGGGTTTGGGGTTT 20  
 |||||  
 Db 8 TTTTGGGGTTTGGGGTTT 27  
 |||||  
 RESULT 15  
 AAV17009  
 ID AAV17009 standard; DNA; 44 BP.  
 XX  
 XX AAV17009;  
 XX  
 XX 13-AUG-1998 (first entry)  
 DT  
 XX Telomerase substrate utilisation primer 28-30.  
 DE  
 XX Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis; prognosis;  
 KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX

PN GB2317891-A.  
 XX  
 XX 08-APR-1998.  
 XX  
 XX 01-OCT-1997; 97GB-00020890.  
 XX  
 XX 01-OCT-1996; 96US-00724643.  
 PR 18-APR-1997; 97US-00844419.  
 PR 25-APR-1997; 97US-00846017.  
 PR 06-MAY-1997; 97US-00851843.  
 PR 09-MAY-1997; 97US-00854050.  
 PR 14-AUG-1997; 97US-00911312.  
 PR 14-AUG-1997; 97US-00912951.  
 PR 14-AUG-1997; 97US-00915503.  
 XX  
 XX (GERO-) GERON CORP.  
 PA (UYTB-) UNIV TECHNOLOGY CORP.  
 PA  
 XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;  
 PI Andrews WH;  
 PI  
 XX WPI; 1998-171633/16.  
 DR  
 XX Pure and recombinant human Telomerase Reverse Transcriptase and its  
 PT variants - are useful in the diagnosis, prognosis and treatment of cell  
 PT proliferation conditions especially cancer and ageing.  
 XX  
 XX Example 1; Page 200; 387pp; English.  
 XX  
 XX The present sequence represents a primer from the present invention which  
 CC describes human telomerase reverse transcriptase (hTERT). The present  
 CC invention also describes the following methods: (A) determining whether a  
 CC test compound is a modulator of hTERT, by detecting the change in hTERT  
 CC recombinant protein or polynucleotide, on administration of the compound;  
 CC (B) preparation of recombinant telomerase by contacting a protein  
 CC preparation of hTERT with a telomerase RNA component; (C) detection of the  
 CC hTERT RNA or protein in a sample by binding a relevant probe to the sample  
 CC and detecting the product and correlating the presence of complex or  
 CC amplifying the product and correlating the presence of complex or  
 CC amplification product with presence of hTERT in the sample; and (D)  
 CC increasing the proliferation of a vertebrate cell by increasing hTERT  
 CC expression; and (E) the use of an agent that causes an increase in cell  
 CC vertebrate cell proliferation to create a medication that inhibits  
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding  
 CC hTERT can be used in the manufacture of medicaments for inhibiting the  
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be used  
 CC to treat conditions that are associated with high telomerase activity. A  
 CC protein preparation of hTERT can also be used in the new methods  
 XX  
 XX Sequence 44 BP; 10 A; 10 C; 12 G; 12 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 2; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTTGGGGTTTGGGGTTT 20  
 |||||  
 Db 25 TTTTGGGGTTTGGGGTTT 44  
 |||||  
 RESULT 16  
 AAV17008  
 ID AAV17008 standard; DNA; 46 BP.  
 XX  
 XX AAV17008;  
 XX  
 XX 13-AUG-1998 (first entry)  
 DT  
 XX Telomerase substrate utilisation primer 25-27.  
 DE  
 XX Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis; prognosis;  
 KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.  
 XX  
 XX

```

OS Synthetic.
OS Homo sapiens.
PN GB2317891-A.
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-00020890.
XX
XX 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERON CORP.
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
XX Andrews WH;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
XX variants - are useful in the diagnosis, prognosis and treatment of cell
XX proliferation conditions especially cancer and ageing.
XX
XX Example 1; Page 200; 387pp; English.
XX
XX The present sequence represents a primer from the present invention which
XX describes human telomerase reverse transcriptase (hTERT). The present
XX invention also describes the following methods: (A) determining whether a
XX test compound is a modulator of hTERT, by detecting the change in hTERT
XX recombinant protein or polynucleotide, on administration of the compound;
XX (B) preparation of recombinant telomerase by contacting a protein
XX preparation of hTERT with a telomerase RNA component; (C) detection of the
XX hTERT RNA or protein in a sample by binding a relevant probe to the sample
XX and detecting the complex formed or in the case of RNA detection,
XX amplifying the product and correlating the presence of complex or
XX amplification product with presence of hTERT in the sample; and (D)
XX increasing the proliferation of a vertebrate cell by increasing hTERT
XX expression; and (E) the use of an agent that causes an increase in cell
XX vertebrate cell proliferation to create a medicament that inhibits
XX ageing. A protein preparation of hTERT and the polynucleotide encoding
XX hTERT can be used in the manufacture of medicaments for inhibiting the
XX effect of ageing or cancer. Inhibitors of telomerase activity can be used
XX to treat conditions that are associated with high telomerase activity. A
XX protein preparation of hTERT can also be used in the new methods
XX
XX Sequence 46 BP; 10 A; 12 C; 12 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 46;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTTCGGGTTTT 20
Db |||||
Db 27 TTTTGGGTTTTCGGGTTTT 46

RESULT 17
AAV17007
ID AAV17007 standard; DNA; 48 BP.
XX
XX AAV17007;
XX
XX 13-AUG-1998 (first entry)
XX
XX Telomerase substrate utilisation primer 22-24.
XX

```

---

```

KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX GB2317891-A.
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-00020890.
XX
XX 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERON CORP.
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
XX Andrews WH;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
XX variants - are useful in the diagnosis, prognosis and treatment of cell
XX proliferation conditions especially cancer and ageing.
XX
XX Example 1; Page 200; 387pp; English.
XX
XX The present sequence represents a primer from the present invention which
XX describes human telomerase reverse transcriptase (hTERT). The present
XX invention also describes the following methods: (A) determining whether a
XX test compound is a modulator of hTERT, by detecting the change in hTERT
XX recombinant protein or polynucleotide, on administration of the compound;
XX (B) preparation of recombinant telomerase by contacting a protein
XX preparation of hTERT with a telomerase RNA component; (C) detection of the
XX hTERT RNA or protein in a sample by binding a relevant probe to the sample
XX and detecting the complex formed or in the case of RNA detection,
XX amplifying the product and correlating the presence of complex or
XX amplification product with presence of hTERT in the sample; and (D)
XX increasing the proliferation of a vertebrate cell by increasing hTERT
XX expression; and (E) the use of an agent that causes an increase in cell
XX vertebrate cell proliferation to create a medicament that inhibits
XX ageing. A protein preparation of hTERT and the polynucleotide encoding
XX hTERT can be used in the manufacture of medicaments for inhibiting the
XX effect of ageing or cancer. Inhibitors of telomerase activity can be used
XX to treat conditions that are associated with high telomerase activity. A
XX protein preparation of hTERT can also be used in the new methods
XX
XX Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 48;
XX Best Local Similarity 100.0%; Pred. No. 54;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTTCGGGTTTT 20
Db |||||
Db 29 TTTTGGGTTTTCGGGTTTT 48

RESULT 18
AAV17004
ID AAV17004 standard; DNA; 48 BP.
XX
XX AAV17004;
XX
XX 13-AUG-1998 (first entry)
XX

```

```
XX Telomerase substrate utilisation primer 13-15.
DE Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
XX Synthetic.
OS Homo sapiens.
XX GB2317891-A.
XX 08-APR-1998.
XX 01-OCT-1997; 97GB-00020890.
XX 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX Cecch TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX WPI; 1998-171633/16.
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX Example 1; Page 200; 387pp; English.
XX The present sequence represents a primer from the present invention which
CC describes human telomerase reverse transcriptase (hTERT). The present
CC invention also describes the following methods: (A) determining whether a
CC test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC amplification product with presence of hTERT in the sample; and (D)
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 20; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGGGTTTGGGGTTTT 20
DB 29 TTTTGGGTTTGGGGTTTT 48
RESULT 19
AAV17006
ID AAV17006 standard; DNA; 50 BP.
XX
```

---

```
AC AAV17006;
XX 13-AUG-1998 (first entry)
DE Telomerase substrate utilisation primer 19-21.
XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
XX Synthetic.
OS Homo sapiens.
XX GB2317891-A.
XX 08-APR-1998.
XX 01-OCT-1997; 97GB-00020890.
XX 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX Cecch TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX WPI; 1998-171633/16.
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX Example 1; Page 200; 387pp; English.
XX The present sequence represents a primer from the present invention which
CC describes human telomerase reverse transcriptase (hTERT). The present
CC invention also describes the following methods: (A) determining whether a
CC test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC amplification product with presence of hTERT in the sample; and (D)
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX Sequence 50 BP; 12 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 20; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTTGGGTTTGGGGTTTT 20
DB 31 TTTTGGGTTTGGGGTTTT 50
RESULT 20
```

ADF69702	
ID	ADF69702 standard; DNA; 29 BP.
XX	
AC	ADF69702;
XX	
DT	11-MAR-2004 (first entry)
XX	
DE	Human HLTf methylation detection PCR primer.
XX	
KW	human; SLC5A8; cell surface protein; cytostatic; gene therapy;
KW	SLC5A8-associated cancer; colon cancer; breast cancer; thyroid cancer;
KW	stomach cancer; cancer; HLTf; PCR primer; ss.
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO2003104427-A2.
XX	
PD	18-DEC-2003.
XX	
PF	05-JUN-2003; 2003WO-US019239.
XX	
PR	05-JUN-2002; 2002US-0386653P.
XX	
PA	(UYCA-) UNIV CASE WESTERN RESERVE.
XX	
PI	Markowitz SD;
XX	
DR	WPI; 2004-062348/06.
XX	
XX	New SLC5A8 polypeptide, useful for detecting and treating SLC5A8-
PT	associated cancer, e.g. colon, breast, thyroid or stomach cancer.
XX	
PS	Claim 77; Page 99; 207pp; English.
XX	
CC	The present invention describes the human SLC5A8 protein (I), which is a
CC	cell surface protein. (I) has cytostatic activity, and can be used in
CC	gene therapy. (I) can be used in detecting and treating SLC5A8-associated
CC	cancer, e.g. colon cancer, breast cancer, thyroid cancer or stomach
CC	cancer. (I) is also useful in screening assays, predictive medicine and
CC	in diagnostic and prognostic assays. The human SLC5A8 gene is located on
CC	chromosome 12. The present sequence is used in the exemplification of the
CC	present invention.
XX	
SQ	Sequence 29 BP; 1 A; 0 C; 9 G; 19 T; 0 U; 0 Other;
	Query Match 92.0%; Score 18.4; DB 12; Length 29;
	Best Local Similarity 95.0%; Pred. No. 2.4e+02;
	Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 TTTTGGGGTTTGGGGTTT 20
Db	3 TTTTGGGGTTTGTGGTTT 22
	RESULT 21
	ADV09385
ID	ADV09385 standard; DNA; 29 BP.
XX	
AC	ADV09385;
XX	
DT	24-FEB-2005 (first entry)
XX	
DE	Human HLTf 5' unmethylated DNA amplifying PCR primer, P-HLTf1347UF.
XX	
KW	DNA methylation; HLTf; helicase-like transcription factor; HPI16a; Zbul;
KW	RUSHia; Smarca; proliferative disease; colon neoplasia; cytostatic; PCR;
KW	primer; gene therapy; ss.
XX	
OS	Homo sapiens.
XX	
PN	US2004242510-A1.
XX	
	Query Match 92.0%; Score 18.4; DB 14; Length 29;
	Best Local Similarity 95.0%; Pred. No. 2.4e+02;
	Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 TTTTGGGGTTTGGGGTTT 20
Db	3 TTTTGGGGTTTGTGGTTT 22
	RESULT 22
	ADV09348
ID	ADV09348 standard; DNA; 29 BP.
XX	
AC	ADV09348;
XX	
DT	24-FEB-2005 (first entry)
XX	
DE	Human HLTf unmethylated DNA amplifying forward PCR primer, 1347UF.
XX	
KW	DNA methylation; HLTf; helicase-like transcription factor; HPI16a; Zbul;
KW	RUSHia; Smarca; proliferative disease; colon neoplasia; cytostatic; PCR;
KW	primer; gene therapy; ss.
XX	
OS	Homo sapiens.
XX	
PN	US2004242510-A1.
XX	
PD	02-DEC-2004.
XX	
PF	07-OCT-2002; 2002US-00266103.
XX	
PR	05-OCT-2001; 2001US-0327537P.
XX	
PA	(MARK/) MARKOWITZ S D.
XX	
PI	Markowitz SD;
XX	
DR	WPI; 2005-011663/01.
XX	
	Query Match 92.0%; Score 18.4; DB 14; Length 29;
	Best Local Similarity 95.0%; Pred. No. 2.4e+02;
	Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 TTTTGGGGTTTGGGGTTT 20
Db	3 TTTTGGGGTTTGTGGTTT 22
	RESULT 22
	ADV09348
ID	ADV09348 standard; DNA; 29 BP.
XX	
AC	ADV09348;
XX	
DT	24-FEB-2005 (first entry)
XX	
DE	Human HLTf unmethylated DNA amplifying forward PCR primer, 1347UF.
XX	
KW	DNA methylation; HLTf; helicase-like transcription factor; HPI16a; Zbul;
KW	RUSHia; Smarca; proliferative disease; colon neoplasia; cytostatic; PCR;
KW	primer; gene therapy; ss.
XX	
OS	Homo sapiens.
XX	
PN	US2004242510-A1.
XX	
PD	02-DEC-2004.
XX	
PF	07-OCT-2002; 2002US-00266103.
XX	
PR	05-OCT-2001; 2001US-0327537P.
XX	
PA	(MARK/) MARKOWITZ S D.
XX	
PI	Markowitz SD;
XX	
DR	WPI; 2005-011663/01.
XX	

PT Detecting differential methylation patterns in an HLTf nucleotide  
PT sequence, useful for diagnosing or treating colon neoplasia, comprises  
PT assay samples for the presence of methylation within a specific  
PT nucleotide sequence.

XX Claim 10; SEQ ID NO 13; 117pp; English.

CC The present invention relates to a method for detecting differential  
CC methylation patterns in an helicase-like transcription factor (HLTF, also  
CC called HPI16a, Zbul, RUSH1a and Smarca) nucleotide sequence. The method  
CC involves obtaining samples from a patient and a healthy subject, assaying  
CC the samples for the presence of methylation within a nucleotide sequence  
CC and comparing the methylation patterns in the sample from the subject to  
CC those in the normal sample. HLTF modulator is useful for treating an HLTF  
CC -associated proliferative disease in a subject, where the disease is  
CC associated with methylation of an HLTF nucleic acid sequence, i.e. colon  
CC neoplasia and the compound induces HLTF expression. The method of the  
CC invention is useful in gene therapy. The present sequence is the human  
CC HLTF unmethylated DNA amplifying PCR primer.

XX Sequence 29 BP; 1 A; 0 C; 9 G; 19 T; 0 U; 0 Other;

Query Match 92.0%; Score 18.4; DB 14; Length 29;  
Best Local Similarity 95.0%; Pred. No. 2.4e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 TTTTGGGGTTTGGGGTTT 22

RESULT 23  
AAT28342  
ID AAT28342 standard; DNA; 18 BP.

XX AC AAT28342;

XX 20-NOV-1996 (first entry)

XX Multi-G oligonucleotide T3-G4-T4-G4-T3.

XX Multi-G oligonucleotide; antisense sequence; c-myb; nuclease resistant;  
KW phosphorothioate linkage; phosphorodithioate linkage; inhibitor; therapy;  
KW cell proliferation; smooth muscle cell; proliferation protein;  
KW vascular restenosis; arterial restenosis; ss.

XX Synthetic.

XX WO9611265-A2.

XX 18-APR-1996.

XX 03-OCT-1995; 95WO-US012770.

XX 05-OCT-1994; 94US-00318458.

XX (AMGE-) AMGEN INC.

XX Burgess TL, Farrell CL, Fisher EF;  
XX WPI; 1996-209848/21.

XX New modified oligo:nucleotide(s) contg. consecutive guanine residues -  
PT inhibit proliferation of smooth muscle cells, esp. to prevent arterial  
PT restenosis.

XX Example 6; Page 32; 67pp; English.

XX AAT28317-T28347 represent multi-G oligonucleotides. AAT28336-T28347 are  
CC multi-G oligonucleotides with multiple G strings or G strings of 4 bases  
CC and over. These sequences are oligonucleotides of the invention. These  
CC sequences can be modified to become more nuclease resistant, using  
CC phosphorothioate, phosphorodithioate, or 3'-carbon modified links. To

CC screen for modified multi-G sequences that inhibit cell proliferation,  
CC cultured smooth muscle cells that are arrested in the G0 phase, are  
CC induced to proliferate in the presence of the multi-G sequence. The  
CC cultured smooth muscle cells used in this method are attached to a solid  
CC support, and growth arrest is achieved on a starvation medium, followed  
CC by transfer to a normal growth medium to induce proliferation. The  
CC compounds that provide over 50% inhibition at a set dosage are selected  
CC as being useful for inhibiting vascular restenosis. The multi-G  
CC oligonucleotides are used to inhibit proliferation of smooth muscle  
CC cells, such as to prevent arterial restenosis. These sequences are not  
CC antisense sequences, but are thought to work in a similar way. The  
CC sequences are thought to act by binding to proteins involved in the  
CC proliferation process. Compounds containing these multi-G  
CC oligonucleotides are not toxic, and their effect on cell proliferation is  
CC fully reversible

XX Sequence 18 BP; 0 A; 0 C; 8 G; 10 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTTGGGGTTTGGGGTTT 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 TTTGGGGTTTGGGGTTT 18

RESULT 24  
AAV17006/C  
ID AAV17006 standard; DNA; 50 BP.

XX AC AAV17006;

XX 13-AUG-1998 (first entry)

XX Telomerase substrate utilisation primer 19-21.

XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;  
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.

XX Synthetic.

XX Homo sapiens.

XX GB2317891-A.

XX 08-APR-1998.

XX 01-OCT-1997; 97GB-00020890.

XX 01-OCT-1996; 96US-00724643.

XX 18-APR-1997; 97US-00844419.

XX 25-APR-1997; 97US-00846017.

XX 06-MAY-1997; 97US-00851843.

XX 09-MAY-1997; 97US-00854050.

XX 14-AUG-1997; 97US-00911312.

XX 14-AUG-1997; 97US-00912951.

XX 14-AUG-1997; 97US-00915503.

XX (GERO-) GERON CORP.  
XX (UYTE-) UNIV TECHNOLOGY CORP.

XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;  
XX Andrews WH;  
XX WPI; 1998-171633/16.

XX Pure and recombinant human Telomerase Reverse Transcriptase and its  
PT variants - are useful in the diagnosis, prognosis and treatment of cell  
PT proliferation conditions especially cancer and ageing.

XX Example 1; Page 200; 387pp; English.

XX The present sequence represents a primer from the present invention which

CC describes human telomerase reverse transcriptase (hTERT). The present  
 CC invention also describes the following methods: (A) determining whether a  
 CC test compound is a modulator of hTERT, by detecting the change in hTERT  
 CC recombinant protein or polynucleotide, on administration of the compound;  
 CC (B) preparation of recombinant telomerase by contacting a protein  
 CC preparation of hTERT with a telomerase RNA component; (C) detection of the  
 CC hTERT RNA or protein in a sample by binding a relevant probe to the sample  
 CC and detecting the complex formed or in the case of RNA detection,  
 CC amplifying the product and correlating the presence of complex or  
 CC amplification product with presence of hTERT in the sample; and (D)  
 CC increasing the proliferation of a vertebrate cell by increasing hTERT  
 CC expression; and (E) the use of an agent that causes an increase in cell  
 CC vertebrate cell proliferation to create a medicament that inhibits  
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding the  
 CC hTERT can be used in the manufacture of medicaments for inhibiting the  
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be used  
 CC to treat conditions that are associated with high telomerase activity. A  
 CC protein preparation of hTERT can also be used in the new methods  
 XX  
 SQ Sequence 50 BP; 12 A; 14 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 18  
 Db 18 TTTTGGGGTTTGGGGTTT 1

RESULT 25  
 AAQ44008  
 ID AAQ44008 standard; DNA; 26 BP.

XX AAQ44008;  
 XX 25-MAR-2003 (revised)  
 DT 28-OCT-1993 (first entry)  
 XX Target sequence #4.  
 DE  
 XX Purine; pyrimidine; tracts; therapeutic; diagnostic; control;  
 KW gene expression; mRNA synthesis suppression; ds.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9312230-A1.  
 PN  
 XX 24-JUN-1993.  
 PD  
 XX 11-DEC-1992; 92WO-US010792.  
 PF  
 XX 13-DEC-1991; 91US-00808452.  
 PR  
 XX 21-JAN-1992; 92US-00826934.  
 PR  
 XX (STRI ) SRI INT.  
 PA  
 XX Jayasena SD, Johnston BH;  
 PI  
 XX WPI; 1993-214172/26.  
 DR  
 XX New oligo:nucleotide(s) forming triple helix with target nucleic acid -  
 PT contain purine and pyrimidine tracts in specific orientations, useful  
 PT therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.  
 XX  
 PS Example; Fig 14a; 101pp; English.

XX The sequence is that of the target sequence #4 which was used in an  
 CC experiment to determine the in vitro cleavage of target duplexes to  
 CC evaluate the lengths of purine and pyrimidine tracts which are useful in  
 CC obtaining oligonucleotides capable of triple helix formation with target  
 CC nucleic acids. The complementary strand overhangs the 3' end by the  
 CC sequence CTAG and the sense strand overhangs the complementary strand by

CC the sequence AATT. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 26 BP; 2 A; 1 C; 13 G; 10 T; 0 U; 0 Other;  
 Query Match 87.0%; Score 17.4; DB 2; Length 26;  
 Best Local Similarity 94.7%; Pred. No. 6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 TTTGGGGTTTGGGGTTT 20  
 Db 3 TTTGGGGTTTGGGGTTT 21  
 RESULT 26  
 AAQ04992  
 ID AAQ04992 standard; DNA; 28 BP.  
 XX AAQ04992;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 31-OCT-1990 (first entry)  
 XX  
 DE Sequence binding to and inhibiting the gene controlling Alzheimer's  
 DE disease plaque formation.  
 DE  
 XX C-myc; cancer; HIV-1; AIDS; collagenase; Alzheimers disease; EGF;  
 KW epidermal growth factor; GSTpi; HMGCoA; thalassaemia;  
 KW Herpes simplex virus; nerve growth factor receptor; globin; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX EP375408-A.  
 PN  
 XX 27-JUN-1990.  
 PD  
 XX 20-DEC-1989; 89EP-00313391.  
 PF  
 XX 20-DEC-1988; 88US-00287359.  
 PR  
 XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
 PA (HOGA/) HOGAN M E.  
 PA  
 XX Hogan ME, Kessler DJ;  
 PI  
 XX WPI; 1990-195509/26.  
 DR  
 XX Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming co-  
 PT linear triplex to control transcription process in gene-specific fashion.  
 PT  
 XX Claim 35; Page 30; 40pp; English.

XX Sequence forms triplex with the double stranded target sequence with G  
 CC binding to G-C and T to A-T. The strand runs 3' to 5' in an antiparallel  
 CC orientation and when targeted to a specific sequence will deactivate it.  
 CC This allows for growth inhibition in cancerous cells; manipulation of  
 CC cellular structural protein content; inhibition of IL-2 chain receptor;  
 CC disrupting plaque formation in Alzheimer's disease; inhibiting EGF gene;  
 CC modulating cholesterol synthesis through the HMGCoA gene; suppressing NGF  
 CC gene expression; arresting HSV-1 replication and suppressing Beta- globin  
 CC expression in thalassaemia and sickle cell anaemia patients. (Updated on  
 CC 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 XX  
 SQ Sequence 28 BP; 0 A; 0 C; 9 G; 19 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 2; Length 28;  
 Best Local Similarity 90.0%; Pred. No. 1.1e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20  
 Db 6 TTTTGGGGTTTGGGGTTT 25



```
RESULT 27
AAQ36268
ID AAQ36268 standard; DNA; 28 BP.
XX
AC AAQ36268;
XX
DT 25-MAR-2003 (revised)
DT 07-JUN-1993 (first entry)
XX
DE APP4par, targetted to a region of APP770 gene.
XX
KW Alzheimer's disease; amyloid precursor protein; plaque; triplex; target;
KW duplex; ss.
XX
OS Synthetic.
XX
PN US5176996-A.
XX
PD 05-JAN-1993.
XX
PF 22-DEC-1989; 89US-00453532.
XX
PR 20-DEC-1988; 88US-00287359.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI Hogan ME, Kessler DJ;
XX
WPI; 1993-035718/04.
XX
PT Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT which bind to target sequence in duplex DNA forming colinear triplex by
PT binding to major groove.
XX
PS Example 6; Col 22; 29pp; English.
XX
CC The APP770 gene is the precursor protein responsible for production of
CC plaque in Alzheimer's disease. Expression of this gene may be prevented
CC by the formation of a triplex between the duplex target DNA sequence and
CC an anti parallel or parallel synthetic oligonucleotide. A suitable target
CC sequence is that from base -434 to -407 of the APP770 gene and a suitable
CC antiparallel synthetic oligonucleotide sequence is shown. See also
CC AAQ36219-362. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 28 BP; 0 A; 0 C; 9 G; 19 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 2; Length 28;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
   ||||| ||||| ||||| |||||
Db 6 TTTTGGGGTTTGGGGTTT 25

RESULT 28
AAQ36269
ID AAQ36269 standard; DNA; 28 BP.
XX
AC AAQ36269;
XX
DT 25-MAR-2003 (revised)
DT 07-JUN-1993 (first entry)
XX
DE APP4anti, targetted to a region of APP770 gene.
XX
KW Alzheimer's disease; amyloid precursor protein; plaque; triplex; target;
KW 3'-5'; duplex; ss.
XX
OS Synthetic.
XX
PN US5176996-A.

Query Match 84.0%; Score 16.8; DB 2; Length 28;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
   ||||| ||||| ||||| |||||
Db 6 TTTTGGGGTTTGGGGTTT 25

RESULT 29
AAV17009/c
ID AAV17009 standard; DNA; 44 BP.
XX
AC AAV17009;
XX
DT 13-AUG-1998 (first entry)
XX
DE Telomerase substrate utilisation primer 28-30.
XX
KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN GB2317891-A.
XX
PD 08-APR-1998.
XX
PF 01-OCT-1997; 97GB-00020890.
XX
PR 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
```

PI Andrews WH;  
XX WPI; 1998-171633/16.  
XX  
XX Pure and recombinant human Telomerase Reverse Transcriptase and its  
PT variants - are useful in the diagnosis, prognosis and treatment of cell  
PT proliferation conditions especially cancer and ageing.  
XX  
XX Example 1; Page 200; 387pp; English.  
XX  
XX The present sequence represents a primer from the present invention which  
CC describes human telomerase reverse transcriptase (hTERT). The present  
CC invention also describes the following methods: (A) determining whether a  
CC test compound is a modulator of hTERT, by detecting the change in hTERT  
CC recombinant protein or polynucleotide, on administration of the compound;  
CC (B) preparation of recombinant telomerase by contacting a protein  
CC preparation of hTERT with a telomerase RNA component; (C) detection of the  
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample  
CC and detecting the complex formed or in the case of RNA detection,  
CC amplification the product with presence of hTERT in the sample; and (D)  
CC increasing the proliferation of a vertebrate cell by increasing hTERT  
CC expression; and (E) the use of an agent that causes an increase in cell  
CC vertebrate cell proliferation to create a medicament that inhibits  
CC ageing. A protein preparation of hTERT and the polynucleotide encoding  
CC hTERT can be used in the manufacture of medicaments for inhibiting the  
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used  
CC to treat conditions that are associated with high telomerase activity. A  
CC protein preparation of hTERT can also be used in the new methods  
XX  
XX Sequence 44 BP; 10 A; 10 C; 12 G; 12 T; 0 U; 0 Other;  
SQ  
Query Match 84.0%; Score 16.8; DB 2; Length 44;  
Best Local Similarity 90.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 20 TGTGGGGGTTTGGGGTTTT 1  
RESULT 30  
AAV17008/c  
ID AAV17008 standard; DNA; 46 BP.  
XX  
XX AAV17008;  
AC  
XX  
XX 13-AUG-1998 (first entry)  
DT  
XX  
XX Telomerase substrate utilisation primer 25-27.  
DE  
XX  
XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;  
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.  
XX  
XX Synthetic.  
OS  
XX Homo sapiens.  
XX  
XX GB2317891-A.  
PN  
XX  
XX 08-APR-1998.  
PD  
XX  
XX 01-OCT-1997; 97GB-00020890.  
XX  
XX 01-OCT-1996; 96US-00724643.  
PR 18-APR-1997; 97US-00844419.  
PR 25-APR-1997; 97US-00846017.  
PR 06-MAY-1997; 97US-00851843.  
PR 14-AUG-1997; 97US-00911312.  
PR 14-AUG-1997; 97US-00912951.  
PR 14-AUG-1997; 97US-00915503.  
XX  
XX (GERO-) GERON CORP.  
PA

PA (UYTE-) UNIV TECHNOLOGY CORP.  
XX  
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;  
PI Andrews WH;  
XX  
XX WPI; 1998-171633/16.  
DR  
XX  
XX Pure and recombinant human Telomerase Reverse Transcriptase and its  
PT variants - are useful in the diagnosis, prognosis and treatment of cell  
PT proliferation conditions especially cancer and ageing.  
XX  
XX Example 1; Page 200; 387pp; English.  
XX  
XX The present sequence represents a primer from the present invention which  
CC describes human telomerase reverse transcriptase (hTERT). The present  
CC invention also describes the following methods: (A) determining whether a  
CC test compound is a modulator of hTERT, by detecting the change in hTERT  
CC recombinant protein or polynucleotide, on administration of the compound;  
CC (B) preparation of recombinant telomerase by contacting a protein  
CC preparation of hTERT with a telomerase RNA component; (C) detection of the  
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample  
CC and detecting the complex formed or in the case of RNA detection,  
CC amplifying the product and correlating the presence of complex or  
CC amplification product with presence of hTERT in the sample; and (D)  
CC increasing the proliferation of a vertebrate cell by increasing hTERT  
CC expression; and (E) the use of an agent that causes an increase in cell  
CC vertebrate cell proliferation to create a medicament that inhibits  
CC ageing. A protein preparation of hTERT and the polynucleotide encoding  
CC hTERT can be used in the manufacture of medicaments for inhibiting the  
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used  
CC to treat conditions that are associated with high telomerase activity. A  
CC protein preparation of hTERT can also be used in the new methods  
XX  
XX Sequence 46 BP; 10 A; 12 C; 12 G; 12 T; 0 U; 0 Other;  
SQ  
Query Match 84.0%; Score 16.8; DB 2; Length 46;  
Best Local Similarity 90.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 22 TGTGGGGGTTTGGGGTTTT 3  
RESULT 31  
AAV17007/c  
ID AAV17007 standard; DNA; 48 BP.  
XX  
XX AAV17007;  
AC  
XX  
XX 13-AUG-1998 (first entry)  
DT  
XX  
XX Telomerase substrate utilisation primer 22-24.  
DE  
XX  
XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;  
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.  
XX  
XX Synthetic.  
OS  
XX Homo sapiens.  
XX  
XX GB2317891-A.  
PN  
XX  
XX 08-APR-1998.  
PD  
XX  
XX 01-OCT-1997; 97GB-00020890.  
XX  
XX 01-OCT-1996; 96US-00724643.  
PR 18-APR-1997; 97US-00844419.  
PR 25-APR-1997; 97US-00846017.  
PR 06-MAY-1997; 97US-00851843.  
PR 09-MAY-1997; 97US-00854050.  
PR 14-AUG-1997; 97US-00911312.  
PR 14-AUG-1997; 97US-00912951.  
PR 14-AUG-1997; 97US-00915503.  
XX  
XX (GERO-) GERON CORP.  
PA

```

PR 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
XX Example 1; Page 200; 387pp; English.
XX
XX The present sequence represents a primer from the present invention which
CC describes human telomerase reverse transcriptase (hTERT). The present
CC invention also describes the following methods: (A) determining whether a
CC test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX
XX Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
SQ
Query Match 84.0%; Score 16.8; DB 2; Length 48;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
Db | | | | | | | | | | | | | | | | | | | |
24 TGTGGGGGTTTGGGGTTT 5

RESULT 32
AAV17004/c
ID AAV17004 standard; DNA; 48 BP.
XX
XX AAV17004;
AC
XX
XX 13-AUG-1998 (first entry)
DT
XX
XX Telomerase substrate utilisation primer 13-15.
DE
XX
XX Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein; primer; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX GB2317891-A.
PN
XX
XX 08-APR-1998.
PD
XX
XX 01-OCT-1997; 97GB-00020890.
PF
XX
XX 01-OCT-1996; 96US-00724643.
PR
XX 18-APR-1997; 97US-00844419.
PR
XX 25-APR-1997; 97US-00846017.
PR
XX 06-MAY-1997; 97US-00851843.
PR

```

---

```

PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX WPI; 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
XX Example 1; Page 200; 387pp; English.
XX
XX The present sequence represents a primer from the present invention which
CC describes human telomerase reverse transcriptase (hTERT). The present
CC invention also describes the following methods: (A) determining whether a
CC test compound is a modulator of hTERT, by detecting the change in hTERT
CC recombinant protein or polynucleotide, on administration of the compound;
CC (B) preparation of recombinant telomerase by contacting a protein
CC preparation of hTERT with a telomerase RNA component; (C) detection of the
CC hTERT RNA or protein in a sample by binding a relevant probe to the sample
CC and detecting the complex formed or in the case of RNA detection,
CC amplifying the product and correlating the presence of complex or
CC increasing the proliferation of a vertebrate cell by increasing hTERT
CC expression; and (E) the use of an agent that causes an increase in cell
CC vertebrate cell proliferation to create a medicament that inhibits
CC ageing. A protein preparation of hTERT and the polynucleotide encoding
CC hTERT can be used in the manufacture of medicaments for inhibiting the
CC effect of ageing or cancer. Inhibitors of telomerase activity can be used
CC to treat conditions that are associated with high telomerase activity. A
CC protein preparation of hTERT can also be used in the new methods
XX
XX Sequence 48 BP; 10 A; 14 C; 12 G; 12 T; 0 U; 0 Other;
SQ
Query Match 84.0%; Score 16.8; DB 2; Length 48;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
Db | | | | | | | | | | | | | | | | | | | |
24 TGTGGGGGTTTGGGGTTT 5

RESULT 33
ABZ05743
ID ABZ05743 standard; DNA; 50 BP.
XX
XX ABZ05743;
AC
XX
XX 09-JAN-2003 (first entry)
DT
XX
XX Human leukocyte gene expression profiling probe SEQ ID NO 5734.
DE
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
XX Homo sapiens.
OS
XX WO200257414-A2.
PN
XX
XX 25-JUL-2002.
PD
XX
XX 22-OCT-2001; 2001WO-US047856.
PF
XX

```

```

PR 20-OCT-2000; 2000US-02411994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quettermous T, Johnson F;
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1; Page 513; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
XX Sequence 50 BP; 6 A; 6 C; 20 G; 18 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 6; Length 50;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
DB 14 TGTGGGTTTGGGGTTTT 33

RESULT 34
AAA39694/C
ID AAA39694 standard; DNA; 20 BP.
XX
XX AAA39694;
XX
XX 18-SEP-2000 (first entry)
XX
XX S. lemmnae alpha-tubulin telomerase primer DNA.
XX
XX Regulatory sequence; eukaryotic protist; telomere; alpha-tubulin; primer;
XX ss.
XX
XX Stylonychia lemnae.
XX
XX WO200023604-A1.
XX
XX 27-APR-2000.
XX
XX 20-OCT-1999; 99WO-EP007958.
XX
XX 21-OCT-1998; 98DE-01048485.
XX
XX 21-OCT-1998; 98DE-01048486.
XX
XX (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
XX Gallert K, Huels C, Muellner S, Steinbrueck G, Jacob NK;
XX WPI; 2000-339703/29.
XX
XX Expression vector functional in eukaryotic protist, useful for expression
XX of heterologous proteins, contains a coding sequence and regulatory
XX flanking regions from a protist.

PR 20-OCT-2000; 2000US-02411994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quettermous T, Johnson F;
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1; Page 513; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
XX Sequence 50 BP; 6 A; 6 C; 20 G; 18 T; 0 U; 0 Other;

Query Match 84.0%; Score 16.8; DB 6; Length 50;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
DB 14 TGTGGGTTTGGGGTTTT 33

RESULT 34
AAA39694/C
ID AAA39694 standard; DNA; 20 BP.
XX
XX AAA39694;
XX
XX 18-SEP-2000 (first entry)
XX
XX S. lemmnae expression vector construct primer XbaApatel.
XX
XX Regulatory sequence; eukaryotic protist; telomere; primer; ss.
XX
XX Stylonychia lemnae.
XX
XX WO200023604-A1.
XX
XX 27-APR-2000.
XX
XX 20-OCT-1999; 99WO-EP007958.
XX
XX 21-OCT-1998; 98DE-01048485.
XX
XX 21-OCT-1998; 98DE-01048486.
XX
XX (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
XX Gallert K, Huels C, Muellner S, Steinbrueck G, Jacob NK;
XX WPI; 2000-339703/29.
XX
XX Expression vector functional in eukaryotic protist, useful for expression
XX of heterologous proteins, contains a coding sequence and regulatory
XX flanking regions from a protist.

```

```

XX
XX Claim 4; Page 45; 51pp; German.
XX
XX This invention describes a novel expression vector (A) for eukaryotic
XX protists comprises a sequence (I) encoding a protein and having, at its
XX 3' and 5'-ends, native flanking regulatory sequences (RS) selected from
XX Stylonychia lemnae and with terminal telomeric sequences. (A) are used
XX for production of proteins in protists, particularly functional
XX heterologous proteins. (A) provide overexpression of foreign proteins in
XX protists, e.g. at 7-15% of total proteins. Eukaryotic protists can be
XX grown simply and on a large scale to high cell density with short
XX generation times and have metabolic and other properties similar to those
XX of multicellular organisms (contrast prokaryotes). In the macronucleus
XX genome of protists, most genes are amplified, resulting in high
XX expression rates even under normal conditions. This sequence represents a
XX primer used in the construction of the expression vector described in the
XX invention
XX
XX Sequence 20 BP; 8 A; 12 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGG 16
DB 16 TTTTGGGGTTTGGGG 1

RESULT 35
AAA39699/C
ID AAA39699 standard; DNA; 30 BP.
XX
XX AAA39699;
XX
XX 18-SEP-2000 (first entry)
XX
XX S. lemmnae expression vector construct primer XbaApatel.
XX
XX Regulatory sequence; eukaryotic protist; telomere; primer; ss.
XX
XX Stylonychia lemnae.
XX
XX WO200023604-A1.
XX
XX 27-APR-2000.
XX
XX 20-OCT-1999; 99WO-EP007958.
XX
XX 21-OCT-1998; 98DE-01048485.
XX
XX 21-OCT-1998; 98DE-01048486.
XX
XX (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
XX Gallert K, Huels C, Muellner S, Steinbrueck G, Jacob NK;
XX WPI; 2000-339703/29.
XX
XX Expression vector functional in eukaryotic protist, useful for expression
XX of heterologous proteins, contains a coding sequence and regulatory
XX flanking regions from a protist.
XX
XX Example 1; Page 27; 51pp; German.
XX
XX This invention describes a novel expression vector (A) for eukaryotic
XX protists comprises a sequence (I) encoding a protein and having, at its
XX 3' and 5'-ends, native flanking regulatory sequences (RS) selected from
XX Stylonychia lemnae and with terminal telomeric sequences. (A) are used
XX for production of proteins in protists, particularly functional
XX heterologous proteins. (A) provide overexpression of foreign proteins in
XX protists, e.g. at 7-15% of total proteins. Eukaryotic protists can be
XX grown simply and on a large scale to high cell density with short
XX generation times and have metabolic and other properties similar to those

```

CC of multicellular organisms (contrast prokaryotes). In the macronucleus  
CC genome of protists, most genes are amplified, resulting in high  
CC expression rates even under normal conditions. This sequence represents a  
CC primer used in the construction of the expression vector described in the  
CC invention  
XX

SQ Sequence 30 BP; 10 A; 13 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 80.0%; Score 16; DB 3; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGG 16  
| | | | | | | | | |  
Db 28 TTTTGGGGTTTGGG 13

RESULT 36  
ADV45884/c  
ID ADV45884 standard; DNA; 19 BP.  
XX  
AC ADV45884;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE Human CpG site probe SEQ ID NO 1411.  
XX  
DE DNA methylation; ss; probe; cancer; neoplasm; squamous cell carcinoma.  
XX  
OS Homo sapiens.  
XX  
PN WC2004110246-A2.  
XX  
PD 23-DEC-2004.  
XX  
PF 14-MAY-2004; 2004WO-US015382.  
XX  
PR 15-MAY-2003; 2003US-0471488P.  
XX  
PA (ILLU-) ILLUMINA INC.  
XX  
PI Fan J, Bibikova M;  
XX  
DR WPI; 2005-057693/06.  
XX

PS Identifying differentially methylated genomic CpG dinucleotide sequences  
PT associated with cancer, comprises measuring level of methylated genomic  
PT CpG dinucleotide sequences for genomic targets in sample and comparing to  
PT reference level.  
XX  
PS Claim 28; SEQ ID NO 1411; 89pp; English.  
XX

CC The invention relates to a method of identifying differentially  
CC methylated genomic CpG dinucleotide sequences associated with cancer,  
CC comprising measuring the level of methylated genomic CpG dinucleotide  
CC sequences for two or more of the genomic targets in sample, and comparing  
CC the level of methylation at genomic CpG dinucleotide sequences in the  
CC sample to a reference level of methylated genomic CpG dinucleotide  
CC sequences. The method is useful for identifying differentially methylated  
CC genomic CpG dinucleotide sequences associated with cancer in an  
CC individual. The level of methylation of the differentially methylated  
CC genomic CpG dinucleotide sequences is used to diagnose cancer in the  
CC individual, predict the course of cancer, predict the susceptibility of  
CC cancer, stage the progression of cancer, predict the likelihood of  
CC overall survival, and predict the likelihood of recurrence of cancer for  
CC individual. The level of methylation of the differentially methylated  
CC genomic CpG dinucleotide sequences in the sample is also used to  
CC determine the effectiveness of a treatment course undergone by the  
CC individual. The cancer is preferably adenocarcinoma or squamous cell  
CC carcinoma. The probes are useful for detecting methylation of genomic CpG  
CC dinucleotide sequences of two or more genomic targets. The present  
CC sequence represents a CpG site probe.  
XX

SQ Sequence 19 BP; 11 A; 8 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 77.0%; Score 15.4; DB 14; Length 19;  
Best Local Similarity 94.1%; Pred. No. 3.9e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTGGGGTTT 20  
| | | | | | | | | |  
Db 19 TGGGGTTTGGGGTTT 3

RESULT 37  
ACF58129  
ID ACF58129 standard; DNA; 43 BP.  
XX  
AC ACF58129;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE HLTF non-methylation-specific PCR forward primer.  
XX  
KW Disease diagnostic; CpG; nucleic acid amplification; cancer detection;  
KW p14; HLTF; MINT31; MINT2; methylation; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WC2003087390-A2.  
XX  
PD 23-OCT-2003.  
XX  
PF 11-APR-2003; 2003WO-US011023.  
XX  
PR 11-APR-2002; 2002US-00123071.  
XX  
PA (EXAC-) EXACT SCI CORP.  
XX  
PI Shuber AP;  
XX  
DR WPI; 2003-845337/78.  
XX

PT Detecting an indicium of a disease in a heterogeneous biological sample  
PT comprises contacting the nucleic acid sample with an agent that modifies  
PT unmethylated cytosine, and detecting hypermethylated or hypomethylated  
PT nucleic acid.  
XX

PS Example 4; Page 17; Opp; English.  
XX

CC The invention relates to detecting an indicium of a disease in a  
CC heterogeneous biological sample. The method involves (a) isolating a  
CC heterogeneous nucleic-acid sample comprising a CpG-containing target  
CC template from a heterogeneous biological sample; (b) contacting the  
CC nucleic acid sample with an agent that modifies unmethylated cytosine;  
CC (c) performing an amplification reaction on the target template using at  
CC least one chimeric primer that comprises a first portion that is not  
CC specific for the target template and a second portion 3' to the first  
CC portion, where the second portion is specific for the CpG-containing  
CC target template if the template comprises an unmethylated cytosine at a  
CC predetermined position; and (d) detecting the presence of an  
CC amplification product as an indicium of a disease. The method is useful  
CC for detecting indicia of cancer in a biological sample, for detecting  
CC abnormal methylation in a homogenous sample, such as a biopsy sample. The  
CC method is especially suitable in clinical assays involving sporadic  
CC cancer detection, for infectious disease diagnostics, or inherited  
CC disease diagnostics. The new method makes it possible to detect a disease  
CC in a biological sample without using an invasive procedure. Sequences  
CC ACF58127-134 represent non-methylation-specific primer used for PCR  
CC assaying of hypermethylation markers on genes p14, HLTF, MINT31 and  
CC MINT2, used in detection of hypermethylation at multiple loci, which  
CC indicate a higher risk of colorectal cancer  
XX

SQ Sequence 43 BP; 4 A; 5 C; 16 G; 18 T; 0 U; 0 Other;  
Query Match 77.0%; Score 15.4; DB 10; Length 43;

Best Local Similarity 94.1%; Pred. No. 4e+03; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTGGGGTTT 20  
 |||||  
 Db 20 TGGGGTTTGGGGTTT 36

RESULT 38  
 ADW84828/c  
 ID ADW84828 standard; DNA; 20 BP.  
 AC ADW84828;  
 XX  
 DT 07-APR-2005 (first entry)  
 XX  
 DE MAP3K9 marker amplification reverse primer #1146.  
 XX  
 KW mixed lineage kinase; MLK; asthma; at-risk haplotype; MAP3K9;  
 KW antiasthmatic; respiratory-gen.; antiinflammatory; antirheumatic;  
 KW antiarthritic; antipsoriatic; neuroprotective; gastrointestinal-gen.;  
 KW respiratory disease; chronic obstructive pulmonary disease;  
 KW chronic bronchitis; inflammation; ss; primer; PCR.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2005007144-A2.  
 XX  
 PD 27-JAN-2005.  
 XX  
 PF 14-JUL-2004; 2004WO-US022446.  
 XX  
 PR 14-JUL-2003; 2003US-0487072P.  
 PR 05-APR-2004; 2004US-0559611P.  
 XX  
 PA (DECO-) DECODE GENETICS EHF.  
 XX  
 PI Hakonarson H, Gurney ME, Halapi E;  
 XX  
 DR WPI; 2005-122681/13.  
 XX  
 PT Use of mixed lineage kinase family kinase inhibitor in the manufacture of  
 PT a medicament for treatment of asthma associated at-risk haplotype for  
 PT asthma, at-risk haplotype in MAP3K9 gene or increased MLK1 protein  
 PT expression or activity.  
 XX  
 PS Disclosure; Fig 12; 640pp; English.  
 XX  
 CC The invention relates to the novel use of a mixed lineage kinase (MLK)  
 CC family kinase inhibitor for treating asthma. Where the asthma is  
 CC associated with a risk factor selected from an at-risk haplotype for  
 CC asthma, at-risk haplotype in MAP3K9 gene, polymorphism in MAP3K9 nucleic  
 CC acid, dysregulation of MAP3K9 mRNA expression, dysregulation of a MAP3K9  
 CC mRNA isoform, and/or increased MLK1 protein expression. The invention  
 CC further comprises: a method for the diagnosis or identification of  
 CC susceptibility to asthma; a method for the use of a first nucleic acid  
 CC molecule for diagnosing asthma or susceptibility to asthma in a sample; a  
 CC method for assaying the presence of a first nucleic acid molecule in a  
 CC sample; a method for assessing the response to treatment with an MLK  
 CC family kinase nucleic acid inhibitor in a target population or in an  
 CC individual with an at-risk haplotype for asthma, at-risk haplotype in the  
 CC MAP3K9 gene, polymorphism in the MAP3K9 nucleic acid, dysregulation of  
 CC MAP3K9 mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased  
 CC MLK1 protein expression, increased MLK1 biochemical activity or increased  
 CC MLK1 protein isoform expression; a method for assessing the response to  
 CC treatment with an MLK1 inhibitor in a target population including an  
 CC individual with an at-risk haplotype for asthma, as above; a kit for  
 CC assaying a sample for the presence or absence of at least one haplotype  
 CC comprising 2 or more alleles associated with asthma comprising: at least  
 CC one nucleic acid capable of detecting the presence or absence of at least  
 CC one specific allele; a reagent kit for assaying the presence of at least  
 CC one haplotype comprising 2 or more alleles comprising: at least one  
 CC labeled nucleic acid capable of detecting at least one specific allele of

CC the haplotype, and reagents for detection of the label; and a reagent kit  
 CC for assaying a sample for the presence of at least one haplotype  
 CC comprising 2 or more alleles comprising: at least one nucleic acid  
 CC complementary to a part of nucleotide sequence that is at least partially  
 CC acting as a primer for a primer extension reaction and capable of  
 CC detecting 2 or more specific alleles of the haplotype. The MLK family  
 CC kinase inhibitor has the following activities: antiasthmatic, respiratory  
 CC -gen., antiinflammatory, antirheumatic, antiarthritic, antipsoriatic,  
 CC neuroprotective, and gastrointestinal-gen. The MLK family kinase  
 CC inhibitor is useful for the treatment of asthma associated with a risk  
 CC factor selected from at-risk haplotype for asthma, at-risk haplotype in  
 CC MAP3K9 gene, polymorphism in MAP3K9 nucleic acid, dysregulation of MAP3K9  
 CC mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased MLK1  
 CC protein expression, increased MLK1 biochemical activity and/or increased  
 CC MLK1 protein isoform expression; and in diagnosis or identification of  
 CC susceptibility to asthma. The inhibitor is also useful for the treatment  
 CC of other respiratory diseases associated with MAP3K9 or other members of  
 CC the JNK pathway such as chronic obstructive pulmonary disease, chronic  
 CC bronchitis and other inflammatory diseases such as rheumatoid arthritis,  
 CC psoriasis, multiple sclerosis and inflammatory bowel disease. This  
 CC polynucleotide sequence represents a reverse primer which is used in  
 CC amplifying a marker of the MAP3K9 kinase, where MAP3K9 is a part of  
 CC Mitogen-Activated Protein Kinase (MAPK) signal transduction pathways, of  
 CC the invention.  
 XX  
 SQ Sequence 20 BP; 11 A; 8 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 14; Length 20;  
 Best Local Similarity 85.0%; Pred. No. 4.7e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20  
 |||||  
 Db 20 TTGTGGTGTGGGGATT 1

RESULT 39  
 AEA51773  
 ID AEA51773 standard; DNA; 22 BP.  
 XX  
 AC AEA51773;  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE Prostate cancer gene PCR primer SEQ ID NO 376.  
 XX  
 KW gene expression; cell proliferation; hyperproliferation; cytostatic;  
 KW neoplasm; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005054517-A2.  
 XX  
 PD 16-JUN-2005.  
 XX  
 PF 01-DEC-2004; 2004WO-US040289.  
 XX  
 PR 01-DEC-2003; 2003EP-00090414.  
 PR 10-FEB-2004; 2004EP-00090040.  
 PR 10-MAY-2004; 2004EP-00090187.  
 PR 21-JUL-2004; 2004EP-00090292.  
 XX  
 PA (EPIC-) EPICENOMICS AG.  
 XX  
 PI Day KJ, Cottrell S, Distler J, Morotti A, Yamamura S, Dekker S;  
 PI Ocamp Y, Devos T;  
 XX  
 DR WPI; 2005-425434/43.  
 XX  
 PT Detecting and/or differentiating prostate cell proliferative disorders in  
 PT a subject by contacting genomic with reagent(s) that distinguishes  
 PT between methylated and non-methylated CpG dinucleotides in target nucleic



```
QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 2 TTTAGGGGTTTAGGGGTTT 21

RESULT 42
ABZ01038
ID ABZ01038 standard; DNA; 50 BP.
XX
AC ABZ01038;
XX
DT 09-JAN-2003 (first entry)
XX
DE Human leukocyte gene expression profiling probe SEQ ID NO 1029.
XX
KW T7; leukocyte; gene expression profiling; allograft rejection;
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200257414-A2.
XX
PD 25-JUL-2002.
XX
PF 22-OCT-2001; 2001WO-US047856.
XX
PR 20-OCT-2000; 2000US-0241994P.
PR 08-JUN-2001; 2001US-0296764P.
XX
PA (BIOC-) BIOCARDIA INC.
XX
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
PI Ly N, Woodward R, Quertermous T, Johnson F;
DR WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
PT or congestive heart failure, comprises diagnostic oligonucleotides.
XX
PS Claim 1; Page 357; Opp; English.
XX
CC The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 13 A; 6 C; 14 G; 17 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 6; Length 50;
Best Local Similarity 85.0%; Pred. No. 4.9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 9 TTTTGTATTGGGGTTTT 28

RESULT 43
AAF99500
ID AAF99500 standard; DNA; 24 BP.
XX
AC AAF99500;
XX
DE Immunostimulatory nucleic acid #794.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #616.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 52; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 24 BP; 0 A; 0 C; 7 G; 17 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 4; Length 24;
Best Local Similarity 88.9%; Pred. No. 6.9e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 18
Db 7 TTTTGTGGTTTGTGGTT 24

RESULT 44
AAF99678
ID AAF99678 standard; DNA; 24 BP.
XX
AC AAF99678;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #794.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
XX
```



KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
XX Synthetic.  
OS  
XX WO200122972-A2.  
PN  
XX  
XX  
PD 05-APR-2001.  
XX  
XX 25-SEP-2000; 2000WO-US026383.  
PF  
XX  
XX 25-SEP-1999; 99US-0156113P.  
PR  
XX 27-SEP-1999; 99US-0156135P.  
PR  
XX 23-AUG-2000; 2000US-0227436P.  
PR  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA (COLE-) COLEY PHARM GMBH.  
XX  
XX Krieg AM, Schetter C, Vollmer J;  
XX WPI; 2001-273485/28.  
DR  
XX  
XX Vaccinating against tumors, infectious diseases, allergies and asthma  
PT using immunostimulatory Py-rich and TG nucleic acids.  
XX  
XX Claim 101; Page 55; 338pp; English.  
PS  
XX The present invention relates to a method for stimulating an immune  
CC response. The method comprises administering an immunostimulatory nucleic  
CC acid to a non-rodent subject in sufficient quantity to stimulate an  
CC immune response. The present sequence is one such immunostimulatory  
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
CC also useful for preventing cancer, asthma, infectious disease, allergy or  
CC immune deficiency. The present sequence can also be used to redirect a  
CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
CC present sequence may have a phosphorothioate backbone  
XX  
XX Sequence 24 BP; 0 A; 2 C; 8 G; 14 T; 0 U; 0 Other;  
SQ

Query Match 74.0%; Score 14.8; DB 4; Length 24;  
Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 18  
||||| ||||||| |||||  
Db 7 TTTTGGGGTTTGGGGTTT 24

RESULT 45  
AAF99498  
ID AAF99498 standard; DNA; 24 BP.  
XX  
AC AAF99498;  
XX  
DT 12-JUN-2001 (first entry)  
XX  
XX Immunostimulatory nucleic acid #614.  
DE  
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
KW immunostimulatory; tumour; viral infection; bacterial infection;  
KW fungal infection; parasitic infection; cancer; asthma;  
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
XX  
OS Synthetic.  
XX  
XX WO200122972-A2.  
FN  
XX  
XX 05-APR-2001.  
PD  
XX

PF 25-SEP-2000; 2000WO-US026383.  
XX  
XX 25-SEP-1999; 99US-0156113P.  
PR  
XX 27-SEP-1999; 99US-0156135P.  
PR  
XX 23-AUG-2000; 2000US-0227436P.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA (COLE-) COLEY PHARM GMBH.  
XX  
XX Krieg AM, Schetter C, Vollmer J;  
XX WPI; 2001-273485/28.  
DR  
XX  
XX Vaccinating against tumors, infectious diseases, allergies and asthma  
PT using immunostimulatory Py-rich and TG nucleic acids.  
XX  
XX Claim 101; Page 52; 338pp; English.  
PS  
XX The present invention relates to a method for stimulating an immune  
CC response. The method comprises administering an immunostimulatory nucleic  
CC acid to a non-rodent subject in sufficient quantity to stimulate an  
CC immune response. The present sequence is one such immunostimulatory  
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
CC also useful for preventing cancer, asthma, infectious disease, allergy or  
CC immune deficiency. The present sequence can also be used to redirect a  
CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
CC present sequence may have a phosphorothioate backbone  
XX  
XX Sequence 24 BP; 0 A; 1 C; 7 G; 16 T; 0 U; 0 Other;  
SQ

Query Match 74.0%; Score 14.8; DB 4; Length 24;  
Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 18  
||||| ||||||| |||||  
Db 7 TTTTGGGGTTTGGGGTTT 24

RESULT 46  
AAF61386  
ID AAF61386 standard; DNA; 24 BP.  
XX  
AC AAF61386;  
XX  
DT 04-JUN-2001 (first entry)  
XX  
XX Strand displacement amplification reporter primer SEQ ID 4.  
DE  
XX Strand displacement amplification; primer; detection; probe; reporter;  
KW fluorescent donor; quencher dye; ss.  
XX  
XX Unidentified.  
OS  
XX EP1087020-A2.  
FN  
XX 28-MAR-2001.  
PD  
XX 23-AUG-2000; 2000EP-00118032.  
PF  
XX 27-SEP-1999; 99US-00406074.  
PR  
XX (BECT ) BECTON DICKINSON & CO.  
PA  
XX Nadeau JG, Linn CP, Pitner JB, Dean CH, Walker GT;  
PI WPI; 2001-259636/27.  
XX  
XX

PT Novel signal primer for detecting nucleic acid target sequences by  
PT fluorescence quenching mechanisms, comprising a reporter probe and an  
PT adaptor oligonucleotide hybridized to the probe.

XX Example 2; Page 11; 16pp; English.

XX This invention describes a novel signal primer (I) comprising a reporter  
CC probe (II) and an adapter oligonucleotide (III) hybridized to (II), such  
CC that (I) comprises intermolecularly base-paired portion and a single-  
CC stranded target binding sequence. (I) comprises (II), which in the  
CC absence of hybridization to a complementary sequence assumes a  
CC conformational structure which brings a fluorescent donor/quencher dye  
CC pair linked to it into sufficiently close spatial proximity to quench  
CC donor fluorescence, and an adapter oligonucleotide (III) hybridized to  
CC (II), such that (I) comprises an intermolecularly base-paired portion and  
CC a single-stranded target binding sequence. (I) is useful for detecting a  
CC nucleic acid target sequence: (I) by: (a) hybridizing with the target  
CC sequence such that formation of a secondary structure is substantially  
CC prevented; (b) separating (II) from (III) in a target-dependent manner;  
CC and (c) detecting the formation of secondary structure as an indication  
CC of the presence of the target sequence; or (2) by: (a) hybridizing (I) to  
CC the target sequence, where (I) comprises an adapter oligonucleotide  
CC hybridized to a second oligonucleotide complementary to (I) which forms a  
CC secondary structure when not hybridized to a complementary sequence; (b)  
CC separating the second oligonucleotide from (III) in a target-dependent  
CC manner; and (c) detecting the hybridization of second oligonucleotide to  
CC (I) as an indication of the presence of target sequence. Detection of a  
CC variety of different targets is simplified as the adapter polynucleotide  
CC to which the second oligonucleotide hybridizes comprises a sequence which  
CC does not hybridize to the target, as a result the 5' adapter sequence may  
CC be selected such that it is the same in a variety of adapter  
CC oligonucleotides with different target binding sequences. A single  
CC labeled reporter probe may be used for detection of a variety of  
CC different target sequences. The adapter oligonucleotides are easier, and  
CC less costly, to synthesize than reporter probes as they do not require  
CC labeling for use

XX Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 5; Length 24;  
Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTGGGGTTTGGGTTT 19

DB 4 TTTGGGGTTTGGGTTT 21

RESULT 47

ABS78208

ID ABS78208 standard; DNA; 24 BP.

XX ABS78208;

XX 13-DEC-2002 (first entry)

DE Angiogenesis inhibitory oligonucleotide #692.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophiliac joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.

XX Synthetic.

XX WO200253141-A2.

XX 11-JUL-2002.

XX

PF 14-DEC-2001; 2001WO-US048458.

XX

PR 14-DEC-2000; 2000US-0255534P.

XX

PA (COLE-) COLEY PHARM GROUP INC.

XX

PI Bratzler RL;

XX

DR WPI; 2002-566690/60.

XX

PT Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.

PS Claim 2; Page 31; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention

XX Sequence 24 BP; 0 A; 1 C; 7 G; 16 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 6; Length 24;

Best Local Similarity 88.9%; Pred. No. 6.9e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGTTT 18

DB 7 TTTTGGGGTTTGGGTTT 24

RESULT 48

ABS78399

ID ABS78399 standard; DNA; 24 BP.

XX

AC ABS78399;

XX

DT 13-DEC-2002 (first entry)

XX

DE Angiogenesis inhibitory oligonucleotide #883.

XX

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophiliac joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.

XX Synthetic.

XX WO200253141-A2.

PN

PD 11-JUL-2002.

XX

PF 14-DEC-2001; 2001WO-US048458.

XX

PR 14-DEC-2000; 2000US-0255534P.

XX

PA (COLE-) COLEY PHARM GROUP INC.

XX

PI Bratzler RL;

XX WPI; 2002-566690/60.  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 XX Claim 2; Page 35; 276pp; English.  
 XX The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma, and  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX Sequence 24 BP; 0 A; 2 C; 8 G; 14 T; 0 U; 0 Other;  
 SQ  
 Query Match 74.0%; Score 14.8; DB 6; Length 24;  
 Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1 TTTTGGGGTTTGGGTT 18  
 7 TTTTGGGGTTTGGGTT 24  
 QY  
 DB  
 RESULT 49  
 ABS78210  
 ID ABS78210 standard; DNA; 24 BP.  
 XX  
 AC ABS78210;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Angiogenesis inhibitory oligonucleotide #694.  
 XX  
 DE Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KW plaque neovascularisation; telangiectasia; haemophilic joint;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200253141-A2.  
 XX  
 XX 11-JUL-2002.  
 XX  
 XX 14-DEC-2001; 2001WO-US048458.  
 XX  
 XX 14-DEC-2000; 2000US-0255534P.  
 XX (COLE-) COLEY PHARM GROUP INC.  
 XX Bratzler RL;  
 XX  
 XX WPI; 2002-566690/60.  
 XX  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 XX Claim 2; Page 31; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma, and  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX Sequence 24 BP; 0 A; 0 C; 7 G; 17 T; 0 U; 0 Other;  
 SQ  
 Query Match 74.0%; Score 14.8; DB 6; Length 24;  
 Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1 TTTTGGGGTTTGGGTT 18  
 7 TTTTGGGGTTTGGGTT 24  
 QY  
 DB  
 RESULT 50  
 ABL39306  
 ID ABL39306 standard; DNA; 24 BP.  
 XX  
 AC ABL39306;  
 XX  
 DT 16-APR-2002 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid SEQ ID NO: 735.  
 XX  
 KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
 KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..24  
 FT /\*tag= a  
 FT /mcd\_base= OTHER  
 FT /note= "phosphorothioate backbone"  
 XX WO200197843-A2.  
 XX  
 XX 27-DEC-2001.  
 XX  
 XX 22-JUN-2001; 2001WO-US020154.  
 XX  
 XX 22-JUN-2000; 2000US-0213346P.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 XX Weiner G, Hartmann G;  
 XX WPI; 2002-154611/20.  
 XX  
 XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
 PT administering immunostimulatory nucleic acids that induce expression of  
 PT cell surface antigens and antibodies to a subject having or at risk of  
 PT developing cancer.  
 XX  
 XX Disclosure; Page 283; 312pp; English.  
 XX  
 XX The present invention relates to methods for treating or preventing  
 CC cancer, involving administering to a subject having or at risk of  
 CC developing cancer immunostimulatory nucleic acids that induce expression  
 CC of cell surface antigens and antibodies. The methods are useful for

CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention

XX

SQ Sequence 24 BP; 0 A; 2 C; 8 G; 14 T; 0 U; 0 Other;

Query Match 74.0%; Score 14.8; DB 6; Length 24;  
Best Local Similarity 88.9%; Pred. No. 6.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTT 18  
      |||||  
Db 7 TTTTGGGGTTTGGGGTT 24

Search completed: February 15, 2006, 18:06:46  
Job time : 161.744 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:07:43 ; Search time 1330.25 Seconds  
(without alignments)  
703.434 Million cell updates/sec

Title: US-09-669-187A-73  
Perfect score: 20  
Sequence: 1 ttttgggttttgggggtttt 20

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database :

EST:.\*  
1: gb\_est1:.\*  
2: gb\_est2:.\*  
3: gb\_est3:.\*  
4: gb\_est4:.\*  
5: gb\_est5:.\*  
6: gb\_est6:.\*  
7: gb\_est7:.\*  
8: gb\_est8:.\*  
9: gb\_est9:.\*  
10: gb\_est10:.\*  
11: gb\_est11:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.8	84.0	37	6	CF301952 7LEAF--07
C 2	16	80.0	37	1	AA916364 Q29509.5
C 3	16	80.0	43	1	AI813791 WK79107.x
C 4	15.2	76.0	31	1	AI468834
C 5	14.8	74.0	31	10	AL756692 Arabidops
C 6	14.8	74.0	32	9	AZ794869 2M0048017
C 7	14.4	72.0	27	9	AZ807733 2M0070H16
C 8	14.4	72.0	39	10	AJ590961 Arabidops
C 9	14.4	72.0	40	1	AI671079 t217H03.x
C 10	14.4	72.0	46	1	AI264859 qx66h12.x
C 11	14.4	72.0	46	1	AI564592 tp98409.x
C 12	14.4	72.0	48	10	CZ918128 4021008B1
C 13	14.4	72.0	49	1	AI475390 t182G01.x
C 14	14.4	72.0	49	10	AL943577 Arabidops
C 15	14.4	72.0	50	10	CZ559680 FL00447-5
C 16	14.2	71.0	33	10	BX535866 Arabidops
C 17	14.2	71.0	37	11	CG722753 1119073D0
C 18	14.2	71.0	43	10	CG722753 1119073D0
C 19	14.2	71.0	50	10	CZ470781 C06535-5D
C 20	14.2	71.0	50	10	CG729919 111311E50
C 21	13.8	69.0	31	10	AL940076 Arabidops
C 22	13.8	69.0	46	8	H71330 yu55d08.sl

c 96	12.6	63.0	46	1	AV966826	AV966826	169	12	60.0	39	1	AL041218	AL041218	DKF2p434J
c 97	12.6	63.0	47	3	CC897341	CC897341	170	12	60.0	39	1	AV949716	AV949716	AV949716
c 98	12.6	63.0	48	3	BJ040279	BJ040279	171	12	60.0	39	1	AZ767935	AZ767935	IM0567E12
c 99	12.6	63.0	49	8	D20657	D20657	c 172	12	60.0	39	11	DR42B18T	DR42B18T	AL974899
c 100	12.6	63.0	50	9	BH855874	BH855874	c 173	12	60.0	40	1	AI362383	AI362383	qu55h04.x
c 101	12.6	63.0	50	1	AU107052	AU107052	c 174	12	60.0	40	1	AI560710	AI560710	tq55e01.x
c 102	12.6	63.0	50	1	AU107060	AU107060	175	12	60.0	40	9	BH146179	BH146179	BG02782-5
c 103	12.6	63.0	50	3	BM069725	BM069725	c 176	12	60.0	40	10	C2484867	C2484867	f02361-5p
c 104	12.6	63.0	50	6	CA339922	CA339922	c 177	12	60.0	40	10	BX127424	BX127424	Danio rer
c 105	12.4	62.0	19	1	AI641650	AI641650	c 178	12	60.0	41	9	AZ655083	AZ655083	IM0529C19
c 106	12.4	62.0	25	9	AZ377955	AZ377955	c 179	12	60.0	41	9	BX242916	BX242916	Danio rer
c 107	12.4	62.0	34	1	AA932536	AA932536	180	12	60.0	42	9	AZ625468	AZ625468	IM0464N22
c 108	12.4	62.0	42	8	DN955340	DN955340	c 181	12	60.0	42	10	BX163193	BX163193	Danio rer
c 109	12.4	62.0	46	1	AI719194	AI719194	c 182	12	60.0	43	1	AA878752	AA878752	of85d03.s
c 110	12.4	62.0	49	9	AZ579577	AZ579577	183	12	60.0	43	7	CN546803	CN546803	EST.18574
c 111	12.2	61.0	23	9	AZ779474	AZ779474	184	12	60.0	44	9	AZ433032	AZ433032	IM0218M12
c 112	12.2	61.0	26	5	C21526	C21526	185	12	60.0	44	9	AZ504238	AZ504238	IM0344A23
c 113	12.2	61.0	29	9	AZ414397	AZ414397	186	12	60.0	45	2	BE336369	BE336369	601086943
c 114	12.2	61.0	30	9	AZ513419	AZ513419	187	12	60.0	45	9	BH853498	BH853498	SALK.0770
c 115	12.2	61.0	30	10	CZ489705	CZ489705	188	12	60.0	45	10	AJ598952	AJ598952	Arabidops
c 116	12.2	61.0	31	1	AA937745	AA937745	c 189	12	60.0	45	10	BX219077	BX219077	Danio rer
c 117	12.2	61.0	31	1	AI768947	AI768947	c 190	12	60.0	46	1	AI223398	AI223398	qx12h07.x
c 118	12.2	61.0	33	9	AZ320037	AZ320037	c 191	12	60.0	46	1	AI471447	AI471447	Em11f04.x
c 119	12.2	61.0	38	9	BZ291479	BZ291479	c 192	12	60.0	46	1	AI749628	AI749628	at25d10.x
c 120	12.2	61.0	39	9	CC057363	CC057363	193	12	60.0	46	9	AZ767539	AZ767539	IM0566H17
c 121	12.2	61.0	40	1	AA876140	AA876140	c 194	12	60.0	47	9	AZ639767	AZ639767	IM0501K24
c 122	12.2	61.0	40	10	BX227306	BX227306	c 195	12	60.0	47	10	BX121950	BX121950	Danio rer
c 123	12.2	61.0	41	9	BH861613	BH861613	196	12	60.0	48	1	AJ663346	AJ663346	Arabidops
c 124	12.2	61.0	42	9	BH791460	BH791460	197	12	60.0	48	9	AZ514368	AZ514368	IM0361D04
c 125	12.2	61.0	43	9	AZ860401	AZ860401	c 198	12	60.0	48	9	BZ354073	BZ354073	SALK.1225
c 126	12.2	61.0	45	10	CZ469757	CZ469757	199	12	60.0	49	1	AA954745	AA954745	on56a04.s
c 127	12.2	61.0	47	9	AZ805016	AZ805016	c 200	12	60.0	49	1	AI056265	AI056265	oz02e04.x
c 128	12.2	61.0	48	9	AZ949234	AZ949234	c 201	12	60.0	49	1	AI587491	AI587491	tr51d10.x
c 129	12.2	61.0	49	1	AI005607	AI005607	c 202	12	60.0	49	1	AI744850	AI744850	tr16a04.x
c 130	12.2	61.0	49	9	BH630562	BH630562	c 203	12	60.0	49	5	BQ625383	BQ625383	rd92f01.y
c 131	12.2	61.0	50	1	AU104045	AU104045	204	12	60.0	49	10	CZ490512	CZ490512	f07777-5p
c 132	12.2	61.0	50	1	AW643187	AW643187	c 205	12	60.0	50	1	AU103941	AU103941	Arabidops
c 133	12	60.0	19	1	AA248820	AA248820	206	12	60.0	50	1	AU107056	AU107056	Danio rer
c 134	12	60.0	22	1	AA999803	AA999803	c 207	12	60.0	50	2	BG538913	BG538913	602568565
c 135	12	60.0	22	9	AZ844290	AZ844290	c 208	12	60.0	50	2	BE887296	BE887296	601510120
c 136	12	60.0	25	2	BG244523	BG244523	c 209	12	60.0	50	3	BX125541	BX125541	rc69f06.y
c 137	12	60.0	25	10	AJ590986	AJ590986	210	12	60.0	50	5	BQ724604	BQ724604	EC724604
c 138	12	60.0	26	1	AI288386	AI288386	211	12	60.0	50	9	BZ378836	BZ378836	SALK.1120
c 139	12	60.0	28	1	AI376644	AI376644	c 212	12	60.0	50	10	AL948306	AL948306	Arabidops
c 140	12	60.0	28	1	AI376644	AI376644	c 213	12	60.0	50	10	BX198108	BX198108	Danio rer
c 141	12	60.0	28	11	TA3236A02P	TA3236A02P	c 214	12	60.0	50	11	CR155014	CR155014	Forward s
c 142	12	60.0	29	10	AJ589262	AJ589262	c 215	11.8	59.0	21	9	AZ447989	AZ447989	IM045UJ19
c 143	12	60.0	30	5	BX569324	BX569324	c 216	11.8	59.0	21	9	AZ991107	AZ991107	2M0275E08
c 144	12	60.0	30	10	CZ475631	CZ475631	c 217	11.8	59.0	24	5	BQ589506	BQ589506	E012561-0
c 145	12	60.0	31	1	AI735691	AI735691	c 218	11.8	59.0	25	9	AZ462617	AZ462617	IM0269A11
c 146	12	60.0	31	9	AZ792134	AZ792134	c 219	11.8	59.0	27	9	AZ846947	AZ846947	2M0147P15
c 147	12	60.0	31	9	AZ801379	AZ801379	c 220	11.8	59.0	28	1	AI912424	AI912424	tz05606.x
c 148	12	60.0	32	1	AV959908	AV959908	c 221	11.8	59.0	31	1	AI560864	AI560864	tq4a06.x
c 149	12	60.0	32	9	AZ465507	AZ465507	c 222	11.8	59.0	31	2	BE308892	BE308892	601096108
c 150	12	60.0	32	9	AZ610577	AZ610577	223	11.8	59.0	36	9	AZ458941	AZ458941	IM0263B05
c 151	12	60.0	33	1	AV959900	AV959900	224	11.8	59.0	36	9	BH907856	BH907856	SALK.0444
c 152	12	60.0	33	10	CG711881	CG711881	225	11.8	59.0	37	1	AI401219	AI401219	tf60g11.x
c 153	12	60.0	34	1	AA948698	AA948698	c 226	11.8	59.0	37	1	AI626589	AI626589	fc05a12.x
c 154	12	60.0	34	1	AI174461	AI174461	c 227	11.8	59.0	37	2	BG569157	BG569157	602588A18
c 155	12	60.0	34	9	CC053791	CC053791	c 228	11.8	59.0	37	10	AL751513	AL751513	Arabidops
c 156	12	60.0	35	9	AZ308581	AZ308581	c 229	11.8	59.0	37	10	BX662468	BX662468	Arabidops
c 157	12	60.0	35	9	BZ6664505	BZ6664505	c 230	11.8	59.0	38	9	AZ504168	AZ504168	IM0344E13
c 158	12	60.0	35	10	CZ484272	CZ484272	c 231	11.8	59.0	40	10	BX200119	BX200119	Danio rer
c 159	12	60.0	36	1	AU012096	AU012096	232	11.8	59.0	42	9	AZ579567	AZ579567	IM0367L09
c 160	12	60.0	37	1	AA939234	AA939234	233	11.8	59.0	43	1	AI000178	AI000178	6645f01.s
c 161	12	60.0	37	1	AI278627	AI278627	c 234	11.8	59.0	43	9	BH903187	BH903187	SALK.1022
c 162	12	60.0	37	1	AI440016	AI440016	c 235	11.8	59.0	45	1	AU256617	AU256617	AU256617
c 163	12	60.0	37	1	AI813747	AI813747	c 236	11.8	59.0	45	9	AZ314853	AZ314853	IM0031A19
c 164	12	60.0	37	8	DR907951	DR907951	c 237	11.8	59.0	45	9	CC796721	CC796721	SALK.1369
c 165	12	60.0	37	9	BZ770609	BZ770609	c 238	11.8	59.0	49	10	BX171885	BX171885	Danio rer
c 166	12	60.0	38	9	AZ372759	AZ372759	239	11.8	59.0	50	1	AU104035	AU104035	Arabidops
c 167	12	60.0	38	10	CZ487976	CZ487976	240	11.8	59.0	50	8	T41178	T41178	ya31h2.82
c 168	12	60.0	39	1	AJ735786	AJ735786	241	11.6	59.0	22	1	AI687266	AI687266	tp94d10.x

```

c 242 11.6 58.0 28 6 CF319829
c 243 11.6 58.0 29 10 CZ478672 e00833-3p
c 244 11.6 58.0 30 9 BZ595207 SALK_0863
c 245 11.6 58.0 30 10 CG726545 111909080
c 246 11.6 58.0 30 11 DR102817S
c 247 11.6 58.0 31 9 BH812156
c 248 11.6 58.0 32 9 BH755332
c 249 11.6 58.0 33 1 BH755392 SALK_0490
c 250 11.6 58.0 33 1 AU266959 AU266959
c 251 11.6 58.0 37 1 A1679997 tu68f03.x
c 252 11.6 58.0 37 9 AZ395256 1M0159D22
c 253 11.6 58.0 38 10 AJ595611 Arabidops
c 254 11.6 58.0 40 1 AA908388 og77c01.s
c 255 11.6 58.0 40 1 AV965080 AV965080
c 256 11.6 58.0 40 8 T49499 ya76a12.r1
c 257 11.6 58.0 40 10 AG228871 Lotus cor
c 258 11.6 58.0 41 3 BJ080710 BJ080710
c 259 11.6 58.0 41 3 AZ390426 1M0151I17
c 260 11.6 58.0 41 10 AG196430 Fan trogl
c 261 11.6 58.0 42 1 AM698626 5578 glan
c 262 11.6 58.0 42 6 CF301078 7LEAF--05
c 263 11.6 58.0 42 10 BX189109 Danio rer
c 264 11.6 58.0 43 10 CZ484701 f02189-5p
c 265 11.6 58.0 43 10 CZ484703 f02190-5p
c 266 11.6 58.0 44 1 AJ649055 AJ649055
c 267 11.6 58.0 44 1 AV947752 AV947752
c 268 11.6 58.0 44 9 BH629051 1007076B0
c 269 11.6 58.0 46 8 H24541 y130f06.r1
c 270 11.6 58.0 46 8 N55368 YV47g02.s1
c 271 11.6 58.0 46 9 AZ404140 1M0172J15
c 272 11.6 58.0 46 9 BH905634 SALK_1075
c 273 11.6 58.0 46 10 AJ588341 Arabidops
c 274 11.6 58.0 47 7 CO787749 NT002B_D0
c 275 11.6 58.0 47 10 BX130415 Danio rer
c 276 11.6 58.0 47 10 BX231697 Danio rer
c 277 11.6 58.0 48 3 BJ083933 BJ083933
c 278 11.6 58.0 48 9 BH909144 SALK_0522
c 279 11.6 58.0 48 10 AL758859 Arabidops
c 280 11.6 58.0 49 3 BJ083833 BJ083833
c 281 11.6 58.0 49 6 CF276937 14ETL--02
c 282 11.6 58.0 49 9 AZ803783 2M0064B22
c 283 11.6 58.0 49 9 BH865521 SALK_0987
c 284 11.6 58.0 49 10 BX153515 Danio rer
c 285 11.6 58.0 49 10 BX946089 Arabidops
c 286 11.6 58.0 50 1 AU104243 AU104243
c 287 11.6 58.0 50 1 AU107920 AU107920
c 288 11.6 58.0 50 1 AU107921 AU107921
c 289 11.6 58.0 50 2 BG063099 H3002808-
c 290 11.6 58.0 50 5 BQ613522 r08f05.y
c 291 11.6 58.0 50 9 AZ387152 1M0146A20
c 292 11.6 58.0 50 9 BZ596617 SALK_0928
c 293 11.4 57.0 28 1 A1633299 ts66C05.x
c 294 11.4 57.0 28 9 AZ587121 1M0394G05
c 295 11.4 57.0 30 9 AZ796681 2M0052G05
c 296 11.4 57.0 32 9 AZ340099 1M0071E24
c 297 11.4 57.0 33 6 CA794368 Cac BL 13
c 298 11.4 57.0 34 1 A1000996 A1000996 os45h07.s
c 299 11.4 57.0 34 1 A1567122 tg85e11.x
c 300 11.4 57.0 39 10 CZ476003 d07939-5p

```

CF319829 HD--10-HI  
CZ478672 e00833-3p  
BZ595207 SALK\_0863  
CG726545 111909080  
AL978672 Danio rer  
BH812156 SALK\_0612  
BH755392 SALK\_0490  
AU266959 AU266959  
A1679997 tu68f03.x  
AZ395256 1M0159D22  
AJ595611 Arabidops  
AA908388 og77c01.s  
AV965080 AV965080  
T49499 ya76a12.r1  
AG228871 Lotus cor  
BJ080710 BJ080710  
AZ390426 1M0151I17  
AG196430 Fan trogl  
AM698626 5578 glan  
CF301078 7LEAF--05  
BX189109 Danio rer  
CZ484701 f02189-5p  
CZ484703 f02190-5p  
AJ649055 AJ649055  
AV947752 AV947752  
BH629051 1007076B0  
H24541 y130f06.r1  
N55368 YV47g02.s1  
AZ404140 1M0172J15  
BH905634 SALK\_1075  
AJ588341 Arabidops  
CO787749 NT002B\_D0  
BX130415 Danio rer  
BX231697 Danio rer  
BJ083933 BJ083933  
BH909144 SALK\_0522  
AL758859 Arabidops  
BJ083833 BJ083833  
CF276937 14ETL--02  
AZ803783 2M0064B22  
BH865521 SALK\_0987  
BX153515 Danio rer  
BX946089 Arabidops  
AU104243 AU104243  
AU107920 AU107920  
AU107921 AU107921  
BG063099 H3002808-  
BQ613522 r08f05.y  
AZ387152 1M0146A20  
BZ596617 SALK\_0928  
A1633299 ts66C05.x  
AZ587121 1M0394G05  
AZ796681 2M0052G05  
AZ340099 1M0071E24  
CA794368 Cac BL 13  
A1000996 os45h07.s  
A1567122 tg85e11.x  
CZ476003 d07939-5p

us-09-669-187a-73.szlm50.rst

ORYZA SATIVA (JAPONICA CULTIVAR-GROUP)  
ORYZA SATIVA (JAPONICA CULTIVAR-GROUP)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 37)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers  
1..37  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="7LEAF--07-A07"  
/issue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 84.0%; Score 16.8; DB 6; Length 37;  
Best Local Similarity 90.0%; Pred. No. 1.4e+04;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 TTTTGGGTTTGGGTTT 20  
|||||  
12 TTTTGGGTTTGGGTTT 31

AA916364 37 bp mRNA linear EST 29-APR-1998  
cg29b09.s1 NCI CGAP Br7 Homo sapiens cDNA clone IMAGE:1441241.3,  
similar to TR:Q29427 Q29427 PROLINE-RICH PROTEIN.; mRNA sequence.  
AA916364.1 GI:3055756  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 37)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
unknown library type  
Trace considered overall poor quality  
Insert Length: 1205 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..37  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1441241"

RESULT 1  
CF301952  
LOCUS  
DEFINITION  
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-A07, mRNA  
sequence.  
ACCESSION  
CF301952  
VERSION  
CF301952.1 GI:33673713  
KEYWORDS

ALIGNMENTS

CF301952 37 bp mRNA linear EST 15-AUG-2003  
7LEAF--07-A07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-A07, mRNA  
sequence.

```
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Bx7"
/notes="Organ: breast; Vector: pCMV-SPORT4; Site.1: Sali;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.2 kb. Life Technologies catalog
#:10985-018"

ORIGIN

Query Match      80.0%; Score 16; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGGTTTGGGGTTT 20
    |||||
Db 34 GGGGTTTGGGGTTT 19
    |||||

RESULT 3
AI813791/c
LOCUS
DEFINITION
wk79f07.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2421637.3.
similar to TR:000599 O00599 CON1.; contains element MSRI repetitive
element ;, mRNA sequence.
ACCESSION
AI813791
VERSION
AI813791.1 GI:5425006
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 43)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

FEATURES
source
Insert Length: 831 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2421637"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Pan1"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site.1: Sali;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN

Query Match      80.0%; Score 16; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGGTTTGGGGTTT 20
    |||||
Db 34 GGGGTTTGGGGTTT 19
    |||||

RESULT 4
AI813791/c
LOCUS
DEFINITION
wk79f07.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2421637.3.
similar to TR:000599 O00599 CON1.; contains element MSRI repetitive
element ;, mRNA sequence.
ACCESSION
AI813791
VERSION
AI813791.1 GI:5425006
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 43)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

FEATURES
source
Insert Length: 831 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2421637"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Pan1"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site.1: Sali;
Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN

Query Match      80.0%; Score 15.2; DB 1; Length 31;
Best Local Similarity 85.0%; Pred. No. 5.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
    |||||
Db 21 TTTTGGGGTTTGGGGTTT 2
    |||||

RESULT 5
AL756692
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-111H11-012331,
genomic survey sequence.
ACCESSION
AL756692
VERSION
AL756692.1 GI:21489190
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1
Li Y., Rosso M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
```



```

JOURNAL      Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED      12874060
REFERENCE
AUTHORS      Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
              Weisshaar, B.
TITLE        An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
              flanking sequence tag-based reverse genetics
JOURNAL      Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED      14756321
REFERENCE
AUTHORS      Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
              Weisshaar, B.
TITLE        High-throughput generation of sequence indexes from T-DNA
              mutagenized Arabidopsis thaliana lines
JOURNAL      Biotechniques 35 (6), 1164-1168 (2003)
PUBMED      14682050
REFERENCE
AUTHORS      Rosso, M.G., Li, Y., Strizhov, N. and Weisshaar, B.
TITLE        Direct Submission
JOURNAL      Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
              Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT      This sequence has been recovered from the right border of the
              T-DNA. It indicates an insertion close to or within gene At1g17190.
              Details on the protocols used for generation of the sequence are
              described in References 1-3. The sequences are generated at the MPI
              for Plant Breeding Research in the context of the GABI-Kat project.
              GABI-Kat is part of the German Plant Genomics program designated
              'GABI'. Information on line availability can be found at:
              http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
source
1. .31
   Location/Qualifiers
   /organism="Arabidopsis thaliana"
   /mol_type="genomic DNA"
   /db_xref="taxon:3702"
   /clone="GK-111H1-012331"
   /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
   /ecotype="Col-0"
   /notes="PCR was performed on DNA from Arabidopsis thaliana
   plants (rt) which were transformed with the T-DNA from
   vector pAC161 (Genbank accession number: AJ537514). The
   lines contain one or more T-DNA insertions. The DNA
   fragment(s) resulting from the PCR were directly sequenced
   to determine the genomic sequence flanking the insertion.
   T-DNA derived sequences were removed."
ORIGIN
Query Match      74.0%; Score 14.8; DB 10; Length 31;
Best Local Similarity 88.9%; Pred. No. 8.3e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 TTGGGGTTTGGGGTTT 20
Db      11 TTAGGGTTTAGGGTTT 28

RESULT 6
AZ794869
LOCUS      2M0048017R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0048017 R, genomic survey sequence.
ACCESSION  AZ794869
VERSION     AZ794869.1 GI:12941283
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 32)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.

JOURNAL      Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED      12874060
REFERENCE
AUTHORS      Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
              Weisshaar, B.
TITLE        An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
              flanking sequence tag-based reverse genetics
JOURNAL      Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED      14756321
REFERENCE
AUTHORS      Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
              Weisshaar, B.
TITLE        High-throughput generation of sequence indexes from T-DNA
              mutagenized Arabidopsis thaliana lines
JOURNAL      Biotechniques 35 (6), 1164-1168 (2003)
PUBMED      14682050
REFERENCE
AUTHORS      Rosso, M.G., Li, Y., Strizhov, N. and Weisshaar, B.
TITLE        Direct Submission
JOURNAL      Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
              Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT      This sequence has been recovered from the right border of the
              T-DNA. It indicates an insertion close to or within gene At1g17190.
              Details on the protocols used for generation of the sequence are
              described in References 1-3. The sequences are generated at the MPI
              for Plant Breeding Research in the context of the GABI-Kat project.
              GABI-Kat is part of the German Plant Genomics program designated
              'GABI'. Information on line availability can be found at:
              http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
source
1. .32
   Location/Qualifiers
   /organism="Mus musculus"
   /mol_type="genomic DNA"
   /strain="C57BL/6J"
   /db_xref="taxon:10090"
   /clone="UUGC2M0048017"
   /sex="Male"
   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
   /clone_lib="Mouse 10kb plasmid UUGC1M library"
   /notes="Vector: PWD42nv; Purified genomic DNA from M.
   musculus C57BL/6J (male) was obtained from the Jackson
   Laboratory Mouse DNA Resource
   (http://www.jax.org/resources/documents/dnares/). The DNA
   was hydrodynamically sheared by repeated passage through a
   0.005 inch orifice at constant velocity. The sheared DNA
   was blunt end-repaired with T4 DNA polymerase and T4
   polynucleotide kinase. Adaptor oligonucleotides were
   ligated to the blunt ends in high molar excess. The
   adaptor DNA was purified and size-selected for a 9.5 to
   10.5 kb range using preparative agarose gel
   electrophoresis. Vector DNA was prepared from a derivative
   of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
   inducible derivative of plasmid R1. The vector was ligated
   with adaptors complementary to the insert adaptors and
   purified. The sheared, adaptor mouse DNA was annealed to
   adaptor vector DNA, and transformed into
   chemically-competent E. coli XL10-Gold (Stratagene) cells
   and selected for ampicillin resistance."
ORIGIN
Query Match      74.0%; Score 14.8; DB 9; Length 32;
Best Local Similarity 88.9%; Pred. No. 8.3e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTTTGGGGTTTGGGGTTT 18
Db      7 TTTTGGGGTTTGGGGTTT 24

RESULT 7
AZ807733
LOCUS      2M0070H16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0070H16 R, genomic survey sequence.
ACCESSION  AZ807733
VERSION     AZ807733.1 GI:12972374
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 27)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.

```



Trace considered overall poor quality  
 Insert Length: 1514 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

## FEATURES

source  
 1. .40  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:228885"  
 /tissue\_type="moderately-differentiated endometrial  
 adenocarcinoma, 3 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut2"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Average insert size 1.85 kb. Life Technologies catalog #:  
 11539-012"

## ORIGIN

Query Match 72.0%; Score 14.4; DB 1; Length 40;  
 Best Local Similarity 93.8%; Pred. NO. 1.2e+05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGG 16  
 ||||| ||||| |||||  
 Db 38 TTTTGGGGTTTGGGG 23

## RESULT 10

AI264859  
 LOCUS  
 DEFINITION  
 QX66h12.x1 NCI CGAP Ov36 Homo sapiens cDNA clone IMAGE:2006375 3'  
 similar to SW:NPX\_HUMAN P55769 NHP2/RS6 FAMILY PROTEIN YEL026W  
 HOMOLOG ;, mRNA sequence.

## ACCESSION

AI264859

## VERSION

AI264859.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

1 (bases 1 to 46)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 200 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .46

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2006375"

/sex="female"

/tissue\_type="borderline ovarian carcinoma"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Ov36"

/note="Organ: ovary; Vector: pAMP1; mRNA made from

## ORIGIN

Query Match 72.0%; Score 14.4; DB 1; Length 46;  
 Best Local Similarity 93.8%; Pred. NO. 1.2e+05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGG 16  
 ||||| ||||| |||||  
 Db 29 TTTTGGGGTTTGGGG 44

## RESULT 11

AI564592/c  
 LOCUS  
 DEFINITION  
 tp98d09.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2207345 3'  
 similar to SW:FRP3\_MOUSE P05143 PROLINE-RICH PROTEIN MP-3 ;, mRNA  
 sequence.

## ACCESSION

AI564592

## VERSION

AI564592.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

1 (bases 1 to 46)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 2382 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

Location/Qualifiers

1. .46

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2207345"

/tissue\_type="poorly-differentiated endometrial  
 adenocarcinoma 2 pooled tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Ut3"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
 Average insert size 1.45 kb. Life Technologies catalog #:  
 11541-018"

## ORIGIN

Query Match 72.0%; Score 14.4; DB 1; Length 46;  
 Best Local Similarity 93.8%; Pred. NO. 1.2e+05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGG 16  
 ||||| ||||| |||||  
 Db 20 TTTTGGGGTTTGGGG 5

borderline ovarian carcinoma, cDNA made by oligo-dr  
 priming. Directionally cloned. Size-selected on agarose  
 gel, average insert size 500 bp. Primary library,  
 non-amplified."

```

RESULT 12
CZ918128
LOCUS      48 bp      DNA      linear      GSS 08-AUG-2005
DEFINITION 4021008B10.1EL.y1 4021 - RescueMu Grid V Zea mays genomic, genomic
survey sequence.
ACCESSION  CZ918128
VERSION     CZ918128
KEYWORDS   CZ918128.1 GI:71937386
SOURCE     GSS.
ORGANISM   Zea mays
            Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 48)
REFERENCE  Walbot,V.
AUTHORS    Walbot,V.
TITLE      Maize genomic sequences found using engineered RescueMu transposon
JOURNAL    Unpublished (2001)
COMMENT    Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Very probable ligation site of ends cut by single endonuclease.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 4021008 row: 1
            Class: transposon-tagged.
FEATURES   Location/Qualifiers
            1..48
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /cultivar="mixed background W23/A188/B73/K55"
            /db_xref="taxon:4577"
            /tissue_type="leaf"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_lib="4021 - RescueMu Grid V"
            /note="Organ: leaf; Vector: RescueMu (engineered from
            pluescript backbone); Site.1: BamHI; Site.2: BglII;
            RescueMu is a 4.9 kb, modified maize Mu transposon
            designed to allow plasmid rescue from total genomic DNA.
            Mu elements insert preferentially into transcription
            units. For more information on RescueMu, go to the web
            site 'http://www.mutransposon.org/project/RescueMu/'. Grid
            V was grown at University of Arizona in 2003. DNA was
            extracted from leaf strips, double digested using BamHI
            and BglII, and ligated to form circular plasmids. DH10B
            cells were transformed and then screened on LB plates with
            ampicillin."
ORIGIN
Query Match      72.0%; Score 14.4; DB 10; Length 48;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  5 GGGGTTTGGGGTTT 20
    |||
DB   6 GGGTTTGGGGTTT 21
    |||

RESULT 13
A1475390/c
LOCUS      49 bp      mRNA      linear      EST 14-APR-1999
DEFINITION t182g01.x1 NCI CGAP Col4 Homo sapiens cDNA clone IMAGE:2153616 3',
similar to SW:PRPM HUMAN P10161 SALIVARY PROLINE-RICH PROTEIN PO
;contains element MSR1 repetitive element ;, mRNA sequence.
ACCESSION  A1475390
VERSION     A1475390.1 GI:4328435
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
            Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
            GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
            Bioinformatics 19 (11), 1441-1442 (2003)
            12874060
            2
            Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
            Weisshaar, B.
            An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
            flanking sequence tag-based reverse genetics

```

---

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE  1 (bases 1 to 49)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1596 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
            1..49
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:2153616"
            /tissue_type="moderately-differentiated adenocarcinoma"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP Col4"
            /note="Organ: Colon; Vector: PCMV-SPORT6; Site.1: SalI;
            Site.2: NotI; Cloned unidirectionally. Primer: Oligo dr.
            Average insert size 1.7 kb. Life Technologies catalog #:
            11531-019"
ORIGIN
Query Match      72.0%; Score 14.4; DB 1; Length 49;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  5 GGGGTTTGGGGTTT 20
    |||
DB   38 GGGGTTTGGGGTTT 23
    |||

RESULT 14
AL943577
LOCUS      49 bp      DNA      linear      GSS 01-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-275E01-015095,
genomic survey sequence.
ACCESSION  AL943577
VERSION     AL943577.1 GI:24400175
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
            1
            Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
            GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
            Bioinformatics 19 (11), 1441-1442 (2003)
            12874060
            2
            Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
            Weisshaar, B.
            An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
            flanking sequence tag-based reverse genetics

```

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
14756321

3 Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weishaar,B.

TITLE  
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

Biotechniques 35 (6), 1164-1168 (2003)  
14682050

4 (bases 1 to 49)

Li,Y., Rosso,M.G., Strizhov,N. and Weishaar,B.

TITLE  
Direct Submission

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT  
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5g11660. Details on the protocols used for generations of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES  
source  
Location/Qualifiers  
1..49  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-275E01-015095"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 72.0%; Score 14.4; DB 10; Length 49;  
Best Local Similarity 93.8%; Pred. No. 1.2e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TGGGGTTTGGGGTTT 19  
|||||  
Db 20 TGGAGTTTGGGGTTT 35  
|||||

RESULT 15  
CZ559680/c  
LOCUS  
DEFINITION

50 bp DNA linear GSS 10-JUN-2005  
PL00447-5prime Drosophila melanogaster PL strains, transposon insertion flanking sequences Drosophila melanogaster genomic sequence recovered from 5' end of piggyBAC, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CZ559680  
CZ559680.1 GI:67486434  
GSS.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  
AUTHORS

1 (bases 1 to 50)  
Levis,R., Hoskins,R., Liao,G., Mozdén,N., Tsang,G., He,Y., Karpen,G., Bellen,H., Rubin,G. and Spradling,A.  
The Berkeley Drosophila Genome Project Gene Disruption Project  
Unpublished (2001)  
Contact: Roger A Hoskins  
Berkeley Drosophila Genome Project  
Lawrence Berkeley National Laboratory  
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA  
Tel: 510 486 4015

Fax: 510 486 6798  
Email: RHoskins@lbl.gov  
Sequence recovery method was inverse PCR.  
Sequence orientation is forward strand relative to 5' end of piggyBAC.  
The piggyBAC insertion position is 47 in the 50 bases. This insertion position refers to the first base of the 4 base target recognition sequence.  
Class: transposon-tagged.  
Location/Qualifiers  
1..50  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone\_lib="Drosophila melanogaster PL strains, transposon insertion flanking sequences"  
/notes="Drosophila melanogaster was mutagenized by remobilization of the piggyBAC vector pBAC(CAL4D,EFPP) (Horn et al. 2003 Genetics 163: 647-661) (FlyBase ID FBtp0017476) as described by Hacker et al. 2003 (Proc Natl Acad Sci USA 100: 7720-7725). Each strain in the collection has an independent insertion of the mutator transposon and the name of each strain begins with the letters PL. Genomic DNA was prepared from samples from each PL strain, DNA segments flanking the transposon insertion sites were amplified by inverse PCR, and the inverse PCR products were sequenced as described by Bellen et al. 2004 (Genetics 167: 761-781)."

ORIGIN

Query Match 72.0%; Score 14.4; DB 10; Length 50;  
Best Local Similarity 93.8%; Pred. No. 1.2e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGG 16  
|||||  
Db 16 TTTTGGGGTTTGGGG 1  
|||||

RESULT 16  
BX535866/c  
LOCUS  
DEFINITION

33 bp DNA linear GSS 04-APR-2004  
Arabidopsis thaliana T-DNA flanking sequence GK-521H07-020048, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BX535866  
BX535866.1 GI:31412996  
GSS.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
AUTHORS  
TITLE

1  
Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weishaar,B.  
GABI-Kat Simplesearch: a flanking sequence tag (fST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
Bioinformatics 19 (11), 1441-1442 (2003)  
12874060

2  
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weishaar,B.  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
14756321

3  
Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weishaar,B.  
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
Biotechniques 35 (6), 1164-1168 (2003)  
14682050

```

REFERENCE 4 (bases 1 to 33)
AUTHORS Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
COMMENT Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
t5e7. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German Plant Genomics program
designated 'GABI'. Information on line availability can be found
at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES             Location/Qualifiers
     source
     1..33
     /organism="Arabidopsis thaliana"
     /mol_type="genomic DNA"
     /db_xref="taxon:3702"
     /clone="GK-521H07-020048"
     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     /ecotypes="Col-0"
     /note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match      71.0%; Score 14.2; DB 10; Length 33;
Best Local Similarity 84.2%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTGGGTTTGGGTTT 20
   ||||| ||||| |||||
DB 22 TTTGGGTTTGGAGTGT 4

RESULT 17
DR63F21T/c 37 bp DNA linear GSS 22-NOV-2002
LOCUS Danio rerio genomic clone DKEY-63F21, genomic survey sequence.
DEFINITION
ACCESSION AL981876
VERSION AL981876.1 GI:25187365
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 37)
AUTHORS Humphray,S.J., Huckle,E. and Hunt,S.E.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquery@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the T7 end of BAC 63F21. 63F21 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES             Location/Qualifiers
     source
     1..37
     /organism="Danio rerio"
     /mol_type="genomic DNA"
     /db_xref="taxon:7955"
     /clone="DKEY-63F21"
     /tissue_type="Testis"
     /note="vector pindigoBAC-536"

ORIGIN
Query Match      71.0%; Score 14.2; DB 11; Length 37;
Best Local Similarity 84.2%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTGGGTTTGGGTTT 20
   ||||| ||||| |||||
DB 19 TTTGGGCTTTGGGTTT 37

RESULT 19
CZ470781 50 bp DNA linear GSS 29-APR-2005
LOCUS c06535-5prime Exelixis piggyBac PB insertions Drosophila
DEFINITION melanogaster genomic Sequence recovered from 5' end of piggyBac,

REFERENCE 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TTTTGGGTTTGGGTTT 19
   ||||| ||||| |||||
DB 37 TTTTGGGTTTAGAGTGT 19

RESULT 18
CG722753 43 bp DNA linear GSS 20-OCT-2003
LOCUS 1119073D02.2ELx1 1119 - RescueMu Grid AA Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION CG722753
VERSION CG722753.1 GI:37757925
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 43)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119073 row: 35
Class: transposon-tagged
FEATURES             Location/Qualifiers
     source
     1..43
     /organism="Zea mays"
     /mol_type="genomic DNA"
     /cultivar="mixed background W23/A188/B73/K55"
     /db_xref="taxon:4577"
     /tissue_type="leaf"
     /dev_stage="adult"
     /lab_host="DH10B"
     /clone_lib="1119 - RescueMu Grid AA"
     /note="Organ: leaf; Vector: RescueMu (engineered from
pBluscript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN
Query Match      71.0%; Score 14.2; DB 10; Length 43;
Best Local Similarity 84.2%; Pred. No. 1.4e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTGGGTTTGGGTTT 20
   ||||| ||||| |||||
DB 19 TTTGGGCTTTGGGTTT 37

RESULT 19
CZ470781 50 bp DNA linear GSS 29-APR-2005
LOCUS c06535-5prime Exelixis piggyBac PB insertions Drosophila
DEFINITION melanogaster genomic Sequence recovered from 5' end of piggyBac,

```

```

genomic survey sequence.
ACCESSION      CZ470781
VERSION        CZ470781.1  GI:62964794
KEYWORDS       GSS.
SOURCE         Drosophila melanogaster (fruit fly)
ORGANISM       Drosophila melanogaster
               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
               Ephydroidea; Drosophilidae; Drosophila.
REFERENCE      1 (bases 1 to 50)
AUTHORS        Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
               Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
               Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
               Greer,K., Hartouni,S.R., Howie,B., Jakkula,L., Joo,D., Killpack,K.,
               Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
               Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
               Swimmer,C., Kopczyński,C., Duyk,G., Winberg,M.L. and Margolis,J.
TITLE          A complementary transposon tool kit for Drosophila melanogaster
               using P and piggyBac
JOURNAL        Nat. Genet. 36 (3), 283-287 (2004)
PUBMED        14981521
COMMENT        Contact: Roger A Hoskins
               Berkeley Drosophila Genome Project
               Lawrence Berkeley National Laboratory
               Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
               Tel: 510 486 4015
               Fax: 510 486 6798
               Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
piggyBac element.
Insertion position is 47 in the 50 bases. This
target recognition sequence.
Class: transposon insertion site.
               Location/Qualifiers
FEATURES       source
               1..50
               /organism="Drosophila melanogaster"
               /mol_type="genomic DNA"
               /strain="isogenic w- strain"
               /db_xref="taxon:7227"
               /clone_lib="Exelixis piggyBac PB insertions"
               /notes="Vector: An isogenic w- Drosophila melanogaster strain
               AY515146; An isogenic w- Drosophila melanogaster strain
               was mutagenized by remobilization of transposable
               elements. We remobilized the PB element using
               Hsp70.piggyBac transposase from a single ammunition
               element on either the X or third chromosome. We induced
               transposase expression by immersing bottles in a
               circulating 37°C water bath for a daily (days 3-10 after
               egg-laying) 1-h heat shock. We outcrossed the resulting
               dysgenic males to an isogenic w- strain. New insertions
               were identified on the basis of a change in eye color
               (third chromosome ammunition) or the appearance of w+ male
               progeny (X chromosome ammunition). All lines were mapped
               to a chromosome by standard genetic methods, examined for
               homozygous viability, and used for recovery of flanking
               genomic sequence by inverse PCR."
ORIGIN
Query Match      71.0%; Score 14.2; DB 10; Length 50;
Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  TTTCGGGTTTTCGGGTTTT 20
        ||| ||||| ||||| |||||
DB      5  TTTCGGGTTTTCGGGTTTT 23

RESULT 20
CG729919
LOCUS       CG729919
DEFINITION  1119116E01.2EL_x1 1119 - RescueMu Grid AA Zea mays genomic, genomic
               50 bp DNA linear GSS 20-OCT-2003
AUTHORS      Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
TITLE        GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
               Arabidopsis.

genomic survey sequence.
ACCESSION      CG729919
VERSION        CG729919.1  GI:37772091
KEYWORDS       GSS.
SOURCE         Zea mays
ORGANISM       Zea mays
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
               clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 50)
AUTHORS        Walbot,V.
TITLE          Maize genomic sequences found using engineered RescueMu transposon
               Unpublished (2001)
JOURNAL
COMMENT        Contact: Walbot V
               Department of Biological Sciences
               Stanford University
               855 California Ave, Palo Alto, CA 94304, USA
               Tel: 650 723 2227
               Fax: 650 725 8221
               Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119116 row: 36
Class: transposon-tagged.
               Location/Qualifiers
FEATURES       source
               1..50
               /organism="Zea mays"
               /mol_type="genomic DNA"
               /cultivar="mixed background W23/A188/B73/K55"
               /db_xref="taxon:4577"
               /dev_stage="adult"
               /tissue_type="leaf"
               /lab_host="DH10B"
               /clone_lib="1119 - RescueMu Grid AA"
               /note="Organ: leaf; Vector: RescueMu (engineered from
               Bluescript backbone); Site 1: BamHI; Site 2: BglII;
               RescueMu is a 4.9 kb, modified maize Mu transposon
               designed to allow plasmid rescue from total genomic DNA.
               Mu elements insert preferentially into transcription
               units. For more information on RescueMu, go to the web
               site 'www.zmndb.iastate.edu' and follow the links for
               'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
               was extracted from leaf strips, double digested using
               BamHI and BglII, and ligated to form circular plasmids.
               DH10B cells were transformed and then screened on LB
               plates with ampicillin."
ORIGIN
Query Match      71.0%; Score 14.2; DB 10; Length 50;
Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  TTTCGGGTTTTCGGGTTTT 20
        ||| ||||| ||||| |||||
DB      19 TTTCGGCCTTTTCGGGTTTT 37

RESULT 21
AL940076/c
LOCUS       AL940076
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-244B11-014397,
               genomic survey sequence.
ACCESSION      AL940076
VERSION        AL940076.1  GI:24396525
KEYWORDS       GSS.
SOURCE         Arabidopsis thaliana (thale cress)
ORGANISM       Arabidopsis thaliana
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE      1
AUTHORS        Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
TITLE        GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
               Arabidopsis.

```

the identification of T-DNA insertion mutants in Arabidopsis thaliana  
bioinformatics 19 (11), 1441-1442 (2003)  
12874060  
2  
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
14756321  
3  
Strizhov,N., Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.  
Weisshaar,B.  
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
Biotechniques 35 (6), 1164-1168 (2003)  
14682050  
4 (bases 1 to 31)  
Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.  
Direct Submission  
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone f26h11. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

Location/Qualifiers  
1. 31  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-244B11-014397"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/scotypes="Col-0"  
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN  
Query Match 69.0%; Score 13.8; DB 10; Length 31;  
Best Local Similarity 88.2%; Pred. No. 2.1e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGCTTTGGGCT 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 17 TGTGGGCTTTGGGCT 1

RESULT 22  
H71330  
LOCUS  
H71330 46 bp mRNA linear EST 26-OCT-1995  
Yu55d08.s1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone IMAGE:230031 3' similar to SP:JC2012 JC2012 RIBOSOMAL PROTEIN 17K - i, mRNA sequence.  
H71330  
ACCESSION H71330.1 GI:1043146  
VERSION H71330.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 46)  
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasakis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
889549  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
Insert Size: 356  
High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Insert Length: 356 Std Error: 0.00  
Seq primer: Promega -21m13  
High quality sequence stop: 1.  
Location/Qualifiers  
1. 46  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:3781127"  
/db\_xref="taxon:9606"  
/clone="IMAGE:230031"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal liver spleen INFUS"  
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACGGAGAAATTAATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN  
Query Match 69.0%; Score 13.8; DB 8; Length 46;  
Best Local Similarity 88.2%; Pred. No. 2.1e+05;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTTGGGCTTTGGGCTT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 TTTGGGATTTTGGGCTT 19

RESULT 23  
AZ774479  
LOCUS  
AZ774479 33 bp DNA linear GSS 16-FEB-2001  
2M0004A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0004A05 F, genomic survey sequence.  
AZ774479  
ACCESSION AZ774479.1 GI:12899972  
VERSION  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 33)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,



Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: rdunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0004 row: A column: 05  
 Seq primer: CGTTGTAACGACGCCACT  
 Class: plasmid ends  
 High quality sequence stop: 33.  
 Location/Qualifiers  
 1. 33  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0004A05"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gl|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**FEATURES**  
 source  
 1. 33  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0004A05"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gl|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**ORIGIN**  
 Query Match 68.0%; Score 13.6; DB 9; Length 33;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 1 TTTTGGGTTTGGGTTTT 20  
 ||||| ||||| ||||| ||||| |||||  
 3 TTTTGGGTTTGGGTTTT 22

**RESULT 24**  
 A1018534/c  
 LOCUS  
 DEFINITION  
 ou24h12.x1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1627271 3, similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST ;contains L1.t1 L1 repetitive element ;, mRNA sequence.  
 A1018534  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 37)

**REFERENCE**  
 1 Soares, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: rdunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0004 row: A column: 05  
 Seq primer: CGTTGTAACGACGCCACT  
 Class: plasmid ends  
 High quality sequence stop: 33.  
 Location/Qualifiers  
 1. 33  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0004A05"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gl|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps@mail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Trace considered overall poor quality  
 Insert Length: 1352 Std Error: 0.00  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 37  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1627271"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares\_NFL\_T\_GBC\_S1"  
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI-CGAP GCBI) were mixed, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

**ORIGIN**  
 Query Match 68.0%; Score 13.6; DB 1; Length 37;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 1 TTTTGGGTTTGGGTTTT 20  
 ||||| ||||| ||||| ||||| |||||  
 37 TGTGTGGTGTGGGTTTT 18

**RESULT 25**  
 A1446151/c  
 LOCUS  
 DEFINITION  
 t107ell.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2140844 3, similar to TR:Q61888 Q61888 PROLINE RICH PROTEIN. ;contains element MSRI repetitive element ;, mRNA sequence.  
 A1446151  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 37)

**REFERENCE**  
 1 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps@mail.nih.gov  
 Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 1210 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES source  
1. .37  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2140844"  
/tissue\_type="poorly differentiated adenocarcinoma with  
signet ring cell features"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Gas4"  
/note="Organ: fToma; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.69 Kb. Life Technologies catalog #: 11549-011"

ORIGIN  
Query Match 68.0%; Score 13.6; DB 1; Length 37;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGGTTTT 20  
||||| |||||  
Db 29 TTTTGGGGGTTGTGGCTTT 10

RESULT 26  
BE974781  
LOCUS  
DEFINITION  
601680831R2 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE:3951175 3',  
mRNA sequence.  
ACCESSION  
BE974781  
VERSION  
BE974781.1 GI:10588117  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 38)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs@mail.nih.gov  
Tissue Procurement: CLONETECH Laboratories, Inc.  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1CM818 row: n column: 08  
High quality sequence stop: 33.  
Location/Qualifiers

FEATURES source  
1. .38  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3951175"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH MGC 83"  
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);  
Site 1: SfiI (ggcgctcgcc); Site 2: SfiI  
(ggccatattggcc); 5' and 3' adaptors were used in cloning  
as follows: 5' adaptor sequence: 5'-CACGCCATTATGCCC-3',  
and 3' adaptor sequence:  
5'-ATTCTAGAGCGCGCGCCGACATG-(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.4  
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts

by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA)."

ORIGIN  
Query Match 68.0%; Score 13.6; DB 2; Length 38;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGGTTTT 20  
||||| |||||  
Db 7 TATTGGGGGCTGGGGTTTT 26

RESULT 27  
CF295607/c  
LOCUS  
DEFINITION  
30DGS--05-K02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa (japonica cultivar-group) cDNA clone 30DGS--05-K02, mRNA  
sequence.  
ACCESSION  
CF295607  
VERSION  
CF295607.1 GI:33664640  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa (japonica cultivar-group)  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
1 (bases 1 to 39)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongui University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source  
1. .39  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="30DGS--05-K02"  
/tissue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

ORIGIN  
Query Match 68.0%; Score 13.6; DB 6; Length 39;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGGTTTT 20  
||||| |||||  
Db 24 TTTTGGGGGGGGGGTTTT 5

RESULT 28  
AZ579518/c  
LOCUS  
DEFINITION  
AZ579518  
ACCESSION  
AZ579518.1 GI:11693947  
KEYWORDS  
GSS.

ORIGIN  
Query Match 68.0%; Score 13.6; DB 6; Length 39;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGGTTTT 20  
||||| |||||  
Db 24 TTTTGGGGGGGGGGTTTT 5

RESULT 28  
AZ579518/c  
LOCUS  
DEFINITION  
AZ579518  
ACCESSION  
AZ579518.1 GI:11693947  
KEYWORDS  
GSS.

**SOURCE**  
ORGANISM  
Mus musculus (house mouse)

**REFERENCE**  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.

**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

**JOURNAL**  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0367 row: G column: 03  
Seq primer: CGTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 42.

**FEATURES**  
source  
1..42  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCIM0367G03"  
/sex="Male"  
/lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**ORIGIN**  
Query Match 68.0%; Score 13.6; DB 9; Length 42;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 23 TTTTGGGTTTGGGGTTTT 4

**RESULT** 29  
BX946019  
LOCUS  
DEFINITION  
Arabisopsis thaliana T-DNA flanking sequence GK-747F04-024638, genomic survey sequence.  
BX946019  
ACCESSION  
VERSION  
BX946019.1 GI:42595705

**KEYWORDS**  
SOURCE  
Arabisopsis thaliana (thale cress)  
Arabisopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

**REFERENCE**  
AUTHORS  
TITLE  
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B. GABI-Kat SimpleSearch: a flanking sequence tag (fST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
Bioinformatics 19 (11), 1441-1442 (2003)  
12874060

**JOURNAL**  
PUBMED  
2  
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
14756321

**REFERENCE**  
AUTHORS  
3  
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weisshaar, B.  
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
Biotechniques 35 (6), 1164-1168 (2003)  
14682050

**TITLE**  
JOURNAL  
PUBMED  
4  
Li, Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.  
Direct Submission  
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3g10360.  
Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German plant genomics program designated 'GABI'. Information on line availability can be found at:  
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

**FEATURES**  
source  
1..42  
/organism="Arabisopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="GK-747F04-024638"  
/clone\_lib="Arabisopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

**ORIGIN**  
Query Match 68.0%; Score 13.6; DB 10; Length 42;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 11 TTTTGGGTTTCTGGTTTT 30

**RESULT** 30  
AI442438  
LOCUS  
DEFINITION  
Gm-cl004-468 5' similar to FR:Q26195 Q26195 PVAL GENE. ;, mRNA sequence.  
AI442438  
ACCESSION

```

VERSION      AI442438.1  GI:4296179
KEYWORDS     EST.
SOURCE       Glycine max (soybean)
ORGANISM     Glycine max

REFERENCE
AUTHORS      Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
              Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
              Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
              Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
              Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
              McCann,R., Waterston,R. and Wilson,R.
              Public Soybean EST Project

TITLE        Unpublished (1999)
JOURNAL      Public Soybean EST Project
COMMENT      Contact: Shoemaker R/Public Soybean EST Project
              Public Soybean EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              When it has been determined, an EST from the other end of this
              clone is listed in the 'Other ESTs on clone' field. Trace
              considered overall poor quality Possible reversed clone: similarity
              on wrong strand This clone is available through: Biogenetic
              Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423
              4163; email: info@biogeneticservices.com)
              Seq primer: -40RP from Gibco
              High quality sequence stop: 1
              POLYA=No. Location/Qualifiers

FEATURES     source
             1..43
                /organism="Glycine max"
                /mol_type="mRNA"
                /cultivar="Williams"
                /db_xref="taxon:3847"
                /clone="GENOME SYSTEMS CLONE ID: Gm-cl004-468"
                /tissue_type="root"
                /lab_host="XL10-Gold"
                /clone_lib="Gm-cl004"
                /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
              XhoI; Root cDNA. The mRNA was isolated from entire roots
              of 8 day old 'Williams' seedlings which were propagated on
              paper towels with distilled water. Stratagene's cDNA
              Synthesis Kit (catalog #200401) was used to synthesize the
              cDNA. First- strand synthesis was performed with 5-methyl
              dCTP, hence the ligated cDNA is hemimethylated.
              Stratagene's first-strand synthesis primer was used
              [GAGAGAGAGAGAGAGAGACTAGTCTCGAG(T)-18]. After
              second-strand synthesis, the cDNA ends were 'polished'
              with clone pfu DNA polymerase, ligated to EcoRI adaptors,
              and phosphorylated. The XhoI site within the first-strand
              synthesis primer was restricted by digestion with XhoI;
              all XhoI sites in the cDNA would be protected by their
              hemimethylated status. The cDNA constructs were
              size-fractionated with a 500bp cutoff, using GibcoBRL Life
              Technologies' cDNA Size Fractionation column. The column
              eluent was then ligated into Stratagene's pBluescript II
              XR Predigested vector (pBluescript II SK(+)) that had been
              digested with EcoRI and XhoI, and phosphorylated). Both
              the white and blue colonies appear to contain recombinant
              plasmids with cDNA inserts. Blue colonies 9n-15 have been
              sequenced, and possess putative cDNA inserts. This library
              was constructed by Dr. Paul Keim & Virginia H. Coryell,
              Department of Biology, Box5640, Northern Arizona
              University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
              Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
              520-523-7500, email: paul.keim@nau.edu,
              virginia.coryell@nau.edu"

Query Match      68.0%; Score 13.6; DB 1; Length 43;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
    ||||| ||||| ||||| |||||
Db 43 TTTCGGGCTTGGGTTTTT 24

RESULT 31
AZ634906/c
LOCUS       43 bp DNA linear GSS 13-DEC-2000
DEFINITION  1M0490P20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0490P20 R, genomic survey sequence.
ACCESSION   AZ634906
VERSION     AZ634906.1 GI:11757096
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 43)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunne@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0490 row: P column: 20
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 43.
              Location/Qualifiers
             1..43
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0490P20"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."

```

## ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 43;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
 ||||| ||||| | |||||  
 Db 21 TTTTGGTGTTCGTCTTT 2

## RESULT 32

CZ472331

LOCUS

DEFINITION CZ472331 43 bp DNA linear GSS 29-APR-2005  
 d01604-3prime Exelixis P element XP insertions Drosophila  
 melanogaster genomic sequence recovered from 3' end of P element,  
 genomic survey sequence.

## ACCESSION

CZ472331

VERSION

CZ472331.1

GI:62966344

SOURCE

GSS.

ORGANISM

Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 43)

Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,

Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,

Ryner,L., Cheung,L.M., Cheng,A., Erickson,C., Fisher,W.W.,

Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Kilpack,K.,

Lauter,A., Mazotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,

Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,

Swimmer,C., Kopczyński,C., Duyk,G., Winberg,M.L. and Margolis,J.

A complementary transposon tool kit for Drosophila melanogaster

using P and piggyBac

Nat. Genet. 36 (3), 283-287 (2004)

14981521

Contact: Roger A Hoskins

Berkeley Drosophila Genome Project

Lawrence Berkeley National Laboratory

Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA

Tel: 510 486 4015

Fax: 510 486 6798

Email: RHoskins@lbl.gov

Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P

element.

The P element insertion position is 1 in the 43 bases. This

insertion position refers to the first base of the 8 base target

recognition sequence.

Class: transposon insertion site.

Location/Qualifiers

1..43

/organism="Drosophila melanogaster"

/mol\_type="genomic DNA"

/strain="isogenic w- strain"

/db\_xref="taxon:7227"

/clone\_lib="Exelixis P element XP insertions"

/note="Vector: P element XP (GenBank accession number

AF15149); An isogenic w- Drosophila melanogaster strain

was mutagenized by remobilization of transposable

elements. For the P element XP, we selected an easily

mobilized ammunition element among inserts hopped into the

Biosnycy balancer. New insertions were collected in vials

from dysgenic females using the standard chromosomal

source of transposase, delta2-3. All lines were mapped to

a chromosome by standard genetic methods, examined for

homozygous viability and used for recovery of flanking

genomic sequence by inverse PCR."

## ORIGIN

Query Match 68.0%; Score 13.6; DB 10; Length 43;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;

## Matches

16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
 ||||| ||||| | |||||  
 Db 20 TGTGGGGCTTTGGAGCTTT 39

## RESULT 33

CF300934/c

LOCUS

DEFINITION

CF300934 44 bp mRNA linear EST 15-AUG-2003

7LEAF--05-J13.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa (japonica cultivar-group) cDNA clone 7LEAF--05-J13, mRNA

sequence.

ACCESSION

CF300934

VERSION

CF300934.1

GI:33672695

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 44)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..44

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clone="7LEAF--05-J13"

/tissue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EORI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

## ORIGIN

Query Match 68.0%; Score 13.6; DB 6; Length 44;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
 ||||| ||||| | |||||  
 Db 34 TTTTGTGTTTGGGATTTT 15

## RESULT 34

AZ476389/c

LOCUS

DEFINITION

AZ476389 44 bp DNA linear GSS 04-OCT-2000

1M0295E09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic

clone UUGCIM0295E09 F, genomic survey sequence.

ACCESSION

AZ476389

VERSION

AZ476389.1

GI:10634514

KEYWORDS

GSS.

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 44)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R. and Nahm,B.H.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0295 row: E column: 09  
 Seq primer: CTTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 44.  
 Location/Qualifiers  
 1..44  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0295E09"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnarses/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 68.0%; Score 13.6; DB 9; Length 44;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
 ||||| ||||| ||||| |||||  
 Db 30 TTTTGGTTTGGGTTTTT 11

RESULT 35  
 CF298361/c  
 LOCUS  
 DEFINITION  
 45 bp mRNA linear EST 15-AUG-2003  
 Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-L10, mRNA  
 sequence.  
 CF298361  
 CF298361.1 GI:33670122  
 EST.  
 SOURCE  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

Query Match 68.0%; Score 13.6; DB 9; Length 44;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
 ||||| ||||| ||||| |||||  
 Db 30 TTTTGGTTTGGGTTTTT 11

RESULT 35  
 CF298361/c  
 LOCUS  
 DEFINITION  
 45 bp mRNA linear EST 15-AUG-2003  
 Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-L10, mRNA  
 sequence.  
 CF298361  
 CF298361.1 GI:33670122  
 EST.  
 SOURCE  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 45)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 JOURNAL  
 COMMENT  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..45  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="7LEAF--01-L10"  
 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 68.0%; Score 13.6; DB 6; Length 45;  
 Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
 ||||| ||||| ||||| |||||  
 Db 22 TTTTGTGTTTGGGATTTT 3

RESULT 36  
 CN751963/c  
 LOCUS  
 DEFINITION  
 45 bp mRNA linear EST 19-MAY-2004  
 APhL3SD-XXI-A6 APhL3SD Acyrthosiphon pisum cDNA clone APhL3SDXXIA6  
 5', mRNA sequence.  
 CN751963  
 CN751963.1 GI:47516960  
 EST.  
 KEYWORDS  
 SOURCE  
 Acyrthosiphon pisum (pea aphid)  
 ORGANISM  
 Acyrthosiphon pisum  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;  
 Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.  
 Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,  
 Stern,D., Tagu,D. and Wincker,P.  
 An expressed sequence tags database for the pea aphid Acyrthosiphon  
 pisum  
 Unpublished (2004)  
 Contact: D. Tagu  
 INRA Rennes  
 UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France  
 Tel: +33.2.23.48.51.65  
 Fax: +33.2.23.48.51.50  
 Risk of contamination by bacterial sequences from obligatory  
 (Buchnera) or facultative endosymbionts.  
 PCR PRIMERS  
 FORWARD: GCCGATAACTTCGTATAGCA  
 Plate: XXI row: A column: 6.  
 Location/Qualifiers  
 1..45  
 /organism="Acyrthosiphon pisum"  
 /mol\_type="mRNA"  
 /cultivar="yr2"  
 /db\_xref="taxon:7029"  
 /clone="APHL3SDXXIA6"

/tissue\_type="head"  
/dev\_stage="third instar nymph (L3)"  
/lab\_host="TOP10"  
/clone\_lib="AphL3SD"

/note="Vector: PDNR-LIB; Site 1: SfiIA; Site 2: SfiIB;  
Sample name: AphL3SD ; Plant growth place: INRA-Rennes,  
UMR BIO3P, BP 35327, 35653 Le Rheu cedex, France ; Soil  
conditions: peat ; Sowing date: 20/03/2003 ; Harvesting  
date: 10/04/2003 ; Stress date: no stress ; Description:  
aphids inoculated on one-week old Vicia faba germinations  
under non sterile conditions. ; experimental condition:  
short photoperiod (12-hr light/12-hr dark at 18 c)"

## ORIGIN

Query Match 68.0%; Score 13.6; DB 7; Length 45;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
||||| ||||| ||||| |||||  
Db 45 TTTTGGGGTTTGGGGTTTT 26

## RESULT 37

AZ793049/c

LOCUS

DEFINITION 2M0045M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0045M14 R, genomic survey sequence.

ACCESSION AZ793049

VERSION AZ793049.1

KEYWORDS GI:12937434

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 46)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0045 row: M column: 14

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 46.

Location/Qualifiers

1. .46

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0045M14"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

## ORIGIN

Query Match 68.0%; Score 13.6; DB 9; Length 46;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
||||| ||||| ||||| |||||  
Db 26 TTTTGGGGTTTGGGGTTTT 7

## RESULT 38

AZ786064

LOCUS

DEFINITION 2M0030G22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0030G22 R, genomic survey sequence.

ACCESSION AZ786064

VERSION AZ786064.1

KEYWORDS GI:12923450

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 47)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0030 row: G column: 22

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 47.

Location/Qualifiers

1. .47

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0030G22"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."





```

Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
mhi@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nleayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
    source
        1..24
            /location/Qualifiers
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="131b05"
ORIGIN
    Query Match          67.0%; Score 13.4; DB 11; Length 24;
    Best Local Similarity 93.3%; Pred. No. 2.9e+05;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TGGGGTTTGGGGTTT 18
      ||| ||||| |||
Db      24 TGGCGTTTGGGGTTT 10

RESULT 42
CZ916406/c
LOCUS
DEFINITION
    4021001C10.2EL_Y1 4021 - RescueMu Grid V Zea mays genomic, genomic
    survey sequence.
ACCESSION
CZ916406
VERSION
CZ916406.1 GI:71934408
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 30)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021001 row: C column: 10
Class: transposon-tagged.
FEATURES
    source
        1..30
            /location/Qualifiers
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /cultivar="mixed background W23/A186/B73/K55"
            /db_xref="taxon:4577"
            /tissue_type="leaf"
            /dev_stage="adult"
            /lab_host="DH10B"

Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
mhi@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nleayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
    source
        1..24
            /location/Qualifiers
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="131b05"
ORIGIN
    Query Match          67.0%; Score 13.4; DB 11; Length 24;
    Best Local Similarity 93.3%; Pred. No. 2.9e+05;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TGGGGTTTGGGGTTT 18
      ||| ||||| |||
Db      24 TGGCGTTTGGGGTTT 10

RESULT 42
CZ916406/c
LOCUS
DEFINITION
    4021001C10.2EL_Y1 4021 - RescueMu Grid V Zea mays genomic, genomic
    survey sequence.
ACCESSION
CZ916406
VERSION
CZ916406.1 GI:71934408
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 30)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021001 row: C column: 10
Class: transposon-tagged.
FEATURES
    source
        1..30
            /location/Qualifiers
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /cultivar="mixed background W23/A186/B73/K55"
            /db_xref="taxon:4577"
            /tissue_type="leaf"
            /dev_stage="adult"
            /lab_host="DH10B"

/clone_lib="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
ORIGIN
    Query Match          67.0%; Score 13.4; DB 10; Length 30;
    Best Local Similarity 93.3%; Pred. No. 2.9e+05;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TTTGGGGTTTGGGG 16
      ||| ||||| |||
Db      15 TTTTGGGTTTGGGG 1

RESULT 43
AI439312/c
LOCUS
DEFINITION
    ti59e12.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134798 3',
    similar to SW:PRP2_HUMAN P02812 SALIVARY PROLIN-RIICH PROTEIN
    PRECURSOR ;contains MER22.B2 TAR1 repetitive element ;, mRNA
    sequence.
ACCESSION
AI439312
VERSION
AI439312.1 GI:4303441
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 34)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 861 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
FEATURES
    Location/Qualifiers
        1..34
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:2134798"
            /issue_type="lymphoma, follicular mixed small and large
            cell"
            /lab_host="DH10B"
            /clone_lib="NCI_CGAP_Lym12"
            /note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1:
            SalI; Site 2: NotI; Cloned unidirectionally. Primer:
            Oligo dt. Average insert size 1.25 kb. Life Technologies
            catalog #: 11547-015"
ORIGIN
    Query Match          67.0%; Score 13.4; DB 1; Length 34;

```

Best Local Similarity 93.3%; Pred. No. 3e+05; Mismatches 0; Indels 1; Gaps 0;  
Matches 14; Conservative 0;

Qy 5 GGGGTTTGGGGTTT 19  
|||||  
Db 34 GGGGTTTGGGGTTT 20  
|||||

## RESULT 44

AI280814/c

## LOCUS

DEFINITION qw11603.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:1990780 3',  
similar to SW:PRP1\_HUMAN P04280 SALIVARY PROLINE-RICH PROTEIN  
PRECURSOR ; contains element MSRI repetitive element ;, mRNA  
sequence.

ACCESSION AI280814 GI:3919047

## VERSION

AI280814.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

1 (bases 1 to 37)

## AUTHORS

NCI-CGAP

## TITLE

http://www.ncbi.nlm.nih.gov/ncicgap.

## JOURNAL

Tumor Gene Index

## COMMENT

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 890 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..37

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1990780"

/tissue\_type="poorly-differentiated endometrial

adenocarcinoma, 2 pooled tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Ut3"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site.1: SalI;

Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.45 kb. Life Technologies catalog #:

11541-018"

## ORIGIN

Query Match

Best Local Similarity 93.3%; Pred. No. 3e+05;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGG 15  
|||||Db 15 TTATGGGGTTTGGG 1  
|||||

## RESULT 45

AI865173/c

## LOCUS

DEFINITION wk09b01.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2411785 3',  
similar to WP:R148.5 CE12856 ;, mRNA sequence.

## ACCESSION

AI865173

## VERSION

AI865173.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 49)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov

Life Technologies catalog #: 11547-015

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 808 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..49

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2411785"

/tissue\_type="lymphoma, follicular mixed small and large

cell"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Lym12"

/note="Organ: lymph node; Vector: pCMV-SPORT6; Site.1:

SalI; Site.2: NotI; Cloned unidirectionally. Primer:

Oligo dt. Average insert size 1.25 kb. Life Technologies

catalog #: 11547-015"

## ORIGIN

Query Match

Best Local Similarity 93.3%; Pred. No. 3e+05;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGGTTTGGGGTTT 20  
|||||Db 44 GGGTTTGGGGTTT 30  
|||||

## RESULT 46

AI2761211

## LOCUS

DEFINITION

IM0555122F Mouse 10kb plasmid UUC1M library Mus musculus genomic

clone UUC1M0555122 F, genomic survey sequence.

ACCESSION AI2761211

## VERSION

AI2761211.1

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

## REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0555 row: 1 column: 22  
Seq primer: CGTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES  
source  
1. .22  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0555122"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN  
Query Match 66.0%; Score 13.2; DB 9; Length 22;  
Best Local Similarity 83.3%; Pred. No. 3.5e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGTTT 18  
|||||  
Db 5 TTTTGGGTTTGGGTTT 22

RESULT 47  
AJ590891  
LOCUS  
DEFINITION  
24 bp DNA linear GSS 15-JAN-2004  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone 576D12, genomic survey sequence.

ACCESSION  
AJ590891 GI:37940515  
VERSION  
GSS; left border; T-DNA flanking sequence.  
KEYWORDS  
Arabidopsis thaliana  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
1  
AUTHORS  
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
EMBO Rep. 3 (12), 1152-1157 (2002)  
12446565

TITLE  
JOURNAL  
PUBMED  
REFERENCE  
2 (bases 1 to 24)

Balzerque, S.  
Direct Submission  
TITLE  
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT  
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

FEATURES  
source  
1. .24  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3702"  
/clone="576D12"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Wassilewskija"  
misc\_feature  
1..24  
/note="T-DNA flanking sequence left border"

ORIGIN  
Query Match 66.0%; Score 13.2; DB 10; Length 24;  
Best Local Similarity 83.3%; Pred. No. 3.5e+05;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGTTT 18  
|||||  
Db 7 TTATGGGTTTGGGGGT 24

RESULT 48  
AZ509683  
LOCUS  
DEFINITION  
37 bp DNA linear GSS 05-OCT-2000  
1M0352C18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0352C18 R, genomic survey sequence.

ACCESSION  
AZ509683 GI:10690999  
VERSION  
GSS.  
KEYWORDS  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 37)  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0352 row: C column: 18  
Seq primer: CACACGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 37.

FEATURES  
source  
1. .37  
Location/Qualifiers

```

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0352C18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN

Query Match 66.0%; Score 13.2; DB 9; Length 37;  
 Best Local Similarity 83.3%; Pred. No. 3.6e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTTGGGTTTTCGGGTTT 19  
 |||||  
 Db 19 TTTGGGACATGGGGTTT 36

RESULT 49  
 BX120037/c  
 LOCUS  
 DEFINITION Danio rerio genomic clone DKEY-61C20, genomic survey sequence.  
 ACCESSION BX120037  
 VERSION BX120037.1 GI:27950952  
 KEYWORDS GSS.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 40)  
 Humphray, S.J., Huckle, E. and Durham, J.L.  
 Direct Submission  
 Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Unpublished  
 This sequence was generated from the T7 end of BAC 61C20. 61C20 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:  
 http://www.sanger.ac.uk/Projects/D\_rerio/  
 Location/Qualifiers  
 1..40  
 /organism="Danio rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="DKEY-61C20"  
 /tissue\_type="testis"  
 /note="vector pindigobAC-536"

ORIGIN

Query Match 66.0%; Score 13.2; DB 10; Length 40;  
 Best Local Similarity 78.9%; Pred. No. 3.6e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TTTGGGTTTTCGGGTTT 20  
 |||||  
 Db 39 TTTGGGTTTTCGGTNTT 21

RESULT 50  
 AL944738/c  
 LOCUS  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-284D09-015289, genomic survey sequence.  
 ACCESSION AL944738  
 VERSION AL944738.1 GI:24401360  
 KEYWORDS GSS.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 1  
 Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.  
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana  
 Bioinformatics 19 (11), 1441-1442 (2003)  
 12874060

REFERENCE

2 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.  
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
 14756321  
 3 Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weisshaar, B.  
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
 BioTechniques 35 (6), 1164-1168 (2003)  
 14682050  
 4 (bases 1 to 41)  
 Li, Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.  
 Direct Submission  
 Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone F3F19. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.  
 Location/Qualifiers  
 1..41  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="GK-284D09-015289"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Col-0"  
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

FEATURES

source

ORIGIN

Query Match 66.0%; Score 13.2; DB 10; Length 41;  
 Best Local Similarity 83.3%; Pred. No. 3.6e+05;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTT 20  
| | | | | | | | | |  
Db 41 TAGGGGTTTAGGGTATT 24

Search completed: February 15, 2006, 21:09:47  
Job time : 1353.25 secs

**THIS PAGE BLANK (USPTO)**







244 12 60.0 30 2 US-08-744-139-53 Sequence 53, Appl  
245 12 60.0 30 3 US-08-987-574-12 Sequence 12, Appl  
246 12 60.0 30 3 US-08-535-168-12 Sequence 12, Appl  
247 12 60.0 30 3 US-09-017-974-12 Sequence 12, Appl  
248 12 60.0 30 3 US-08-682-255A-12 Sequence 12, Appl  
249 12 60.0 30 3 US-09-429-130-12 Sequence 12, Appl  
250 12 60.0 30 3 US-08-779-599-53 Sequence 53, Appl  
251 12 60.0 30 6 PCT-US95-06639-55 Sequence 55, Appl  
252 12 60.0 30 6 PCT-US95-06639-61 Sequence 61, Appl  
253 12 60.0 30 6 PCT-US96-11786-12 Sequence 12, Appl  
254 12 60.0 32 3 US-10-053-883-56 Sequence 56, Appl  
255 12 60.0 32 3 US-10-053-883-89 Sequence 89, Appl  
256 12 60.0 34 2 US-07-753-7388-3 Sequence 3, Appl  
257 12 60.0 36 3 US-10-053-883-67 Sequence 67, Appl  
258 12 60.0 36 6 PCT-US93-07743-4 Sequence 4, Appl  
259 12 60.0 36 6 PCT-US93-07743-9 Sequence 9, Appl  
260 12 60.0 38 6 PCT-US93-08329-9 Sequence 9, Appl  
261 12 60.0 38 6 PCT-US93-08329-10 Sequence 10, Appl  
262 12 60.0 45 2 US-08-171-389-27 Sequence 27, Appl  
263 12 60.0 45 2 US-08-123-936-27 Sequence 27, Appl  
264 12 60.0 45 2 US-08-475-228A-27 Sequence 27, Appl  
265 12 60.0 45 3 US-08-482-080A-27 Sequence 27, Appl  
266 12 60.0 45 3 US-09-354-947-27 Sequence 27, Appl  
267 12 60.0 45 3 US-09-993-346-27 Sequence 27, Appl  
268 12 60.0 45 6 PCT-US93-12388-27 Sequence 27, Appl  
269 12 60.0 46 3 US-10-053-883-65 Sequence 65, Appl  
270 12 60.0 47 3 US-09-345-882-50 Sequence 50, Appl  
271 12 60.0 47 3 US-10-071-179-50 Sequence 50, Appl  
272 12 60.0 50 3 US-10-131-827-1904 Sequence 1904, Ap  
273 12 60.0 50 3 US-10-131-827-5760 Sequence 5760, Ap  
274 11.8 59.0 20 2 US-08-117-952-297 Sequence 297, Appl  
275 11.8 59.0 20 3 US-08-755-587-89 Sequence 89, Appl  
276 11.8 59.0 20 3 US-09-166-186-183 Sequence 183, App  
277 11.8 59.0 20 3 US-09-313-932-183 Sequence 183, App  
278 11.8 59.0 24 2 US-08-844-521-46 Sequence 46, Appl  
279 11.8 59.0 24 3 US-08-891-463-24 Sequence 24, Appl  
280 11.8 59.0 24 3 US-08-766-528-46 Sequence 46, Appl  
281 11.8 59.0 24 3 US-08-766-528-47 Sequence 47, Appl  
282 11.8 59.0 24 3 US-08-817-575-7 Sequence 7, Appl  
283 11.8 59.0 24 3 US-09-769-352-7 Sequence 7, Appl  
284 11.8 59.0 24 3 US-09-151-376-58 Sequence 58, Appl  
285 11.8 59.0 24 3 US-09-661-858-46 Sequence 46, Appl  
286 11.8 59.0 24 3 US-09-661-858-47 Sequence 47, Appl  
287 11.8 59.0 25 3 US-09-396-196G-27658 Sequence 27658, A  
288 11.8 59.0 26 2 US-08-033-320-2 Sequence 2, Appl  
289 11.8 59.0 26 2 US-08-336-069-2 Sequence 2, Appl  
290 11.8 59.0 27 2 US-08-483-743-13 Sequence 13, Appl  
291 11.8 59.0 27 2 US-08-483-743-14 Sequence 14, Appl  
292 11.8 59.0 27 2 US-08-474-624-13 Sequence 13, Appl  
293 11.8 59.0 27 3 US-09-109-957-1 Sequence 1, Appl  
294 11.8 59.0 27 3 US-09-109-957-2 Sequence 2, Appl  
295 11.8 59.0 28 3 US-09-296-840A-8 Sequence 8, Appl  
296 11.8 59.0 30 6 PCT-US93-01901-34 Sequence 34, Appl  
297 11.8 59.0 35 3 US-09-302-620B-11 Sequence 11, Appl  
298 11.8 59.0 35 3 US-09-912-161-21 Sequence 21, Appl  
299 11.8 59.0 35 3 US-09-911-781-25 Sequence 25, Appl  
300 11.8 59.0 35 3 US-10-400-902-25 Sequence 25, Appl

## ALIGNMENTS

RESULT 1  
US-08-403-888A-121  
; Sequence 121, Application US/08403888A  
; Patent No. 5952490  
; GENERAL INFORMATION:  
; APPLICANT: Hanecak et al.  
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core  
; TITLE OF INVENTION: Sequence  
; NUMBER OF SEQUENCES: 146  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP

; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,888A  
; FILING DATE: 12-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/954,185  
; FILING DATE: 29-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul K. Legaard  
; REGISTRATION NUMBER: 38,534  
; REFERENCE/DOCKET NUMBER: ISIS-1229  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 121:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: N is A or C or G or T/U  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 2  
; OTHER INFORMATION: N is A or C or G or T/U  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 3  
; OTHER INFORMATION: N is A or C or G or T/U  
; US-08-403-888A-121  
Query Match 100.0%; Score 20; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 6.9;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTTTGGGGTTTGGGGTTTT 20  
Db 8 TTTTGGGGTTTGGGGTTTT 27  
RESULT 2  
US-08-851-843A-42  
; Sequence 42, Application US/08851843A  
; Patent No. 6093809  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6093809el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America



```

; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/08/854,050
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; US-08-854-050-42

```

```

Query Match 100.0%; Score 20; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 25 TTTTGGGGTTTGGGGTTTT 44

```

```

RESULT 5
US-09-430-323-42
; Sequence 42, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.

```

```

; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/09/430,323
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
; US-09-430-323-42

```

```

Query Match 100.0%; Score 20; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 25 TTTTGGGGTTTGGGGTTTT 44

```

```

RESULT 6
US-09-402-181B-568
; Sequence 568, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:

```

ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181B  
FILING DATE: 29-Sep-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 568:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..44  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 25 TTTTGGGTTTGGGGTTTT 44

## RESULT 7

US-09-721-456-568  
Sequence 568, Application US/09721456  
Patent No. 6617110  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.

Morin, Gregg B.  
Harley, Calvin B. H.  
Andrews, William B. H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,456  
FILING DATE: 22-No. 6617110-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 568:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..44  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 568:  
US-09-721-456-568

Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 25 TTTTGGGTTTGGGGTTTT 44

## RESULT 8

US-09-766-253-42  
; Sequence 42, Application US/09766253  
; Patent No. 6808880  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. 6808880el Telomerase  
; NUMBER OF SEQUENCES: 171  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/766,253  
; FILING DATE: 19-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/846,017  
; FILING DATE: 1997-04-25  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002920US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
US-09-766-253-42  
Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
DB 25 TTTTGGGGTTTGGGGTTTT 44  
RESULT 9  
US-10-054-295-42  
; Sequence 42, Application US/10054295  
; Patent No. 6921664  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND  
; TITLE OF INVENTION: TELOMERASE VARIANTS  
; FILE REFERENCE: 018/062  
; CURRENT APPLICATION NUMBER: US/09/438,486A  
; CURRENT FILING DATE: 1999-11-12

Harley, Calvin  
Andrews, William H.  
; TITLE OF INVENTION: No. 6921664el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/054,295  
; FILING DATE: 18-Jan-2002  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/854,050  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
US-10-054-295-42  
Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
DB 25 TTTTGGGGTTTGGGGTTTT 44  
RESULT 10  
US-09-438-486A-42  
; Sequence 42, Application US/09438486A  
; Patent No. 6927285  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: LINGNER, JOACHIM  
; APPLICANT: NAKAMURA, TORU  
; APPLICANT: CHAPMAN, KAREN B.  
; APPLICANT: MORIN, GREGG B.  
; APPLICANT: HARLEY, CALVIN  
; APPLICANT: ANDREWS, WILLIAM H.  
; TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND  
; TITLE OF INVENTION: TELOMERASE VARIANTS  
; FILE REFERENCE: 018/062  
; CURRENT APPLICATION NUMBER: US/09/438,486A  
; CURRENT FILING DATE: 1999-11-12

```
/ PRIOR APPLICATION NUMBER: 08/851,843
/ PRIOR FILING DATE: 1997-05-06
/ PRIOR APPLICATION NUMBER: 08/846,017
/ PRIOR FILING DATE: 1997-04-25
/ PRIOR APPLICATION NUMBER: 08/844,419
/ PRIOR FILING DATE: 1997-04-18
/ PRIOR APPLICATION NUMBER: 08/724,643
/ PRIOR FILING DATE: 1996-10-01
/ NUMBER OF SEQ ID NOS: 223
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 42
/ LENGTH: 44
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-438-486A-42

Query Match          100.0%; Score 20; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20
   |||||
Db 25 TTTTGGGTTTGGGGTTT 44

RESULT 11
US-08-851-843A-41
/ Sequence 41, Application US/08851843A
/ Patent No. 6093809
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: No. 6093809el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/851,843A
/ FILING DATE: 06-MAY-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
```

```
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
US-08-851-843A-41

Query Match          100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20
   |||||
Db 27 TTTTGGGTTTGGGGTTT 46

RESULT 12
US-08-974-549A-567
/ Sequence 567, Application US/08974549A
/ Patent No. 6166178
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin B.
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/974,549A
/ FILING DATE: 19-NOV-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 567:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..46
; OTHER INFORMATION: /note= "hairpin primer"
;
US-08-974-549A-567

Query Match 100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 27 TTTTGGGTTTGGGGTTTT 46

RESULT 13
US-08-854-050-41
; Sequence 41, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..46
; OTHER INFORMATION: /desc = "DNA"
;
US-08-854-050-41

Query Match 100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 27 TTTTGGGTTTGGGGTTTT 46

RESULT 14
US-09-430-323-41
; Sequence 41, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
```

```
/
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-430-323-41

Query Match      100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTTGGGGTTTGGGGTTTT 20
        |||||
Db      27 TTTTGGGGTTTGGGGTTTT 46

RESULT 15
US-09-402-181B-567
/ Sequence 567, Application US/09402181B
/ Patent No. 6610839
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,181B
/ FILING DATE: 29-Sep-1997
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/
```

```
/
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ausenhus, Scott L.
/ REGISTRATION NUMBER: 42,271
/ REFERENCE/DOCKET NUMBER: 015389-002620US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 567:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..46
/ OTHER INFORMATION: /note= "hairpin primer"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 567:
US-09-402-181B-567

Query Match      100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTTGGGGTTTGGGGTTTT 20
        |||||
Db      27 TTTTGGGGTTTGGGGTTTT 46

RESULT 16
US-09-721-456-567
/ Sequence 567, Application US/09721456
/ Patent No. 6617110
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/721,456
/ FILING DATE: 22-No. 6617110-2000
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/974,549A
/ FILING DATE: 19-NOV-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/
```





/ FILING DATE: 18-APR-1997  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002930US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 41:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 46 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "DNA"  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-10-054-295-41

Query Match 100.0%; Score 20; DB 3; Length 46;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 27 TTTTGGGGTTTGGGGTTTT 46

RESULT 19  
US-09-438-486A-41  
/ Sequence 41, Application US/09438486A  
/ Patent No. 6927285  
/ GENERAL INFORMATION:  
/ APPLICANT: CECHE, THOMAS R.  
/ APPLICANT: LINGNER, JOACHIM  
/ APPLICANT: NAKAMURA, TORU  
/ APPLICANT: CHAPMAN, KAREN B.  
/ APPLICANT: MORIN, GREGG B.  
/ APPLICANT: HARLEY, CALVIN  
/ APPLICANT: ANDREWS, WILLIAM H.  
/ TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND  
/ TITLE OF INVENTION: TELOMERASE VARIANTS  
/ FILE REFERENCE: 018/062  
/ CURRENT APPLICATION NUMBER: US/09/438,486A  
/ CURRENT FILING DATE: 1999-11-12  
/ PRIOR APPLICATION NUMBER: 08/851,843  
/ PRIOR FILING DATE: 1997-05-06  
/ PRIOR APPLICATION NUMBER: 08/846,017  
/ PRIOR FILING DATE: 1997-04-25  
/ PRIOR APPLICATION NUMBER: 08/844,419  
/ PRIOR FILING DATE: 1997-04-18  
/ PRIOR APPLICATION NUMBER: 08/724,643  
/ PRIOR FILING DATE: 1996-10-01  
/ NUMBER OF SEQ ID NOS: 23  
/ SOFTWARE: PatentIn Ver. 3.2  
/ SEQ ID NO 41  
/ LENGTH: 46  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide  
US-09-438-486A-41

Query Match 100.0%; Score 20; DB 3; Length 46;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 27 TTTTGGGGTTTGGGGTTTT 46

RESULT 20  
US-08-851-843A-37  
/ Sequence 37, Application US/08851843A  
/ Patent No. 6093809  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ APPLICANT: Lingner, Joachim  
/ APPLICANT: Nakamura, Toru  
/ APPLICANT: Chapman, Karen B.  
/ APPLICANT: Morin, Gregg B.  
/ APPLICANT: Harley, Calvin  
/ APPLICANT: Andrews, William H.  
/ TITLE OF INVENTION: No. 6093809el Telomerase  
/ NUMBER OF SEQUENCES: 225  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/851,843A  
/ FILING DATE: 06-MAY-1997  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/846,017  
/ FILING DATE: 25-APR-1997  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/844,419  
/ FILING DATE: 18-APR-1997  
/ CLASSIFICATION:  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ CLASSIFICATION:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002930US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 37:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 48 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "DNA"  
US-08-851-843A-37

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 21  
US-08-851-843A-40  
/ Sequence 40, Application US/08851843A  
/ Patent No. 6093809

GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin H.  
TITLE OF INVENTION: No. 6093809e1 Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-843A-40

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTGGGGTTT 20  
Db 29 TTTTGGGTTTGGGGTTT 48

RESULT 22  
US-08-974-549A-564  
Sequence 564, Application US/08974549A  
Patent No. 6166178  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin H.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 564:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..48  
OTHER INFORMATION: /note= "hairpin primer"  
US-08-974-549A-564

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;



QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 25  
US-09-430-323-37  
; Sequence 37, Application US/09430323  
; Patent No. 6309867  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.

TITLE OF INVENTION: No. 6309867el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/430,323  
FILING DATE: 29-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-430-323-37  
Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 26  
US-09-430-323-40  
; Sequence 40, Application US/09430323  
; Patent No. 6309867  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.  
; TITLE OF INVENTION: No. 6309867el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/430,323  
FILING DATE: 29-Oct-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-09-430-323-40  
Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 27  
US-09-402-181B-564  
; Sequence 564, Application US/09402181B  
; Patent No. 6610839  
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181B  
FILING DATE: 29-Sep-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 564:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..48  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 564:  
US-09-402-181B-564

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 28  
US-09-721-456-564  
Sequence 564, Application US/09721456  
Patent No. 6617110  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/721,456  
FILING DATE: 22-No. 6617110-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 564:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..48  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 564:

US-09-721-456-564

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
DB 29 TTTTGGGTTTGGGGTTTT 48

RESULT 29

US-09-766-253-37

; Sequence 37, Application US/09766253

; Patent No. 6808880

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: No. 6808880el Telomerase

; NUMBER OF SEQUENCES: 171

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/766,253

; FILING DATE: 19-Jan-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/846,017

; FILING DATE: 1997-04-25

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002920US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 48 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "DNA"

; SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-766-253-37

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
DB 29 TTTTGGGTTTGGGGTTTT 48

RESULT 30

US-09-766-253-40

; Sequence 40, Application US/09766253

; Patent No. 6808880

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: No. 6808880el Telomerase

; NUMBER OF SEQUENCES: 171

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/766,253

; FILING DATE: 19-Jan-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/846,017

; FILING DATE: 1997-04-25

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002920US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 48 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "DNA"

; SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-766-253-40

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
DB 29 TTTTGGGTTTGGGGTTTT 48

RESULT 31

US-10-054-295-37

; Sequence 37, Application US/10054295

; Patent No. 6921664

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

Andrews, William H.  
TITLE OF INVENTION: No. 6921664e1 Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/054,295  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/854,050  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-10-054-295-37  
Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTTGGGGTTTT 20  
Db 29 TTTTGGGGTTTTGGGGTTTT 48  
RESULT 32  
US-10-054-295-40  
Sequence 40, Application US/10054295  
Patent No. 6921664  
GENERAL INFORMATION:  
APPLICANT: Cecch, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. 6921664e1 Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco

STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/054,295  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/854,050  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-10-054-295-40  
Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTTGGGGTTTT 20  
Db 29 TTTTGGGGTTTTGGGGTTTT 48  
RESULT 33  
US-09-438-486A-37  
Sequence 37, Application US/09438486A  
Patent No. 6927285  
GENERAL INFORMATION:  
APPLICANT: CECH, THOMAS R.  
APPLICANT: LINGNER, JOACHIM  
APPLICANT: NAKAMURA, TORU  
APPLICANT: CHAPMAN, KAREN B.  
APPLICANT: MORIN, GREGG B.  
APPLICANT: HARLEY, CALVIN  
APPLICANT: ANDREWS, WILLIAM H.  
TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND  
TITLE OF INVENTION: TELOMERASE VARIANTS  
FILE REFERENCE: 018/062  
CURRENT APPLICATION NUMBER: US/09/438,486A  
CURRENT FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 08/851,843  
PRIOR FILING DATE: 1997-05-06  
PRIOR APPLICATION NUMBER: 08/846,017  
PRIOR FILING DATE: 1997-04-25  
PRIOR APPLICATION NUMBER: 08/844,419  
PRIOR FILING DATE: 1997-04-18  
PRIOR APPLICATION NUMBER: 08/724,643  
PRIOR FILING DATE: 1996-10-01



; NUMBER OF SEQ ID NOS: 223  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 37  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide  
US-09-438-486A-37

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||  
DB 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 34  
US-09-438-486A-40  
; Sequence 40, Application US/09438486A  
; Patent No. 6927285  
; GENERAL INFORMATION:  
; APPLICANT: CECHE, THOMAS R.  
; APPLICANT: LINGNER, JOACHIM  
; APPLICANT: NAKAMURA, TORU  
; APPLICANT: CHAPMAN, KAREN B.  
; APPLICANT: MORIN, GREGG B.  
; APPLICANT: HARLEY, CALVIN  
; APPLICANT: ANDREWS, WILLIAM H.  
; TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND  
; FILE REFERENCE: 018/062  
; CURRENT APPLICATION NUMBER: US/09/438,486A  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 08/851,843  
; PRIOR FILING DATE: 1997-05-06  
; PRIOR APPLICATION NUMBER: 08/846,017  
; PRIOR FILING DATE: 1997-04-25  
; PRIOR APPLICATION NUMBER: 08/844,419  
; PRIOR FILING DATE: 1997-04-18  
; PRIOR APPLICATION NUMBER: 08/724,643  
; PRIOR FILING DATE: 1996-10-01  
; NUMBER OF SEQ ID NOS: 223  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 40  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide  
US-09-438-486A-40

Query Match 100.0%; Score 20; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||  
DB 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 35  
US-08-851-843A-39  
; Sequence 39, Application US/08851843A  
; Patent No. 6093809  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6093809el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/851,843A  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-08-851-843A-39

Query Match 100.0%; Score 20; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||  
DB 31 TTTTGGGGTTTGGGGTTTT 50

RESULT 36  
US-08-974-549A-566  
; Sequence 566, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:

```
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/974,549A
;; FILING DATE: 19-NOV-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/844,419
;; FILING DATE: 18-APR-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/911,312
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/912,951
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/915,503
;; FILING DATE: 14-AUG-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17618
;; FILING DATE: 01-OCT-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US97/17885
;; FILING DATE: 01-OCT-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph Ted
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002610US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 566:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 50 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; NAME/KEY: -
;; LOCATION: 1..50
;; OTHER INFORMATION: /note= "hairpin primer"
US-08-974-549A-566
```

```
Query Match 100.0%; Score 20; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTTTGGGTTTGGGGTTTT 20
    |||||||
Db 31 TTTTGGGTTTGGGGTTTT 50
```

```
RESULT 37
US-08-854-050-39
; Sequence 39, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-854-050-39
```

```
Query Match 100.0%; Score 20; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TTTTGGGTTTGGGGTTTT 20
    |||||||
Db 31 TTTTGGGTTTGGGGTTTT 50
```

## RESULT 38

US-09-430-323-39

; Sequence 39, Application US/09430323

; Patent No. 6309867

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: No. 6309867el Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/430,323

; FILING DATE: 29-Oct-1999

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002930US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 39:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 50 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "DNA"

; SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-430-323-39

Query Match 100.0%; Score 20; DB 3; Length 50;

Best Local Similarity 100.0%; Pred. No. 7.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20

|||||

Db 31 TTTTGGGGTTTGGGGTTTT 50

|||||

## RESULT 39

US-09-402-181B-566

; Sequence 566, Application US/09402181B

; Patent No. 6610839

; GENERAL INFORMATION:

;

APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin B.

; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 633

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/402,181B

; FILING DATE: 29-Sep-1997

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Ausenhus, Scott L.

; REGISTRATION NUMBER: 42,271

; REFERENCE/DOCKET NUMBER: 015389-002620US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 566:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 50 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; FEATURE:

; NAME/KEY: -

; LOCATION: 1..50

; OTHER INFORMATION: /note= "hairpin primer"

; SEQUENCE DESCRIPTION: SEQ ID NO: 566:

US-09-402-181B-566

Query Match 100.0%; Score 20; DB 3; Length 50;

Best Local Similarity 100.0%; Pred. No. 7.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20

|||||

Db 31 TTTTGGGGTTTGGGGTTTT 50

|||||

RESULT 40  
US-09-721-456-566  
; Sequence 566, Application US/09721456  
; Patent No. 6617110  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; ; Lingner, Joachim  
; ; Nakamura, Toru  
; ; Chapman, Karen B.  
; ; Morin, Gregg B.  
; ; Harley, Calvin B.  
; ; Andrews, William H.  
; ;  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/721,456  
; FILING DATE: 22-Nov. 6617110-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 566:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..50  
; OTHER INFORMATION: /note= "hairpin primer"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 566:

US-09-721-456-566  
Query Match 100.0%; Score 20; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||  
Db 31 TTTTGGGGTTTGGGGTTTT 50  
|||  
RESULT 41  
US-09-766-253-39  
; Sequence 39, Application US/09766253  
; Patent No. 6808880  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; ; Lingner, Joachim  
; ; Nakamura, Toru  
; ; Chapman, Karen B.  
; ; Morin, Gregg B.  
; ; Harley, Calvin  
; ; Andrews, William H.  
; ;  
; TITLE OF INVENTION: No. 6808880el Telomerase  
; NUMBER OF SEQUENCES: 171  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/766,253  
; FILING DATE: 19-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/846,017  
; FILING DATE: 1997-04-25  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002920US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-766-253-39  
Query Match 100.0%; Score 20; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||  
Db 31 TTTTGGGGTTTGGGGTTTT 50  
|||

RESULT 42  
US-10-054-295-39  
Sequence 39, Application US/10054295  
Patent No. 6921664  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
LINGNER, JOACHIM  
NAKAMURA, TORU  
CHAPMAN, KAREN B.  
MORIN, GREGG B.  
HARLEY, CALVIN  
ANDREWS, WILLIAM H.  
TITLE OF INVENTION: No. 6921664el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/054,295  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/854,050  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-10-054-295-39  
Query Match 100.0%; Score 20; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 31 TTTTGGGGTTTGGGGTTTT 50  
RESULT 43  
US-09-438-486A-39  
Sequence 39, Application US/09438486A  
Patent No. 6927285  
GENERAL INFORMATION:  
APPLICANT: CECH, THOMAS R.  
LINGNER, JOACHIM

APPLICANT: NAKAMURA, TORU  
APPLICANT: CHAPMAN, KAREN B.  
APPLICANT: MORIN, GREGG B.  
APPLICANT: HARLEY, CALVIN  
APPLICANT: ANDREWS, WILLIAM H.  
TITLE OF INVENTION: GENE FOR HUMAN TELOMERASE REVERSE TRANSCRIPTASE AND  
TELOMERASE VARIANTS  
FILE REFERENCE: 018/062  
CURRENT APPLICATION NUMBER: US/09/438,486A  
CURRENT FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 08/851,843  
PRIOR FILING DATE: 1997-05-06  
PRIOR APPLICATION NUMBER: 08/846,017  
PRIOR FILING DATE: 1997-04-25  
PRIOR APPLICATION NUMBER: 08/844,419  
PRIOR FILING DATE: 1997-04-18  
PRIOR APPLICATION NUMBER: 08/724,643  
PRIOR FILING DATE: 1996-10-01  
NUMBER OF SEQ ID NOS: 223  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 39  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide  
US-09-438-486A-39  
Query Match 100.0%; Score 20; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
Db 31 TTTTGGGGTTTGGGGTTTT 50  
RESULT 44  
US-08-851-843A-39/c  
Sequence 39, Application US/08851843A  
Patent No. 6093809  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6093809el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419

```
/ FILING DATE: 18-APR-1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 39:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ US-08-851-843A-39

Query Match 90.0%; Score 18; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 18
Db 18 TTTTGGGTTTGGGGTTT 1

RESULT 45
US-08-974-549A-566/c
/ Sequence 566, Application US/08974549A
/ Patent No. 6166178
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin B.
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/974,549A
/ FILING DATE: 19-NOV-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/851,843
```

```
/ FILING DATE: 06-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/17618
/ FILING DATE: 01-OCT-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Ted
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 566:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..50
/ OTHER INFORMATION: /note= "hairpin primer"
/ US-08-974-549A-566

Query Match 90.0%; Score 18; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 18
Db 18 TTTTGGGTTTGGGGTTT 1

RESULT 46
US-08-854-050-39/c
/ Sequence 39, Application US/08854050
/ Patent No. 6261836
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: No. 6261836el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
/
/
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/854,050
/ FILING DATE: 09-MAY-1997
/ CLASSIFICATION: 536
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ CLASSIFICATION: 536
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ CLASSIFICATION: 536
/
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ CLASSIFICATION: 536
/
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION: 536
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/
/ INFORMATION FOR SEQ ID NO: 39:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/
/
/ US-08-854-050-39
/
/ Query Match 90.0%; Score 18; DB 3; Length 50;
/ Best Local Similarity 100.0%; Pred. No. 50;
/ Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 TTTTGGGGTTTGGGGTTT 18
/ Db 18 TTTTGGGGTTTGGGGTTT 1
/
/ RESULT 47
/ US-09-430-323-39/c
/ Sequence 39, Application US/09430323
/ Patent No. 6309867
/
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/
/ TITLE OF INVENTION: No. 6309867el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
```

```
/
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/430,323
/ FILING DATE: 29-Oct-1999
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/
/ INFORMATION FOR SEQ ID NO: 39:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 39:
/
/ US-09-430-323-39
/
/ Query Match 90.0%; Score 18; DB 3; Length 50;
/ Best Local Similarity 100.0%; Pred. No. 50;
/ Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 TTTTGGGGTTTGGGGTTT 18
/ Db 18 TTTTGGGGTTTGGGGTTT 1
/
/ RESULT 48
/ US-09-402-181B-566/c
/ Sequence 566, Application US/09402181B
/ Patent No. 6610839
/
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/
/ TITLE OF INVENTION: Human telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,181B
/ FILING DATE: 29-Sep-1997
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/
```

```

; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 566:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..50
; OTHER INFORMATION: /note= "hairpin primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 566:
US-09-402-181B-566
Query Match 90.0%; Score 18; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGTT 18
Db 18 TTTTGGGTTTGGGTT 1

RESULT 49
US-09-721-456-566/c
; Sequence 566, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 566:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..50
; OTHER INFORMATION: /note= "hairpin primer"
; SEQUENCE DESCRIPTION: SEQ ID NO: 566:
US-09-721-456-566
Query Match 90.0%; Score 18; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGTT 18
Db 18 TTTTGGGTTTGGGTT 1

RESULT 50
US-09-766-253-39/c
; Sequence 39, Application US/09766253
; Patent No. 6808880
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6808880el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
```



ADDRESSES: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/766,253  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/846,017  
FILING DATE: 1997-04-25  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002920US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-766-253-39

Query Match 90.0%; Score 18; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTTTGGGGTTTGGGGTT 18  
Db 18 TTTTGGGGTTTGGGGTT 1

Search completed: February 15, 2006, 21:14:09  
Job time : 48.9587 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 01:43:22 ; Search time 290.248 Seconds  
(without alignments)  
569.815 Million cell updates/sec

Title: US-09-669-187A-73

Perfect score: 20

Sequence: 1 ttttgggttttgggggtttt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413469005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications NA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-09-776-479-73 Sequence 73, Appl
2	20	100.0	20	3	US-09-776-479-73 Sequence 73, Appl
3	20	100.0	20	5	US-10-112-653-67 Sequence 67, Appl
4	20	100.0	20	5	US-10-112-653-67 Sequence 67, Appl
5	20	100.0	20	6	US-10-314-578-73 Sequence 73, Appl
6	20	100.0	20	6	US-10-314-578-73 Sequence 73, Appl
7	20	100.0	28	6	US-10-118-854-28 Sequence 28, Appl
8	20	100.0	28	7	US-10-607-455-28 Sequence 28, Appl
9	20	100.0	28	9	US-10-683-480-28 Sequence 28, Appl
10	20	100.0	28	9	US-10-690-984-11 Sequence 11, Appl
11	20	100.0	28	9	US-10-961-479-29 Sequence 29, Appl
12	20	100.0	44	3	US-09-843-676-42 Sequence 42, Appl
13	20	100.0	44	3	US-09-843-676-42 Sequence 42, Appl
14	20	100.0	44	3	US-09-438-486-42 Sequence 42, Appl
15	20	100.0	44	5	US-10-053-758-41 Sequence 42, Appl
16	20	100.0	44	5	US-10-054-295-42 Sequence 42, Appl
17	20	100.0	44	6	US-10-054-611-41 Sequence 42, Appl
18	20	100.0	44	6	US-10-325-810-568 Sequence 568, App
19	20	100.0	44	8	US-10-877-124-568 Sequence 568, App
20	20	100.0	44	8	US-10-877-124-568 Sequence 568, App
21	20	100.0	44	8	US-10-877-146-568 Sequence 568, App
22	20	100.0	46	3	US-09-843-676-41 Sequence 41, Appl
23	20	100.0	46	3	US-09-766-253-41 Sequence 41, Appl

C 97	16.8	84.0	48	5	US-10-053-758-37	Sequence 37, Appl	C 170	14.2	71.0	26	5	US-10-054-611-30	Sequence 30, Appl
C 98	16.8	84.0	48	5	US-10-053-758-40	Sequence 40, Appl	C 171	14.2	71.0	26	5	US-10-054-611-60	Sequence 60, Appl
C 99	16.8	84.0	48	5	US-10-054-295-37	Sequence 37, Appl	C 172	14.2	71.0	26	6	US-10-325-810-557	Sequence 557, App
C 100	16.8	84.0	48	5	US-10-054-295-40	Sequence 40, Appl	C 173	14.2	71.0	26	8	US-10-877-124-557	Sequence 557, App
C 101	16.8	84.0	48	5	US-10-054-611-37	Sequence 37, Appl	C 174	14.2	71.0	26	8	US-10-877-023-557	Sequence 557, App
C 102	16.8	84.0	48	5	US-10-054-611-40	Sequence 40, Appl	C 175	14.2	71.0	26	8	US-10-877-146-557	Sequence 557, App
C 103	16.8	84.0	48	6	US-10-325-810-564	Sequence 564, App	C 176	14.2	71.0	32	6	US-10-369-214-99	Sequence 99, Appl
C 104	16.8	84.0	48	8	US-10-877-124-564	Sequence 564, App	C 177	14.2	71.0	46	10	US-11-049-446-117	Sequence 117, App
C 105	16.8	84.0	48	8	US-10-877-022-564	Sequence 564, App	C 178	14.2	71.0	50	6	US-10-131-827-4217	Sequence 4217, Ap
C 106	16.8	84.0	48	8	US-10-877-146-564	Sequence 564, App	C 179	14.2	71.0	50	6	US-10-131-827-7605	Sequence 7605, Ap
C 107	16.8	84.0	50	6	US-10-131-827-5734	Sequence 5734, Ap	C 180	14	70.0	15	3	US-09-843-676-43	Sequence 43, Appl
C 108	16	80.0	16	3	US-09-843-676-61	Sequence 61, Appl	C 181	14	70.0	15	3	US-09-843-676-45	Sequence 45, Appl
C 109	16	80.0	16	3	US-09-766-253-61	Sequence 61, Appl	C 182	14	70.0	15	3	US-09-766-253-43	Sequence 43, Appl
C 110	16	80.0	16	3	US-09-438-486-61	Sequence 61, Appl	C 183	14	70.0	15	3	US-09-766-253-45	Sequence 45, Appl
C 111	16	80.0	16	5	US-10-053-758-61	Sequence 61, Appl	C 184	14	70.0	15	3	US-09-438-486-43	Sequence 43, Appl
C 112	16	80.0	16	5	US-10-054-295-61	Sequence 61, Appl	C 185	14	70.0	15	3	US-09-438-486-45	Sequence 45, Appl
C 113	16	80.0	16	6	US-10-054-611-61	Sequence 61, Appl	C 186	14	70.0	15	5	US-10-053-758-43	Sequence 43, Appl
C 114	16	80.0	16	6	US-10-325-810-114	Sequence 114, App	C 187	14	70.0	15	5	US-10-053-758-45	Sequence 45, Appl
C 115	16	80.0	16	8	US-10-877-124-114	Sequence 114, App	C 188	14	70.0	15	5	US-10-054-295-43	Sequence 43, Appl
C 116	16	80.0	16	8	US-10-877-022-114	Sequence 114, App	C 189	14	70.0	15	5	US-10-054-295-45	Sequence 45, Appl
C 117	16	80.0	16	8	US-10-877-146-114	Sequence 114, App	C 190	14	70.0	15	5	US-10-054-611-43	Sequence 43, Appl
C 118	15.8	79.0	20	10	US-11-166-990-39	Sequence 39, Appl	C 191	14	70.0	15	5	US-10-054-611-45	Sequence 45, Appl
C 119	15.4	77.0	19	8	US-10-845-667-1035	Sequence 1035, Ap	C 192	14	70.0	15	6	US-10-325-810-113	Sequence 113, App
C 120	15.4	77.0	19	9	US-10-873-783-1416	Sequence 1416, Ap	C 193	14	70.0	15	8	US-10-877-124-113	Sequence 113, App
C 121	15.4	77.0	25	9	US-10-956-157-129722	Sequence 129722,	C 194	14	70.0	15	8	US-10-877-023-113	Sequence 113, App
C 122	15.4	77.0	26	10	US-11-049-446-60	Sequence 60, Appl	C 195	14	70.0	15	8	US-10-877-146-113	Sequence 113, App
C 123	15.2	76.0	26	6	US-10-085-906-51	Sequence 51, Appl	C 196	14	70.0	20	7	US-10-240-454-66	Sequence 66, Appl
C 124	15.2	76.0	50	6	US-10-131-827-1029	Sequence 1029, Ap	C 197	14	70.0	50	6	US-10-131-827-5325	Sequence 5325, Ap
C 125	14.8	74.0	22	9	US-10-708-204-67	Sequence 67, Appl	C 198	13.8	69.0	17	3	US-09-848-754A-1981	Sequence 1981, Ap
C 126	14.8	74.0	22	9	US-10-708-204-1790	Sequence 1790, Ap	C 199	13.8	69.0	24	7	US-10-456-930-32	Sequence 32, Appl
C 127	14.8	74.0	24	3	US-09-888-326-735	Sequence 735, App	C 200	13.8	69.0	24	8	US-10-266-103-11	Sequence 11, Appl
C 128	14.8	74.0	24	3	US-09-776-479-692	Sequence 692, App	C 201	13.8	69.0	24	8	US-10-266-103-48	Sequence 48, Appl
C 129	14.8	74.0	24	3	US-09-776-479-694	Sequence 694, App	C 202	13.8	69.0	25	7	US-10-719-956-257773	Sequence 257773,
C 130	14.8	74.0	24	3	US-09-776-479-883	Sequence 883, App	C 203	13.8	69.0	25	8	US-10-719-900-750629	Sequence 750629,
C 131	14.8	74.0	24	3	US-09-776-479-692	Sequence 692, App	C 204	13.8	69.0	25	2	US-08-781-986A-2244	Sequence 2244, Ap
C 132	14.8	74.0	24	3	US-09-776-479-694	Sequence 694, App	C 205	13.8	69.0	50	7	US-10-329-624-2244	Sequence 2244, Ap
C 133	14.8	74.0	24	3	US-09-776-479-883	Sequence 883, App	C 206	13.6	68.0	22	9	US-10-708-204-371	Sequence 371, App
C 134	14.8	74.0	24	5	US-10-112-653-665	Sequence 665, App	C 207	13.6	68.0	22	9	US-10-708-204-2154	Sequence 2154, Ap
C 135	14.8	74.0	24	5	US-10-112-653-667	Sequence 667, App	C 208	13.6	68.0	25	7	US-10-719-956-474680	Sequence 474680,
C 136	14.8	74.0	24	5	US-10-112-653-854	Sequence 854, App	C 209	13.6	68.0	25	7	US-10-719-956-692527	Sequence 692527,
C 137	14.8	74.0	24	5	US-10-017-995-692	Sequence 692, App	C 210	13.6	68.0	25	10	US-11-036-317-102555	Sequence 102555,
C 138	14.8	74.0	24	5	US-10-017-995-694	Sequence 694, App	C 211	13.6	68.0	25	10	US-11-036-317-433201	Sequence 433201,
C 139	14.8	74.0	24	5	US-10-017-995-883	Sequence 883, App	C 212	13.6	68.0	27	3	US-09-931-583-35	Sequence 35, Appl
C 140	14.8	74.0	24	6	US-10-163-862-4	Sequence 4, Appl	C 213	13.6	68.0	27	8	US-10-649-584-35	Sequence 35, Appl
C 141	14.8	74.0	24	6	US-10-140-013-32	Sequence 32, Appl	C 214	13.6	68.0	29	3	US-09-888-326-131	Sequence 131, App
C 142	14.8	74.0	24	6	US-10-314-578-692	Sequence 692, App	C 215	13.6	68.0	29	3	US-09-776-479-305	Sequence 305, App
C 143	14.8	74.0	24	6	US-10-314-578-694	Sequence 694, App	C 216	13.6	68.0	29	3	US-09-776-479-305	Sequence 305, App
C 144	14.8	74.0	24	6	US-10-314-578-883	Sequence 883, App	C 217	13.6	68.0	29	5	US-10-113-653-295	Sequence 295, App
C 145	14.8	74.0	24	6	US-10-309-775A-6	Sequence 6, Appl	C 218	13.6	68.0	29	5	US-10-017-995-305	Sequence 305, App
C 146	14.8	74.0	24	8	US-10-831-778-692	Sequence 692, App	C 219	13.6	68.0	29	6	US-10-831-778-305	Sequence 305, App
C 147	14.8	74.0	24	8	US-10-831-778-694	Sequence 694, App	C 220	13.6	68.0	29	8	US-10-831-778-305	Sequence 305, App
C 148	14.8	74.0	24	8	US-10-831-778-883	Sequence 883, App	C 221	13.6	68.0	32	3	US-09-888-326-734	Sequence 734, App
C 149	14.8	74.0	46	6	US-10-163-862-3	Sequence 3, Appl	C 222	13.6	68.0	32	3	US-09-776-479-429	Sequence 429, App
C 150	14.4	72.0	17	8	US-10-845-667-285	Sequence 285, App	C 223	13.6	68.0	32	3	US-09-776-479-429	Sequence 429, App
C 151	14.4	72.0	17	9	US-10-973-783-662	Sequence 662, App	C 224	13.6	68.0	32	5	US-10-113-653-411	Sequence 411, App
C 152	14.4	72.0	23	8	US-10-845-667-1250	Sequence 1250, Ap	C 225	13.6	68.0	32	5	US-10-017-995-429	Sequence 429, App
C 153	14.4	72.0	23	8	US-10-845-667-1480	Sequence 1480, Ap	C 226	13.6	68.0	32	5	US-10-207-655-238	Sequence 228, App
C 154	14.4	72.0	50	6	US-10-131-827-5465	Sequence 5465, Ap	C 227	13.6	68.0	32	6	US-10-076-674-1	Sequence 1, Appl
C 155	14.2	71.0	25	7	US-10-719-956-215749	Sequence 215749,	C 228	13.6	68.0	32	6	US-10-314-578-429	Sequence 429, App
C 156	14.2	71.0	25	7	US-10-719-956-215750	Sequence 215750,	C 229	13.6	68.0	32	6	US-10-355-161A-1	Sequence 1, Appl
C 157	14.2	71.0	25	8	US-10-719-900-519045	Sequence 519045,	C 230	13.6	68.0	32	8	US-10-831-778-429	Sequence 429, App
C 158	14.2	71.0	25	8	US-10-719-900-910968	Sequence 910968,	C 231	13.6	68.0	32	9	US-10-627-556-543	Sequence 543, App
C 159	14.2	71.0	25	10	US-11-036-317-624650	Sequence 624650,	C 232	13.6	68.0	42	5	US-10-140-164-70	Sequence 70, Appl
C 160	14.2	71.0	26	3	US-09-843-676-30	Sequence 30, Appl	C 233	13.6	68.0	42	6	US-10-073-333A-38	Sequence 38, Appl
C 161	14.2	71.0	26	3	US-09-843-676-60	Sequence 60, Appl	C 234	13.6	68.0	42	8	US-10-841-471-38	Sequence 38, Appl
C 162	14.2	71.0	26	3	US-09-766-253-30	Sequence 30, Appl	C 235	13.6	68.0	47	6	US-10-349-143-842	Sequence 842, App
C 163	14.2	71.0	26	3	US-09-766-253-60	Sequence 60, Appl	C 236	13.6	68.0	47	6	US-10-349-143-2476	Sequence 2476, Ap
C 164	14.2	71.0	26	3	US-09-438-486-30	Sequence 30, Appl	C 237	13.4	67.0	25	10	US-11-036-317-34432	Sequence 34432, A
C 165	14.2	71.0	26	3	US-09-438-486-60	Sequence 60, Appl	C 238	13.4	67.0	30	6	US-10-369-214-100	Sequence 100, App
C 166	14.2	71.0	26	5	US-10-053-758-30	Sequence 30, Appl	C 239	13.2	66.0	21	3	US-09-253-150-50	Sequence 50, Appl
C 167	14.2	71.0	26	5	US-10-053-758-60	Sequence 60, Appl	C 240	13.2	66.0	21	8	US-10-646-381-50	Sequence 50, Appl
C 168	14.2	71.0	26	5	US-10-054-295-30	Sequence 30, Appl	C 241	13.2	66.0	25	6	US-10-316-194-123	Sequence 123, App
C 169	14.2	71.0	26	5	US-10-054-295-60	Sequence 60, Appl	C 242	13.2	66.0	25	7	US-10-719-956-1069	Sequence 1069, Ap



```
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-67

Query Match          100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 1 TTTTGGGTTTGGGGTTTT 20

RESULT 4
US-10-017-995-73
; Sequence 73, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-73

Query Match          100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 1 TTTTGGGTTTGGGGTTTT 20

RESULT 5
US-10-314-578-73
; Sequence 73, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
US-10-314-578-73

Query Match          100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 1 TTTTGGGTTTGGGGTTTT 20

RESULT 6
US-10-831-778-73
; Sequence 73, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-73

Query Match          100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 1 TTTTGGGTTTGGGGTTTT 20

RESULT 7
US-10-118-854-28
; Sequence 28, Application US/10118854
; Publication No. US20030194754A1
; GENERAL INFORMATION:
; APPLICANT: Bates, Paula J
; APPLICANT: Miller, Donald M
; APPLICANT: Trent, John O
; APPLICANT: Xu, Xiaohua
; TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS AND PROGNOSIS OF MALIGNANT
; FILE REFERENCE: 9799910-
; CURRENT APPLICATION NUMBER: US/10/118,854
; CURRENT FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-118-854-28

Query Match          100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 5 TTTTGGGGTTTGGGGTTTT 24

## RESULT 8

US-10-607-455-28  
; Sequence 28, Application US/10607455  
; Publication No. US20040132049A1  
; GENERAL INFORMATION:  
; APPLICANT: Bates, Paula J  
; APPLICANT: Mi, Yingchang  
; TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS AND PROGNOSIS OF MALIGNANT  
; DISEASES  
; FILE REFERENCE: 09799910-0034  
; CURRENT APPLICATION NUMBER: US/10/607,455  
; CURRENT FILING DATE: 2003-06-26  
; PRIOR APPLICATION NUMBER: 60/392,143  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 28  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
US-10-607-455-28

Query Match 100.0%; Score 20; DB 7; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 5 TTTTGGGGTTTGGGGTTTT 24

## RESULT 9

US-10-683-480-28  
; Sequence 28, Application US/10683480  
; Publication No. US20050053607A1  
; GENERAL INFORMATION:  
; APPLICANT: BATES, PAULA J.  
; APPLICANT: MILLER, DONALD M.  
; APPLICANT: TRENT, JOHN O.  
; APPLICANT: XU, XIAOHUA  
; TITLE OF INVENTION: A NEW METHOD FOR THE DIAGNOSIS AND PROGNOSIS OF  
; MALIGNANT DISEASES  
; FILE REFERENCE: LOU01-012-CIP-US  
; CURRENT APPLICATION NUMBER: US/10/683,480  
; CURRENT FILING DATE: 2003-10-09  
; PRIOR APPLICATION NUMBER: 10/118,854  
; PRIOR FILING DATE: 2002-04-08  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 28  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: polynucleotide sequence  
US-10-683-480-28

Query Match 100.0%; Score 20; DB 9; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||

Db 5 TTTTGGGGTTTGGGGTTTT 24

## RESULT 10

US-10-690-984-11  
; Sequence 11, Application US/10690984  
; Publication No. US20050090671A1  
; GENERAL INFORMATION:  
; APPLICANT: Chang, Ta-Chau  
; APPLICANT: Chang, Cheng-Chung  
; APPLICANT: Wu, Jin-Yi  
; TITLE OF INVENTION: QUADRUPEX STABILIZER  
; FILE REFERENCE: 08919-112001  
; CURRENT APPLICATION NUMBER: US/10/690,984  
; CURRENT FILING DATE: 2003-10-22  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated oligonucleotide  
US-10-690-984-11

Query Match 100.0%; Score 20; DB 9; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 5 TTTTGGGGTTTGGGGTTTT 24

## RESULT 11

US-10-961-479-29  
; Sequence 29, Application US/10961479  
; Publication No. US20050187176A1  
; GENERAL INFORMATION:  
; APPLICANT: BATES, PAULA J.  
; APPLICANT: GIRVAN, ALLICIA C.  
; APPLICANT: BARVE, SHIRISH S.  
; TITLE OF INVENTION: METHOD FOR INHIBITING NF-KAPPA B SIGNALING AND USE TO  
; TREAT OR PREVENT HUMAN DISEASES  
; FILE REFERENCE: LOU01-010-US  
; CURRENT APPLICATION NUMBER: US/10/961,479  
; CURRENT FILING DATE: 2004-10-08  
; PRIOR APPLICATION NUMBER: 60/510,466  
; PRIOR FILING DATE: 2003-10-10  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 29  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: polynucleotide sequence  
US-10-961-479-29

Query Match 100.0%; Score 20; DB 9; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 5 TTTTGGGGTTTGGGGTTTT 24

## RESULT 12

US-09-843-676-42  
; Sequence 42, Application US/09843676  
; Patent No. US20020164786A1

GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. US20020164786A1el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/843,676  
FILING DATE: 26-Apr-2001  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
US-09-843-676-42  
Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTT 20  
DB 25 TTTTGGGGTTTGGGGTTT 44  
RESULT 13  
US-09-766-253-42  
Sequence 42, Application US/09766253  
Publication No. US2002018741A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin

Andrews, William H.  
TITLE OF INVENTION: No. US2002018741A1el Telomerase  
NUMBER OF SEQUENCES: 171  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/766,253  
FILING DATE: 19-Jan-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/846,017  
FILING DATE: 1997-04-25  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002920US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
US-09-766-253-42  
Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGGTTTGGGGTTT 20  
DB 25 TTTTGGGGTTTGGGGTTT 44  
RESULT 14  
US-09-438-486-42  
Sequence 42, Application US/09438486  
Publication No. US20030009019A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. US20030009019A1el Telomerase  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111-3834  
COMPUTER READABLE FORM:



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/438,486  
FILING DATE: 12-NOV-1999  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 536  
APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002931US  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-438-486-42

Query Match 100.0%; Score 20; DB 3; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20  
Db 25 TTTTGGGTTTGGGGTTT 44

RESULT 15  
US-10-053-758-42  
Sequence 42, Application US/10053758  
Publication No. US20030032075A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. US20030032075A1el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/053,758  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
US-10-053-758-42

Query Match 100.0%; Score 20; DB 5; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTT 20  
Db 25 TTTTGGGTTTGGGGTTT 44

RESULT 16  
US-10-054-295-42  
Sequence 42, Application US/10054295  
Publication No. US20030044953A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin  
Andrews, William H.  
TITLE OF INVENTION: No. US20030044953A1el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/054,295

```
/
/ FILING DATE: 18-Jan-2002
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/854,050
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0300
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 44 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-054-295-42

Query Match 100.0%; Score 20; DB 5; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 25 TTTTGGGGTTTGGGGTTTT 44

RESULT 17
US-10-054-611-42
/ Sequence 42, Application US/10054611
/ Publication No. US20030059787A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin
/ Andrews, William H.
/ TITLE OF INVENTION: No. US20030059787A1el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/054,611
/ FILING DATE: 18-Jan-2002
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/854,050
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
```

```
/
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 44 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-054-611-42

Query Match 100.0%; Score 20; DB 5; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 25 TTTTGGGGTTTGGGGTTTT 44

RESULT 18
US-10-325-810-568
/ Sequence 568, Application US/10325810
/ Publication No. US20030204069A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin B.
/ Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/325,810
/ FILING DATE: 20-Dec-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,181
/ FILING DATE: 29-Sep-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/854,050
```

/ FILING DATE: 09-MAY-1997  
/ APPLICATION NUMBER: US 08/911,312  
/ FILING DATE: 14-AUG-1997  
/ APPLICATION NUMBER: US 08/912,951  
/ FILING DATE: 14-AUG-1997  
/ APPLICATION NUMBER: US 08/915,503  
/ FILING DATE: 14-AUG-1997  
/ APPLICATION NUMBER: WO PCT/US97/17885  
/ FILING DATE: 01-OCT-1997  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Aussenhus, Scott L.  
/ REGISTRATION NUMBER: 42,271  
/ REFERENCE/DOCKET NUMBER: 015389-002620US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 568:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 44 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA  
/ FEATURE:  
/ NAME/KEY: -  
/ LOCATION: 1..44  
/ OTHER INFORMATION: /note= "hairpin primer"  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 568:  
US-10-325-810-568  
  
Query Match 100.0%; Score 20; DB 6; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 25 TTTTGGGTTTGGGGTTTT 44  
  
RESULT 19  
US-10-877-124-568  
; Sequence 568, Application US/10877124  
; Publication No. US20040242529A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/877,124  
; FILING DATE: 24-Jun-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,503  
; FILING DATE: 02-Nov-1999  
; APPLICATION NUMBER: 08/974,549

/ FILING DATE: <Unknown>  
/ APPLICATION NUMBER: US 08/844,419  
/ FILING DATE: 18-APR-1997  
/ APPLICATION NUMBER: US 08/846,017  
/ FILING DATE: 25-APR-1997  
/ APPLICATION NUMBER: US 08/851,843  
/ FILING DATE: 06-MAY-1997  
/ APPLICATION NUMBER: US 08/854,050  
/ FILING DATE: 09-MAY-1997  
/ APPLICATION NUMBER: US 08/911,312  
/ FILING DATE: 14-AUG-1997  
/ APPLICATION NUMBER: US 08/912,951  
/ FILING DATE: 14-AUG-1997  
/ APPLICATION NUMBER: US 08/915,503  
/ FILING DATE: 14-AUG-1997  
/ APPLICATION NUMBER: WO PCT/US97/17618  
/ FILING DATE: 01-OCT-1997  
/ APPLICATION NUMBER: WO PCT/US97/17885  
/ FILING DATE: 01-OCT-1997  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph Ted  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002610US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 568:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 44 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA  
/ FEATURE:  
/ NAME/KEY: -  
/ LOCATION: 1..44  
/ OTHER INFORMATION: /note= "hairpin primer"  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 568:  
US-10-877-124-568  
  
Query Match 100.0%; Score 20; DB 8; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTTTGGGTTTGGGGTTTT 20  
|||||  
Db 25 TTTTGGGTTTGGGGTTTT 44  
  
RESULT 20  
US-10-877-022-568  
; Sequence 568, Application US/10877022  
; Publication No. US20040247613A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,022  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 568:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..44  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 568:  
US-10-877-022-568  
Query Match 100.0%; Score 20; DB 8; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 25 TTTTGGGTTTGGGGTTTT 44  
RESULT 21  
US-10-877-146-568  
Sequence 568, Application US/10877146  
Publication No. US20050013825A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,146  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 568:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..44  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 568:  
US-10-877-146-568  
Query Match 100.0%; Score 20; DB 8; Length 44;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 25 TTTTGGGTTTGGGGTTTT 44  
RESULT 22  
US-09-843-676-41  
Sequence 41, Application US/09843676  
Patent No. US20020164786A1

/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ Lingner, Joachim  
/ Nakamura, Toru  
/ Chapman, Karen B.  
/ Morin, Gregg B.  
/ Harley, Calvin  
/ Andrews, William H.  
/ TITLE OF INVENTION: No. US20020164786A1el Telomerase  
/ NUMBER OF SEQUENCES: 225  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/843,676  
/ FILING DATE: 26-Apr-2001  
/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/854,050  
/ FILING DATE: 09-MAY-1997  
/ APPLICATION NUMBER: US 08/846,017  
/ FILING DATE: 25-APR-1997  
/ APPLICATION NUMBER: US 08/844,419  
/ FILING DATE: 18-APR-1997  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002930US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 41:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 46 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "DNA"  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
/ US-09-843-676-41  
/ Query Match 100.0%; Score 20; DB 3; Length 46;  
/ Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
/ Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
/ QY 1 TTTTGGGGTTTGGGGTTTT 20  
/ Db 27 TTTTGGGGTTTGGGGTTTT 46  
/ RESULT 23  
/ US-09-766-253-41  
/ Sequence 41, Application US/09766253  
/ Publication No. US2002018741A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ Lingner, Joachim  
/ Nakamura, Toru  
/ Chapman, Karen B.  
/ Morin, Gregg B.  
/ Harley, Calvin

/ Andrews, William H.  
/ TITLE OF INVENTION: No. US2002018741A1el Telomerase  
/ NUMBER OF SEQUENCES: 171  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/766,253  
/ FILING DATE: 19-Jan-2001  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/846,017  
/ FILING DATE: 1997-04-25  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002920US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 41:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 46 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "DNA"  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
/ US-09-766-253-41  
/ Query Match 100.0%; Score 20; DB 3; Length 46;  
/ Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
/ Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
/ QY 1 TTTTGGGGTTTGGGGTTTT 20  
/ Db 27 TTTTGGGGTTTGGGGTTTT 46  
/ RESULT 24  
/ US-09-438-486-41  
/ Sequence 41, Application US/09438486  
/ Publication No. US20030009019A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ APPLICANT: Lingner, Joachim  
/ APPLICANT: Nakamura, Toru  
/ APPLICANT: Chapman, Karen B.  
/ APPLICANT: Morin, Gregg B.  
/ APPLICANT: Harley, Calvin  
/ APPLICANT: Andrews, William H.  
/ TITLE OF INVENTION: No. US20030009019A1el Telomerase  
/ NUMBER OF SEQUENCES: 223  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111-3834  
/ COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
;
US-09-438-486-41
```

```

Query Match      100.0%; Score 20; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTTTGGGGTTTGGGGTTTT 20
        |||||
Db      27 TTTTGGGGTTTGGGGTTTT 46
```

```

RESULT 25
US-10-053-758-41
; Sequence 41, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;               Lingner, Joachim
;               Nakamura, Toru
;               Chapman, Karen B.
;               Morin, Gregg B.
;               Harley, Calvin
;               Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
;
US-10-053-758-41

Query Match      100.0%; Score 20; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTTGGGGTTTGGGGTTTT 20
        |||||
Db      27 TTTTGGGGTTTGGGGTTTT 46

RESULT 26
US-10-054-295-41
; Sequence 41, Application US/10054295
; Publication No. US2003004953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;               Lingner, Joachim
;               Nakamura, Toru
;               Chapman, Karen B.
;               Morin, Gregg B.
;               Harley, Calvin
;               Andrews, William H.
; TITLE OF INVENTION: No. US2003004953A1e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
```

/ FILING DATE: 18-Jan-2002  
/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/854,050  
/ FILING DATE: <unknown>  
/ APPLICATION NUMBER: US 08/846,017  
/ FILING DATE: 25-APR-1997  
/ APPLICATION NUMBER: US 08/844,419  
/ FILING DATE: 18-APR-1997  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002930US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0300  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 41:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 46 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "DNA"  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-10-054-295-41  
  
Query Match 100.0%; Score 20; DB 5; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 27 TTTTGGGTTTGGGGTTTT 46  
  
RESULT 27  
US-10-054-611-41  
/ Sequence 41, Application US/10054611  
/ Publication No. US20030059787A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ Lingner, Joachim  
/ Nakamura, Toru  
/ Chapman, Karen B.  
/ Morin, Gregg B.  
/ Harley, Calvin  
/ Andrews, William H.  
/ TITLE OF INVENTION: No. US20030059787A1el Telomerase  
/ NUMBER OF SEQUENCES: 225  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, 8th Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: United States of America  
/ ZIP: 94111  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/10/054,611  
/ FILING DATE: 18-Jan-2002  
/ CLASSIFICATION: 536  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/854,050  
/ FILING DATE: <unknown>  
/ APPLICATION NUMBER: US 08/846,017  
/ FILING DATE: 25-APR-1997

/ APPLICATION NUMBER: US 08/844,419  
/ FILING DATE: 18-APR-1997  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Apple, Randolph T.  
/ REGISTRATION NUMBER: 36,429  
/ REFERENCE/DOCKET NUMBER: 015389-002930US  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (415) 576-0200  
/ TELEFAX: (415) 576-0300  
/ INFORMATION FOR SEQ ID NO: 41:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 46 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: other nucleic acid  
/ DESCRIPTION: /desc = "DNA"  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-10-054-611-41  
  
Query Match 100.0%; Score 20; DB 5; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTTTGGGTTTGGGGTTTT 20  
Db 27 TTTTGGGTTTGGGGTTTT 46  
  
RESULT 28  
US-10-325-810-567  
/ Sequence 567, Application US/10325810  
/ Publication No. US20030204069A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Cech, Thomas R.  
/ Lingner, Joachim  
/ Nakamura, Toru  
/ Chapman, Karen B.  
/ Morin, Gregg B.  
/ Harley, Calvin B.  
/ Andrews, William H.  
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
/ NUMBER OF SEQUENCES: 633  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Townsend and Townsend and Crew LLP  
/ STREET: Two Embarcadero Center, Eighth Floor  
/ CITY: San Francisco  
/ STATE: California  
/ COUNTRY: USA  
/ ZIP: 94111-3834  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/10/325,810  
/ FILING DATE: 20-Dec-2002  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/402,181  
/ FILING DATE: 29-Sep-1997  
/ APPLICATION NUMBER: US 08/724,643  
/ FILING DATE: 01-OCT-1996  
/ APPLICATION NUMBER: US 08/844,419  
/ FILING DATE: 18-APR-1997  
/ APPLICATION NUMBER: US 08/846,017  
/ FILING DATE: 25-APR-1997  
/ APPLICATION NUMBER: US 08/851,843  
/ FILING DATE: 06-MAY-1997  
/ APPLICATION NUMBER: US 08/854,050





OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,022  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 567:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..46  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 567:  
US-10-877-022-567  
Query Match 100.0%; Score 20; DB 8; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGTTTT 20  
Db 27 TTTTGGGTTTGGGTTTT 46  
RESULT 31  
US-10-877-146-567  
Sequence 567, Application US/10877146  
Publication No. US20050013825A1  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
Lingner, Joachim  
Nakamura, Toru  
Chapman, Karen B.  
Morin, Gregg B.  
Harley, Calvin B.  
Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/877,146  
FILING DATE: 24-Jun-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/432,503  
FILING DATE: 02-Nov-1999  
APPLICATION NUMBER: 08/974,549  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 567:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..46  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 567:  
US-10-877-146-567  
Query Match 100.0%; Score 20; DB 8; Length 46;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTTTGGGTTTGGGTTTT 20  
Db 27 TTTTGGGTTTGGGTTTT 46  
RESULT 32  
US-09-843-676-37  
Sequence 37, Application US/09843676  
Patent No. US20020164786A1

```
;
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
;
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-843-676-37
Query Match 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 33
US-09-843-676-40
; Sequence 40, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
;
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; 
```

```
;
; Andrews, William H.
;
; TITLE OF INVENTION: No. US20020164786A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/843,676
; FILING DATE: 26-Apr-2001
; CLASSIFICATION: 536
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-843-676-40
Query Match 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 34
US-09-766-253-37
; Sequence 37, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
;
; TITLE OF INVENTION: No. US20020187471A1el Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; 
```

```
/
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/766,253
/ FILING DATE: 19-Jan-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/846,017
/ FILING DATE: 1997-04-25
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002920US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-766-253-37

Query Match 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 35
US-09-766-253-40
/ Sequence 40, Application US/09766253
/ Publication No. US20020187471A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: No. US20020187471A1el Telomerase
/ NUMBER OF SEQUENCES: 171
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/766,253
/ FILING DATE: 19-Jan-2001
```

```
/
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/846,017
/ FILING DATE: 1997-04-25
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002920US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-766-253-40

Query Match 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 36
US-09-438-486-37
/ Sequence 37, Application US/09438486
/ Publication No. US20030009019A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: No. US20030009019A1el Telomerase
/ NUMBER OF SEQUENCES: 223
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111-3834
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/438,486
/ FILING DATE: 12-NOV-1999
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
```

```
/
/ FILING DATE: 18-APR-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002931US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ US-09-438-486-37
Query Match 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 37
US-09-438-486-40
/ Sequence 40, Application US/09438486
/ Publication No. US20030009019A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: No. US20030009019A1 Telomerase
/ NUMBER OF SEQUENCES: 223
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/438,486
/ FILING DATE: 12-NOV-1999
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
```

```
/
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002931US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 40:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ US-09-438-486-40
Query Match 100.0%; Score 20; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 29 TTTTGGGTTTGGGGTTTT 48

RESULT 38
US-10-053-758-37
/ Sequence 37, Application US/10053758
/ Publication No. US20030032075A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: No. US20030032075A1 Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/053,758
/ FILING DATE: 18-Jan-2002
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
```

```
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-053-758-37

Query Match 100.0%; Score 20; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 39
US-10-053-758-40
/ Sequence 40, Application US/10053758
/ Publication No. US20030032075A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin
/ Andrews, William H.
/ TITLE OF INVENTION: No. US20030032075A1el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/053,758
/ FILING DATE: 18-Jan-2002
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/854,050
/ FILING DATE: 09-MAY-1997
/ APPLICATION NUMBER: US/08/851,843
/ FILING DATE: 06-MAY-1997
/ APPLICATION NUMBER: US/08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US/08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US/08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200

Query Match 100.0%; Score 20; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 40
US-10-054-295-37
/ Sequence 37, Application US/10054295
/ Publication No. US20030044953A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ Lingner, Joachim
/ Nakamura, Toru
/ Chapman, Karen B.
/ Morin, Gregg B.
/ Harley, Calvin
/ Andrews, William H.
/ TITLE OF INVENTION: No. US20030044953A1el Telomerase
/ NUMBER OF SEQUENCES: 225
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/054,295
/ FILING DATE: 18-Jan-2002
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/854,050
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US/08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US/08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US/08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 48 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
```

```
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-054-295-37
Query Match      100.0%; Score 20; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 41
US-10-054-295-40
; Sequence 40, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-054-295-40
Query Match      100.0%; Score 20; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48

RESULT 42
US-10-054-611-37
; Sequence 37, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-054-611-37
Query Match      100.0%; Score 20; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20
Db 29 TTTTGGGGTTTGGGGTTTT 48
```

## RESULT 43

US-10-054-611-40  
; Sequence 40, Application US/10054611  
; Publication No. US20030059787A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin  
; Andrews, William H.

TITLE OF INVENTION: No. US20030059787A1 Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Townsend and Townsend and Crew LLP  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/10/054,611  
FILING DATE: 18-Jan-2002  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/854,050  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-10-054-611-40

Query Match 100.0%; Score 20; DB 5; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGGTTTTGGGGTTTT 48

## RESULT 44

US-10-325-810-564  
; Sequence 564, Application US/10325810  
; Publication No. US20030204069A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim

; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 633  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Townsend and Townsend and Crew LLP  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/10/325,810  
FILING DATE: 20-Dec-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,181  
FILING DATE: 29-Sep-1997  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Ausenhus, Scott L.  
REGISTRATION NUMBER: 42,271  
REFERENCE/DOCKET NUMBER: 015389-002620US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 564:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 48 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..48  
OTHER INFORMATION: /note= "hairpin primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 564:

US-10-325-810-564

Query Match 100.0%; Score 20; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGGTTTTGGGGTTTT 48

RESULT 45  
US-10-877-124-564  
; Sequence 564, Application US/10877124  
; Publication No. US20040242529A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/877,124  
; FILING DATE: 24-Jun-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/432,503  
; FILING DATE: 02-Nov-1999  
; APPLICATION NUMBER: 08/974,549  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 564:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 48 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..48  
; OTHER INFORMATION: /note= "hairpin primer"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 564:

US-10-877-124-564

Query Match 100.0%; Score 20; DB 8; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 29 TTTTGGGGTTTGGGGTTTT 48  
|||||

RESULT 46

US-10-877-022-564  
; Sequence 564, Application US/10877022  
; Publication No. US20040247613A1  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.

; Lingner, Joachim  
; Nakamura, Toru  
; Chapman, Karen B.  
; Morin, Gregg B.  
; Harley, Calvin B.  
; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,022

FILING DATE: 24-Jun-2004

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999

APPLICATION NUMBER: 08/974,549

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 564:

SEQUENCE CHARACTERISTICS:





```

; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-843-676-39
Query Match 100.0%; Score 20; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 31 TTTTGGGTTTGGGGTTTT 50

RESULT 49
US-09-766-253-39
; Sequence 39, Application US/09766253
; Publication No. US20020187471A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20020187471A1 Telomerase
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,253
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,017
; FILING DATE: 1997-04-25
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002920US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid

; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-766-253-39
Query Match 100.0%; Score 20; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
Db 31 TTTTGGGTTTGGGGTTTT 50

RESULT 50
US-09-438-486-39
; Sequence 39, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. US20030009019A1 Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002931US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
```

```
; DESCRIPTION: /desc = "DNA"
US-09-438-486-39
Query Match      100.0%; Score 20; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
   ||||||||||||||||
Db 31 TTTTGGGGTTTGGGGTTT 50
```

Search completed: February 16, 2006, 02:34:00  
Job time : 294.248 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 02:03:53 ; Search time 186.446 Seconds  
(without alignments)  
98.157 Million call updates/sec

Title: US-09-669-187A-73

Perfect score: 20

Sequence: 1 ttttggggtttggggtttt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6247088 seqs, 457523669 residues

Total number of hits satisfying chosen parameters: 11812030

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- Published Applications NA New:\*
- 1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
  - 2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
  - 3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
  - 4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
  - 5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
  - 6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
  - 7: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
  - 8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
  - 9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
  - 10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
  - 11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
  - 12: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	100.0	20	11	US-11-127-654-67
C 2	16.8	84.0	23	7	US-10-310-914A-596008
C 3	16.8	84.0	24	7	US-10-310-914A-185978
C 4	16.8	84.0	25	7	US-10-310-914A-596068
C 5	16.8	84.0	27	7	US-10-310-914A-596011
C 6	16.4	82.0	21	7	US-10-310-914A-138168
C 7	16.4	82.0	22	7	US-10-310-914A-138169
C 8	16.4	82.0	22	7	US-10-310-914A-138179
C 9	16.4	82.0	22	7	US-10-310-914A-138228
C 10	16.4	82.0	23	7	US-10-310-914A-138180
C 11	16.4	82.0	24	7	US-10-310-914A-138196
C 12	16.4	82.0	24	7	US-10-310-914A-227183
C 13	16.4	82.0	25	7	US-10-310-914A-138229
C 14	16.4	82.0	26	7	US-10-310-914A-138236
C 15	16.4	82.0	27	7	US-10-310-914A-227197
C 16	15.8	79.0	20	11	US-11-170-693-39
C 17	15.8	79.0	21	7	US-10-310-914A-271479
C 18	15.8	79.0	22	7	US-10-310-914A-1342346
C 19	15.8	79.0	23	7	US-10-310-914A-626125
C 20	15.8	79.0	23	7	US-10-310-914A-626126
C 21	15.8	79.0	23	7	US-10-310-914A-1143293

Sequence 844567,  
Sequence 271527,  
Sequence 271489,  
Sequence 844568,  
Sequence 565951,  
Sequence 60025, A  
Sequence 626220,  
Sequence 626221,  
Sequence 1143338,  
Sequence 626141,  
Sequence 138178,  
Sequence 138235,  
Sequence 626295,  
Sequence 626296,  
Sequence 1143370,  
Sequence 216, App  
Sequence 84509, A  
Sequence 455408,  
Sequence 622070,  
Sequence 675377,  
Sequence 1222901,  
Sequence 238142,  
Sequence 465689,  
Sequence 1222898,  
Sequence 282917,  
Sequence 465697,  
Sequence 501657,  
Sequence 651609,  
Sequence 675445,  
Sequence 675449,  
Sequence 1222897,  
Sequence 84466, A  
Sequence 1222899,  
Sequence 622066,  
Sequence 675446,  
Sequence 651610,  
Sequence 651611,  
Sequence 1036106,  
Sequence 445638,  
Sequence 467816,  
Sequence 596013,  
Sequence 675376,  
Sequence 1342361,  
Sequence 675448,  
Sequence 57940, A  
Sequence 57941, A  
Sequence 57942, A  
Sequence 57943, A  
Sequence 467342,  
Sequence 596007,  
Sequence 465690,  
Sequence 675468,  
Sequence 185950,  
Sequence 185964,  
Sequence 467314,  
Sequence 665, App  
Sequence 667, App  
Sequence 854, App  
Sequence 6, Appli  
Sequence 602539,  
Sequence 626121,  
Sequence 626122,  
Sequence 1143289,  
Sequence 602540,  
Sequence 626219,  
Sequence 1143337,  
Sequence 227210,  
Sequence 238250,  
Sequence 238251,  
Sequence 626123,  
Sequence 626124,  
Sequence 1143292,  
Sequence 138234,

C 95	14.4	72.0	21	7	US-10-310-914A-238162	Sequence 238162,	C 168	14.2	71.0	25	11	US-11-136-527-15527	Sequence 15527, A
C 96	14.4	72.0	22	7	US-10-310-914A-238201	Sequence 238201,	C 169	14.2	71.0	26	7	US-10-310-914A-207665	Sequence 207665,
C 97	14.4	72.0	22	7	US-10-310-914A-238252	Sequence 238252,	C 170	14.2	71.0	26	7	US-10-310-914A-208739	Sequence 208739,
C 98	14.4	72.0	22	7	US-10-310-914A-238252	Sequence 238252,	C 171	14.2	71.0	26	7	US-10-310-914A-348736	Sequence 348736,
C 99	14.4	72.0	22	7	US-10-310-914A-626236	Sequence 626236,	C 172	14.2	71.0	26	7	US-10-310-914A-467814	Sequence 467814,
C 100	14.4	72.0	22	7	US-10-310-914A-626237	Sequence 626237,	C 173	14.2	71.0	26	7	US-10-310-914A-526421	Sequence 526421,
C 101	14.4	72.0	22	7	US-10-310-914A-1143345	Sequence 1143345,	C 174	14.2	71.0	26	7	US-10-310-914A-621501	Sequence 621501,
C 102	14.4	72.0	23	7	US-10-310-914A-238202	Sequence 238202,	C 175	14.2	71.0	26	7	US-10-310-914A-621510	Sequence 621510,
C 103	14.4	72.0	24	7	US-10-310-914A-565981	Sequence 565981,	C 176	14.2	71.0	27	7	US-10-310-914A-803774	Sequence 803774,
C 104	14.4	72.0	25	7	US-10-310-914A-238163	Sequence 238163,	C 177	14.2	71.0	30	7	US-10-310-914A-935038	Sequence 935038,
C 105	14.4	72.0	26	7	US-10-310-914A-138182	Sequence 138182,	C 178	14.2	71.0	30	11	US-11-175-859-30118	Sequence 30118, A
C 106	14.4	72.0	31	7	US-10-310-914A-238203	Sequence 238203,	C 179	14	70.0	18	7	US-10-310-914A-1035984	Sequence 1035984,
C 107	14.2	71.0	19	7	US-10-310-914A-455340	Sequence 455340,	C 180	14	70.0	19	7	US-10-310-914A-519068	Sequence 519068,
C 108	14.2	71.0	20	7	US-10-310-914A-208723	Sequence 208723,	C 181	14	70.0	19	7	US-10-310-914A-995986	Sequence 995986,
C 109	14.2	71.0	20	7	US-10-310-914A-328480	Sequence 328480,	C 182	14	70.0	20	7	US-10-310-914A-57938	Sequence 57938, A
C 110	14.2	71.0	20	7	US-10-310-914A-404785	Sequence 404785,	C 183	14	70.0	20	7	US-10-310-914A-57939	Sequence 57939, A
C 111	14.2	71.0	20	7	US-10-310-914A-621470	Sequence 621470,	C 184	14	70.0	20	7	US-10-310-914A-429806	Sequence 429806,
C 112	14.2	71.0	20	7	US-10-310-914A-935090	Sequence 935090,	C 185	14	70.0	20	7	US-10-310-914A-518940	Sequence 518940,
C 113	14.2	71.0	20	7	US-10-310-914A-1222903	Sequence 1222903,	C 186	14	70.0	21	7	US-10-310-914A-185963	Sequence 185963,
C 114	14.2	71.0	20	7	US-10-310-914A-112276	Sequence 112276,	C 187	14	70.0	21	7	US-10-310-914A-995976	Sequence 995976,
C 115	14.2	71.0	21	7	US-10-310-914A-322150	Sequence 322150,	C 188	14	70.0	22	7	US-10-310-914A-518978	Sequence 518978,
C 116	14.2	71.0	21	7	US-10-310-914A-328481	Sequence 328481,	C 189	14	70.0	22	7	US-10-310-914A-995973	Sequence 995973,
C 117	14.2	71.0	21	7	US-10-310-914A-328482	Sequence 328482,	C 190	14	70.0	22	7	US-10-310-914A-995987	Sequence 995987,
C 118	14.2	71.0	21	7	US-10-310-914A-348738	Sequence 348738,	C 191	14	70.0	22	7	US-10-310-914A-518941	Sequence 518941,
C 119	14.2	71.0	21	7	US-10-310-914A-540890	Sequence 540890,	C 192	14	70.0	23	7	US-10-310-914A-518941	Sequence 518941,
C 120	14.2	71.0	21	7	US-10-310-914A-621471	Sequence 621471,	C 193	14	70.0	23	7	US-10-310-914A-995974	Sequence 995974,
C 121	14.2	71.0	21	7	US-10-310-914A-845458	Sequence 845458,	C 194	14	70.0	24	7	US-10-310-914A-58246	Sequence 58246, A
C 122	14.2	71.0	21	7	US-10-310-914A-845471	Sequence 845471,	C 195	14	70.0	24	7	US-10-310-914A-58247	Sequence 58247, A
C 123	14.2	71.0	22	7	US-10-310-914A-84474	Sequence 84474, A	C 196	14	70.0	24	7	US-10-310-914A-58248	Sequence 58248, A
C 124	14.2	71.0	22	7	US-10-310-914A-208738	Sequence 208738,	C 197	14	70.0	24	7	US-10-310-914A-58249	Sequence 58249, A
C 125	14.2	71.0	22	7	US-10-310-914A-445665	Sequence 445665,	C 198	14	70.0	24	7	US-10-310-914A-227190	Sequence 227190,
C 126	14.2	71.0	22	7	US-10-310-914A-465262	Sequence 465262,	C 199	14	70.0	24	7	US-10-310-914A-518980	Sequence 518980,
C 127	14.2	71.0	22	7	US-10-310-914A-549696	Sequence 549696,	C 200	14	70.0	25	7	US-10-310-914A-995975	Sequence 995975,
C 128	14.2	71.0	22	7	US-10-310-914A-621472	Sequence 621472,	C 201	13.8	69.0	18	7	US-10-310-914A-111256	Sequence 111256,
C 129	14.2	71.0	22	7	US-10-310-914A-803700	Sequence 803700,	C 202	13.8	69.0	18	7	US-10-310-914A-1342360	Sequence 1342360,
C 130	14.2	71.0	22	7	US-10-310-914A-845459	Sequence 845459,	C 203	13.8	69.0	19	7	US-10-310-914A-255657	Sequence 255657,
C 131	14.2	71.0	23	7	US-10-310-914A-845459	Sequence 845459,	C 204	13.8	69.0	19	7	US-10-310-914A-1043347	Sequence 1043347,
C 132	14.2	71.0	23	7	US-10-310-914A-208735	Sequence 208735,	C 205	13.8	69.0	20	7	US-10-310-914A-239913	Sequence 239913,
C 133	14.2	71.0	23	7	US-10-310-914A-208749	Sequence 208749,	C 206	13.8	69.0	20	7	US-10-310-914A-467827	Sequence 467827,
C 134	14.2	71.0	23	7	US-10-310-914A-322142	Sequence 322142,	C 207	13.8	69.0	21	7	US-10-310-914A-111268	Sequence 111268,
C 135	14.2	71.0	23	7	US-10-310-914A-322166	Sequence 322166,	C 208	13.8	69.0	21	7	US-10-310-914A-185961	Sequence 185961,
C 136	14.2	71.0	23	7	US-10-310-914A-328573	Sequence 328573,	C 209	13.8	69.0	21	7	US-10-310-914A-239892	Sequence 239892,
C 137	14.2	71.0	23	7	US-10-310-914A-465292	Sequence 465292,	C 210	13.8	69.0	21	7	US-10-310-914A-239912	Sequence 239912,
C 138	14.2	71.0	23	7	US-10-310-914A-467819	Sequence 467819,	C 211	13.8	69.0	21	7	US-10-310-914A-251546	Sequence 251546,
C 139	14.2	71.0	23	7	US-10-310-914A-467906	Sequence 467906,	C 212	13.8	69.0	21	7	US-10-310-914A-427324	Sequence 427324,
C 140	14.2	71.0	23	7	US-10-310-914A-526398	Sequence 526398,	C 213	13.8	69.0	21	7	US-10-310-914A-565958	Sequence 565958,
C 141	14.2	71.0	23	7	US-10-310-914A-845463	Sequence 845463,	C 214	13.8	69.0	21	7	US-10-310-914A-1043348	Sequence 1043348,
C 142	14.2	71.0	23	7	US-10-310-914A-1035982	Sequence 1035982,	C 215	13.8	69.0	21	7	US-10-310-914A-1222944	Sequence 1222944,
C 143	14.2	71.0	24	7	US-10-310-914A-111296	Sequence 111296,	C 216	13.8	69.0	22	7	US-10-310-914A-239917	Sequence 239917,
C 144	14.2	71.0	24	7	US-10-310-914A-322181	Sequence 322181,	C 217	13.8	69.0	22	7	US-10-310-914A-255658	Sequence 255658,
C 145	14.2	71.0	24	7	US-10-310-914A-348737	Sequence 348737,	C 218	13.8	69.0	22	7	US-10-310-914A-255758	Sequence 255758,
C 146	14.2	71.0	24	7	US-10-310-914A-431969	Sequence 431969,	C 219	13.8	69.0	22	7	US-10-310-914A-887834	Sequence 887834,
C 147	14.2	71.0	24	7	US-10-310-914A-452933	Sequence 452933,	C 220	13.8	69.0	23	7	US-10-310-914A-507619	Sequence 507619,
C 148	14.2	71.0	24	7	US-10-310-914A-465676	Sequence 465676,	C 221	13.8	69.0	23	7	US-10-310-914A-1043651	Sequence 1043651,
C 149	14.2	71.0	24	7	US-10-310-914A-490858	Sequence 490858,	C 222	13.8	69.0	24	7	US-10-310-914A-126736	Sequence 126736,
C 150	14.2	71.0	24	7	US-10-310-914A-526411	Sequence 526411,	C 223	13.8	69.0	24	7	US-10-310-914A-426746	Sequence 426746,
C 151	14.2	71.0	24	7	US-10-310-914A-540871	Sequence 540871,	C 224	13.8	69.0	24	7	US-10-310-914A-251487	Sequence 251487,
C 152	14.2	71.0	24	7	US-10-310-914A-621491	Sequence 621491,	C 225	13.8	69.0	24	7	US-10-310-914A-507599	Sequence 507599,
C 153	14.2	71.0	24	7	US-10-310-914A-621493	Sequence 621493,	C 226	13.8	69.0	24	7	US-10-310-914A-507626	Sequence 507626,
C 154	14.2	71.0	24	7	US-10-310-914A-845464	Sequence 845464,	C 227	13.8	69.0	24	7	US-10-310-914A-1043567	Sequence 1043567,
C 155	14.2	71.0	24	7	US-10-310-914A-1059987	Sequence 1059987,	C 228	13.8	69.0	24	7	US-10-310-914A-1043652	Sequence 1043652,
C 156	14.2	71.0	25	7	US-10-310-914A-1177640	Sequence 1177640,	C 229	13.8	69.0	25	7	US-10-750-185-22623	Sequence 22623, A
C 157	14.2	71.0	25	7	US-10-310-914A-111266	Sequence 111266,	C 230	13.8	69.0	25	7	US-10-750-623-22623	Sequence 22623, A
C 158	14.2	71.0	25	7	US-10-310-914A-208725	Sequence 208725,	C 231	13.8	69.0	25	7	US-10-310-914A-126807	Sequence 126807,
C 159	14.2	71.0	25	7	US-10-310-914A-490843	Sequence 490843,	C 232	13.8	69.0	26	7	US-10-310-914A-271500	Sequence 271500,
C 160	14.2	71.0	25	7	US-10-310-914A-526412	Sequence 526412,	C 233	13.8	69.0	27	7	US-10-310-914A-231883	Sequence 231883,
C 161	14.2	71.0	25	7	US-10-310-914A-540891	Sequence 540891,	C 234	13.8	69.0	29	7	US-10-310-914A-626135	Sequence 626135,
C 162	14.2	71.0	25	7	US-10-310-914A-621517	Sequence 621517,	C 235	13.6	68.0	20	7	US-10-310-914A-95371	Sequence 95371, A
C 163	14.2	71.0	25	7	US-10-310-914A-1107886	Sequence 1107886,	C 236	13.6	68.0	20	7	US-10-310-914A-1182490	Sequence 1182490,
C 164	14.2	71.0	25	11	US-11-121-849-55567	Sequence 55567,	C 237	13.6	68.0	21	7	US-10-310-914A-98327	Sequence 98327, A
C 165	14.2	71.0	25	11	US-11-121-849-55567	Sequence 55567,	C 238	13.6	68.0	21	7	US-10-310-914A-287323	Sequence 287323,
C 166	14.2	71.0	25	11	US-11-136-527-15519	Sequence 15519, A	C 239	13.6	68.0	21	7	US-10-310-914A-429781	Sequence 429781,
C 167	14.2	71.0	25	11	US-11-136-527-15522	Sequence 15522, A	C 240	13.6	68.0	21	7	US-10-310-914A-429785	Sequence 429785,
C 167	14.2	71.0	25	11	US-11-136-527-15523	Sequence 15523, A							

c 241	13.6	68.0	21	7	US-10-310-914A-429807	Sequence 429807,
c 242	13.6	68.0	21	7	US-10-310-914A-727253	Sequence 727253,
c 243	13.6	68.0	21	7	US-10-310-914A-727618	Sequence 727618,
c 244	13.6	68.0	21	7	US-10-310-914A-1058055	Sequence 1058055,
c 245	13.6	68.0	22	7	US-10-310-914A-347390	Sequence 347390,
c 246	13.6	68.0	22	7	US-10-310-914A-352346	Sequence 352346,
c 247	13.6	68.0	22	7	US-10-310-914A-543125	Sequence 543125,
c 248	13.6	68.0	22	7	US-10-310-914A-562535	Sequence 562535,
c 249	13.6	68.0	22	7	US-10-310-914A-562537	Sequence 562537,
c 250	13.6	68.0	22	7	US-10-310-914A-562538	Sequence 562538,
c 251	13.6	68.0	22	7	US-10-310-914A-714531	Sequence 714531,
c 252	13.6	68.0	22	7	US-10-310-914A-727623	Sequence 727623,
c 253	13.6	68.0	22	7	US-10-310-914A-787860	Sequence 787860,
c 254	13.6	68.0	22	7	US-10-310-914A-912484	Sequence 912484,
c 255	13.6	68.0	22	7	US-10-310-914A-995951	Sequence 995951,
c 256	13.6	68.0	22	7	US-10-310-914A-1182519	Sequence 1182519,
c 257	13.6	68.0	22	7	US-10-310-914A-1182520	Sequence 1182520,
c 258	13.6	68.0	22	7	US-10-310-914A-1266554	Sequence 1266554,
c 259	13.6	68.0	22	7	US-10-310-914A-1347304	Sequence 1347304,
c 260	13.6	68.0	22	7	US-10-310-914A-1368901	Sequence 1368901,
c 261	13.6	68.0	23	7	US-10-310-914A-208722	Sequence 208722,
c 262	13.6	68.0	23	7	US-10-310-914A-266818	Sequence 266818,
c 263	13.6	68.0	23	7	US-10-310-914A-353094	Sequence 353094,
c 264	13.6	68.0	23	7	US-10-310-914A-429786	Sequence 429786,
c 265	13.6	68.0	23	7	US-10-310-914A-592413	Sequence 592413,
c 266	13.6	68.0	23	7	US-10-310-914A-622065	Sequence 622065,
c 267	13.6	68.0	23	7	US-10-310-914A-727232	Sequence 727232,
c 268	13.6	68.0	23	7	US-10-310-914A-749812	Sequence 749812,
c 269	13.6	68.0	23	7	US-10-310-914A-766139	Sequence 766139,
c 270	13.6	68.0	23	7	US-10-310-914A-766181	Sequence 766181,
c 271	13.6	68.0	23	7	US-10-310-914A-861266	Sequence 861266,
c 272	13.6	68.0	23	7	US-10-310-914A-1058052	Sequence 1058052,
c 273	13.6	68.0	23	7	US-10-310-914A-1100961	Sequence 1100961,
c 274	13.6	68.0	23	7	US-10-310-914A-1155612	Sequence 1155612,
c 275	13.6	68.0	23	7	US-10-310-914A-1182491	Sequence 1182491,
c 276	13.6	68.0	23	11	US-11-179-574-295	Sequence 295, App
c 277	13.6	68.0	24	7	US-10-310-914A-150268	Sequence 150268,
c 278	13.6	68.0	24	7	US-10-310-914A-150271	Sequence 150271,
c 279	13.6	68.0	24	7	US-10-310-914A-150275	Sequence 150275,
c 280	13.6	68.0	24	7	US-10-310-914A-158172	Sequence 158172,
c 281	13.6	68.0	24	7	US-10-310-914A-164308	Sequence 164308,
c 282	13.6	68.0	24	7	US-10-310-914A-350862	Sequence 350862,
c 283	13.6	68.0	24	7	US-10-310-914A-352379	Sequence 352379,
c 284	13.6	68.0	24	7	US-10-310-914A-427397	Sequence 427397,
c 285	13.6	68.0	24	7	US-10-310-914A-429793	Sequence 429793,
c 286	13.6	68.0	24	7	US-10-310-914A-455404	Sequence 455404,
c 287	13.6	68.0	24	7	US-10-310-914A-622062	Sequence 622062,
c 288	13.6	68.0	24	7	US-10-310-914A-622063	Sequence 622063,
c 289	13.6	68.0	24	7	US-10-310-914A-714554	Sequence 714554,
c 290	13.6	68.0	24	7	US-10-310-914A-817616	Sequence 817616,
c 291	13.6	68.0	24	7	US-10-310-914A-822771	Sequence 822771,
c 292	13.6	68.0	24	7	US-10-310-914A-907648	Sequence 907648,
c 293	13.6	68.0	24	7	US-10-310-914A-1050624	Sequence 1050624,
c 294	13.6	68.0	24	7	US-10-310-914A-1058053	Sequence 1058053,
c 295	13.6	68.0	24	7	US-10-310-914A-1100910	Sequence 1100910,
c 296	13.6	68.0	24	7	US-10-310-914A-1308275	Sequence 1308275,
c 297	13.6	68.0	25	7	US-10-310-914A-98332	Sequence 98332, A
c 298	13.6	68.0	25	7	US-10-310-914A-130272	Sequence 130272,
c 299	13.6	68.0	25	7	US-10-310-914A-714555	Sequence 714555,
c 300	13.6	68.0	25	7	US-10-310-914A-749740	Sequence 749740,

ALIGNMENTS

RESULT 1  
US-11-127-654-67  
; Sequence 67, Application US/11127654  
; Publication No. US20050250726A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

; TITLE OF INVENTION: INFLAMMATORY DISEASES  
; FILE REFERENCE: C1039.70060US01  
; CURRENT APPLICATION NUMBER: US/11/127,654  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 67  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-67  
  
Query Match 100.0%; Score 20; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 1 TTTTGGGGTTTGGGGTTTT 20  
  
RESULT 2  
US-10-310-914A-596008/c  
; Sequence 596008, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 596008  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-596008  
  
Query Match 84.0%; Score 16.8; DB 7; Length 23;  
Best Local Similarity 90.0%; Pred. No. 1.2e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 23 TTTTGGGGTTTGGGGTTTT 4  
  
RESULT 3  
US-10-310-914A-185978/c  
; Sequence 185978, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 185978  
; LENGTH: 24  
; TYPE: RNA

```
; ORGANISM: Human
US-10-310-914A-185978

Query Match      84.0%; Score 16.8; DB 7; Length 24;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   ||||| ||||| ||||| |||||
Db 23 TTTTGGGTTTGGGGTTTT 4

RESULT 4
US-10-310-914A-596068/c
; Sequence 596068, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 596068
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-596068

Query Match      84.0%; Score 16.8; DB 7; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   ||||| ||||| ||||| |||||
Db 25 TTTTGGTTTTGGGGTTTT 6

RESULT 5
US-10-310-914A-596011/c
; Sequence 596011, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 596011
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-596011

Query Match      84.0%; Score 16.8; DB 7; Length 27;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGTTTGGGGTTTT 20
   ||||| ||||| ||||| |||||
Db 21 TTTTGGTTTTGGGGTTTT 2

RESULT 6
US-10-310-914A-138168/c
; Sequence 138168, Application US/10310914A
```

```
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138168
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-138168

Query Match      82.0%; Score 16.4; DB 7; Length 21;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTTT 20
   ||||| ||||| ||||| |||||
Db 18 TTGGGGTTTGGGGTTTT 1

RESULT 7
US-10-310-914A-138169/c
; Sequence 138169, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138169
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-138169

Query Match      82.0%; Score 16.4; DB 7; Length 22;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTTT 20
   ||||| ||||| ||||| |||||
Db 18 TTGGGGTTTGGGGTTTT 1

RESULT 8
US-10-310-914A-138179/c
; Sequence 138179, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138179
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
```



US-10-310-914A-138179

Query Match 82.0%; Score 16.4; DB 7; Length 22;  
Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTT 20  
|||||

Db 22 TTGGGGTTTGGGGTTT 5

RESULT 9

US-10-310-914A-138228/c

; Sequence 138228, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 138228

; LENGTH: 22

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-138228

Query Match 82.0%; Score 16.4; DB 7; Length 22;  
Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTT 20  
|||||

Db 20 TTGGGGTTTGGGGTTT 3

RESULT 10

US-10-310-914A-138180/c

; Sequence 138180, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 138180

; LENGTH: 23

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-138180

Query Match 82.0%; Score 16.4; DB 7; Length 23;  
Best Local Similarity 94.4%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTT 20  
|||||

Db 22 TTGGGGTTTGGGGTTT 5

RESULT 11

US-10-310-914A-138196/c

; Sequence 138196, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 138196

; LENGTH: 24

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-138196

Query Match 82.0%; Score 16.4; DB 7; Length 24;

Best Local Similarity 94.4%; Pred. No. 1.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTT 20  
|||||

Db 21 TTGGGGTTTGGGGTTT 4

RESULT 12

US-10-310-914A-227183/c

; Sequence 227183, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 227183

; LENGTH: 24

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-227183

Query Match 82.0%; Score 16.4; DB 7; Length 24;

Best Local Similarity 94.4%; Pred. No. 1.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGGGGTTTGGGGTTT 19  
|||||

Db 18 TTGGGGTTTGGGGTTT 1

RESULT 13

US-10-310-914A-138229/c

; Sequence 138229, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 138229

; LENGTH: 25

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-138229

```
Query Match      82.0%; Score 16.4; DB 7; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTT 20
Db 20 TTGGGGTTTGGGGTTT 3

RESULT 14
US-10-310-914A-138236/c
; Sequence 138236, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138236
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-138236

Query Match      82.0%; Score 16.4; DB 7; Length 26;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTGGGGTTTGGGGTTT 20
Db 26 TTGGGGTTTGGGGTTT 9

RESULT 15
US-10-310-914A-227197/c
; Sequence 227197, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 227197
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-227197

Query Match      82.0%; Score 16.4; DB 7; Length 27;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTGGGGTTTGGGGTTT 19
Db 19 TTGGGGTTTGGGGTTT 2

RESULT 16
US-11-170-693-39/c
; Sequence 39, Application US/11170693
; Publication No. US20060014186A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Hodge, Timothy A.
; TITLE OF INVENTION: METHODS FOR GENOTYPE SCREENING OF A STRAIN DISPOSED ON AN
; FILE OF INVENTION: ABSORBENT CARRIER
; FILE REFERENCE: 023131.41500
; CURRENT APPLICATION NUMBER: US/11/170,693
; CURRENT FILING DATE: 2005-06-29
; PRIOR APPLICATION NUMBER: 60/230,371
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 09/945,952
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 11/074,995
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 11/
; PRIOR FILING DATE: 2005-06-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: Forward Primer
US-11-170-693-39

Query Match      79.0%; Score 15.8; DB 11; Length 20;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 19
Db 19 TGTGTGGGTTCTGTGGGGTTT 1

RESULT 17
US-10-310-914A-271479/c
; Sequence 271479, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 271479
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-271479

Query Match      79.0%; Score 15.8; DB 7; Length 21;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTTGGGGTTTGGGGTTT 20
Db 19 TTTGTGGTTTTGGGGTTT 1

RESULT 18
US-10-310-914A-1342346/c
; Sequence 1342346, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
```

; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1342346  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1342346

Query Match 79.0%; Score 15.8; DB 7; Length 22;  
Best Local Similarity 89.5%; Pred. No. 3.e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGGGGGTTTGGGGTTT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 22 TTGGGGGTTTGGGGTTT 4

RESULT 19  
US-10-310-914A-626125/c  
; Sequence 626125, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 626125  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626125

Query Match 79.0%; Score 15.8; DB 7; Length 23;  
Best Local Similarity 89.5%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGGGGGTTTGGGGTTT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 23 TGTGGGGTTTGGGGTTT 5

RESULT 20  
US-10-310-914A-626126/c  
; Sequence 626126, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 626126  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626126

Query Match 79.0%; Score 15.8; DB 7; Length 23;  
Best Local Similarity 89.5%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGGGGGTTTGGGGTTT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 23 TGTGGGGTTTGGGGTTT 5

RESULT 21  
US-10-310-914A-1143293/c  
; Sequence 1143293, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1143293  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1143293

Query Match 79.0%; Score 15.8; DB 7; Length 23;  
Best Local Similarity 89.5%; Pred. No. 3.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTGGGGGTTTGGGGTTT 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 23 TGTGGGGTTTGGGGTTT 5

RESULT 22  
US-10-310-914A-844567  
; Sequence 844567, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 844567  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-844567

Query Match 79.0%; Score 15.8; DB 7; Length 24;  
Best Local Similarity 36.8%; Pred. No. 3.1e+02;  
Matches 7; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 19  
:  
Db 1 UUUUGGAUUUCGGGGUUU 19

RESULT 23  
US-10-310-914A-271527/c  
; Sequence 271527, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01



; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 626220  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626220

Query Match 77.0%; Score 15.4; DB 7; Length 19;  
Best Local Similarity 94.1%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
Db 19 TGGGGTTTTGGGGTTTT 3

## RESULT 29

US-10-310-914A-626221/c  
; Sequence 626221, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 626221  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626221

Query Match 77.0%; Score 15.4; DB 7; Length 19;  
Best Local Similarity 94.1%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
Db 19 TGGGGTTTTGGGGTTTT 3

## RESULT 30

US-10-310-914A-1143338/c  
; Sequence 1143338, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 1143338  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1143338

Query Match 77.0%; Score 15.4; DB 7; Length 19;  
Best Local Similarity 94.1%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20

Db 19 TGGGGTTTTGGGGTTTT 3  
|||||  
RESULT 31  
US-10-310-914A-626141/c  
; Sequence 626141, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 626141  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626141

Query Match 77.0%; Score 15.4; DB 7; Length 20;  
Best Local Similarity 94.1%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
Db 20 TGGGGTTTTGGGGTTTT 4

## RESULT 32

US-10-310-914A-138178/c  
; Sequence 138178, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 138178  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-138178

Query Match 77.0%; Score 15.4; DB 7; Length 21;  
Best Local Similarity 94.1%; Pred. No. 4.4e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
Db 21 TGGGGTTTTGGGGTTTT 5

## RESULT 33

US-10-310-914A-138235/c  
; Sequence 138235, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 138235  
; TYPE: RNA  
; LENGTH: 25  
; ORGANISM: Human  
US-10-310-914A-138235

Query Match 77.0%; Score 15.4; DB 7; Length 25;  
Best Local Similarity 94.1%; Pred. No. 4.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
DB 25 TGGGGTTTTGGGGTTTT 9  
|||||

RESULT 34  
US-10-310-914A-626295/c  
; Sequence 626295, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 626295  
; LENGTH: 25  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626295

Query Match 77.0%; Score 15.4; DB 7; Length 25;  
Best Local Similarity 94.1%; Pred. No. 4.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
DB 24 TGGGGTTTTGGGGTTTT 8  
|||||

RESULT 35  
US-10-310-914A-626296/c  
; Sequence 626296, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 626296  
; LENGTH: 25  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-626296

Query Match 77.0%; Score 15.4; DB 7; Length 25;  
Best Local Similarity 94.1%; Pred. No. 4.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||

Db 24 TGGGGTTTTGGGGTTTT 8  
|||||

RESULT 36  
US-10-310-914A-1143370/c  
; Sequence 1143370, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1143370  
; LENGTH: 25  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1143370

Query Match 77.0%; Score 15.4; DB 7; Length 25;  
Best Local Similarity 94.1%; Pred. No. 4.5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGGGGTTTTGGGGTTTT 20  
|||||  
DB 24 TGGGGTTTTGGGGTTTT 8  
|||||

RESULT 37  
US-11-043-752-216/c  
; Sequence 216, Application US/11043752  
; Publication No. US20060014165A1  
; GENERAL INFORMATION:  
; APPLICANT: Hakonarson, Hakon  
; APPLICANT: Gurney, Mark E.  
; APPLICANT: Halapi, Eva  
; TITLE OF INVENTION: METHODS OF DIAGNOSIS AND TREATMENT FOR  
; FILE REFERENCE: 2345.2044-003  
; CURRENT APPLICATION NUMBER: US/11/043,752  
; CURRENT FILING DATE: 2005-01-26  
; PRIOR APPLICATION NUMBER: PCT/US04/022446  
; PRIOR FILING DATE: 2004-07-14  
; PRIOR APPLICATION NUMBER: 60/487,072  
; PRIOR FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: 60/559,611  
; PRIOR FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 4326  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 216  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-043-752-216

Query Match 76.0%; Score 15.2; DB 11; Length 20;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTTGGGGTTTT 20  
|||||  
DB 20 TTGTGGTGTTTGGGGATTT 1  
|||||

RESULT 38  
US-10-310-914A-84509/c  
; Sequence 84509, Application US/10310914A  
; Publication No. US20060003322A1

## ; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 84509  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-84509

Query Match 76.0%; Score 15.2; DB 7; Length 21;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 21 TTTTGGGGTTTGGGGTTTT 2

## RESULT 39

US-10-310-914A-455408/c  
; Sequence 455408, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 455408  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-455408

Query Match 76.0%; Score 15.2; DB 7; Length 21;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 21 TTTTGGGGTTTATGTTTT 2

## RESULT 40

US-10-310-914A-622070/c  
; Sequence 622070, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 622070  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-622070

; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 84509  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-84509

Query Match 76.0%; Score 15.2; DB 7; Length 21;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 21 TTTTGGGGTTTGGGGTTTT 2

## RESULT 39

US-10-310-914A-455408/c  
; Sequence 455408, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 455408  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-455408

Query Match 76.0%; Score 15.2; DB 7; Length 21;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 21 TTTTGGGGTTTATGTTTT 2

## RESULT 40

US-10-310-914A-622070/c  
; Sequence 622070, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 622070  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-622070

Query Match 76.0%; Score 15.2; DB 7; Length 21;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 20 TTTTGTTTTTTTGGGGTTTT 1

## RESULT 41

US-10-310-914A-675377/c  
; Sequence 675377, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 675377  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-675377

Query Match 76.0%; Score 15.2; DB 7; Length 21;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 20 TGTTCGGGGTTTGGGGTTTT 1

## RESULT 42

US-10-310-914A-1222901/c  
; Sequence 1222901, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1222901  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1222901

Query Match 76.0%; Score 15.2; DB 7; Length 21;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGGTTTGGGGTTTT 20  
|||||  
Db 21 TTTTGGGGTTTGTGTTTT 2

## RESULT 43

US-10-310-914A-238142/c  
; Sequence 238142, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

```

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 238142
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-238142

Query Match          76.0%; Score 15.2; DB 7; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
   ||||| ||||| ||||| |||||
Db 22 TTTTGGGGTTTGGGGCAIT 3

RESULT 44
US-10-310-914A-465689/c
; Sequence 465689, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 465689
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-465689

Query Match          76.0%; Score 15.2; DB 7; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
   ||||| ||||| ||||| |||||
Db 22 TTTTGGGGTTTGGGGCAIT 3

RESULT 45
US-10-310-914A-1222898/c
; Sequence 1222898, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1222898
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1222898
```

```

Query Match          76.0%; Score 15.2; DB 7; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
   ||||| ||||| ||||| |||||
Db 22 TTTTGGGGTTTGGGGTTT 3

RESULT 46
US-10-310-914A-282917/c
; Sequence 282917, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 282917
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-282917

Query Match          76.0%; Score 15.2; DB 7; Length 23;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
   ||||| ||||| ||||| |||||
Db 23 TTTTGGGTGTTTGTGTTT 4

RESULT 47
US-10-310-914A-465697/c
; Sequence 465697, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 465697
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-465697

Query Match          76.0%; Score 15.2; DB 7; Length 23;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTGGGGTTTGGGGTTT 20
   ||||| ||||| ||||| |||||
Db 20 TTTTGGGGTTTGGGGTTGT 1

RESULT 48
US-10-310-914A-501657/c
; Sequence 501657, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
```



; APPLICANT: Shiler, Kvizat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 501657  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-501657

Query Match 76.0%; Score 15.2; DB 7; Length 23;  
Best Local Similarity 85.0%; Pred. No. 5.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTTGGGTTTT 20  
||| || ||||| |||||  
Db 21 TTTAGGTGTTTTGGGTTTT 2

## RESULT 49

US-10-310-914A-651609/c  
; Sequence 651609, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvizat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 651609  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-651609

Query Match 76.0%; Score 15.2; DB 7; Length 23;  
Best Local Similarity 85.0%; Pred. No. 5.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTTGGGTTTT 20  
||| || ||||| |||||  
Db 21 TTTTGGGTTTTGGGTTTT 2

## RESULT 50

US-10-310-914A-675445/c  
; Sequence 675445, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvizat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 675445  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-675445

Query Match 76.0%; Score 15.2; DB 7; Length 23;

Best Local Similarity 85.0%; Pred. No. 5.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTTTGGGTTTTGGGTTTT 20  
||| || ||||| |||||  
Db 22 TGTTTGGGTTTGGGTTTT 3

Search completed: February 16, 2006, 02:52:56  
Job time : 188.446 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:51:58 ; Search time 455.843 Seconds  
(without alignments)  
2369.293 Million cell updates/sec

Title: US-09-669-187A-80

Perfect score: 19

Sequence: 1 ggggtgaagcttcagggggg 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172563 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.in.\*

3: gb.env.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pr.\*

9: gb.ro.\*

10: gb.sts.\*

11: gb.sy.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.htg.\*

15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	19	100.0	19	6	AX103888 Sequence
2	19	100.0	19	6	AX355419 Sequence
3	19	100.0	19	6	AX546941 Sequence
4	17.4	91.6	19	6	AX103890 Sequence
5	17.4	91.6	19	6	AX355420 Sequence
6	17.4	91.6	19	6	AX546943 Sequence
7	14.2	74.7	20	6	AR096686 Sequence
8	14.2	74.7	20	6	AR135030 Sequence
9	14.2	74.7	20	6	AR182891 Sequence
10	14.2	74.7	20	6	AR607454 Sequence
11	14.2	74.7	20	6	AX104032 Sequence
12	14.2	74.7	20	6	AX342378 Sequence
13	14.2	74.7	20	6	AX342405 Sequence
14	14.2	74.7	20	6	AX342438 Sequence
15	14.2	74.7	20	6	AX355421 Sequence
16	14.2	74.7	20	6	AX547085 Sequence
17	14	73.7	39	6	AR337615 Sequence
18	13.4	70.5	22	6	AR137717 Sequence

CQ874726	Sequence	30	6	CQ874726	70.5	13.4	19
AX514115	Sequence	41	6	AX514115	70.5	13.4	C 20
AX520264	Sequence	41	6	AX520264	70.5	13.4	C 21
AX104329	Sequence	20	6	AX104329	69.5	13.2	C 22
AX104332	Sequence	20	6	AX104332	69.5	13.2	C 23
AX355395	Sequence	20	6	AX355395	69.5	13.2	C 24
AX355396	Sequence	20	6	AX355396	69.5	13.2	C 25
AX547382	Sequence	20	6	AX547382	69.5	13.2	C 26
AX547385	Sequence	20	6	AX547385	69.5	13.2	C 27
CS121639	Sequence	32	6	CS121639	69.5	13.2	C 28
AX805700	Sequence	32	6	AX805700	69.5	13.2	C 29
CS087335	Sequence	47	6	CS087335	69.5	13.2	C 30
CS087338	Sequence	47	6	CS087338	69.5	13.2	C 31
CS087376	Sequence	47	6	CS087376	69.5	13.2	C 32
CS087377	Sequence	47	6	CS087377	69.5	13.2	C 33
AX455113	Sequence	20	6	AX455113	68.4	13	C 34
CQ827797	Sequence	19	6	CQ827797	67.4	12.8	C 35
AR135661	Sequence	20	6	AR135661	67.4	12.8	C 36
CQ775024	Sequence	20	6	CQ775024	67.4	12.8	C 37
AX814043	Sequence	20	6	AX814043	67.4	12.8	C 38
CQ760615	Sequence	21	6	CQ760615	67.4	12.8	C 39
CQ760697	Sequence	21	6	CQ760697	67.4	12.8	C 40
AX249619	Sequence	31	6	AX249619	67.4	12.8	C 41
AR029533	Sequence	32	6	AR029533	67.4	12.8	C 42
AR098486	Sequence	32	6	AR098486	67.4	12.8	C 43
141446	Sequence 43	32	6	141446	67.4	12.8	C 44
AR494995	Sequence	32	6	AR494995	67.4	12.8	C 45
AX441412	Sequence	32	6	AX441412	67.4	12.8	C 46
AX453908	Sequence	32	6	AX453908	67.4	12.8	C 47
AX514624	Sequence	41	6	AX514624	67.4	12.8	C 48
M18006 Flavobacter		50	1	FVBFOKIB	67.4	12.8	C 49
AX190133	Sequence	50	6	AX190133	67.4	12.8	C 50
AX104784	Sequence	50	6	AX104784	66.3	12.6	C 51
AX104854	Sequence	19	6	AX104854	66.3	12.6	C 52
AX105129	Sequence	19	6	AX105129	66.3	12.6	C 53
AX547907	Sequence	19	6	AX547907	66.3	12.6	C 54
AR140453	Sequence	20	6	AR140453	66.3	12.6	C 55
AR154761	Sequence	20	6	AR154761	66.3	12.6	C 56
BD069974	Sequence	20	6	BD069974	66.3	12.6	C 57
BD190419	Microemul	20	6	BD190419	66.3	12.6	C 58
BD251267	Enhanceme	20	6	BD251267	66.3	12.6	C 59
AR182880	Sequence	20	6	AR182880	66.3	12.6	C 60
AR182887	Sequence	20	6	AR182887	66.3	12.6	C 61
AR222213	Sequence	20	6	AR222213	66.3	12.6	C 62
AR432435	Sequence	20	6	AR432435	66.3	12.6	C 63
AR607443	Sequence	20	6	AR607443	66.3	12.6	C 64
AR607450	Sequence	20	6	AR607450	66.3	12.6	C 65
AX063578	Sequence	20	6	AX063578	66.3	12.6	C 66
AX088932	Sequence	20	6	AX088932	66.3	12.6	C 67
AX104327	Sequence	20	6	AX104327	66.3	12.6	C 68
AX104575	Sequence	20	6	AX104575	66.3	12.6	C 69
AX104717	Sequence	20	6	AX104717	66.3	12.6	C 70
AX104776	Sequence	20	6	AX104776	66.3	12.6	C 71
AX105103	Sequence	20	6	AX105103	66.3	12.6	C 72
AX105107	Sequence	20	6	AX105107	66.3	12.6	C 73
AX105236	Sequence	20	6	AX105236	66.3	12.6	C 74
AX105237	Sequence	20	6	AX105237	66.3	12.6	C 75
AX135634	Sequence	20	6	AX135634	66.3	12.6	C 76
AX194489	Sequence	20	6	AX194489	66.3	12.6	C 77
AX355408	Sequence	20	6	AX355408	66.3	12.6	C 78
AX355409	Sequence	20	6	AX355409	66.3	12.6	C 79
AX355415	Sequence	20	6	AX355415	66.3	12.6	C 80
AX465439	Sequence	20	6	AX465439	66.3	12.6	C 81
AX468483	Sequence	20	6	AX468483	66.3	12.6	C 82
AX547380	Sequence	20	6	AX547380	66.3	12.6	C 83
AX547628	Sequence	20	6	AX547628	66.3	12.6	C 84
AX547770	Sequence	20	6	AX547770	66.3	12.6	C 85
AX547829	Sequence	20	6	AX547829	66.3	12.6	C 86
AX547830	Sequence	20	6	AX547830	66.3	12.6	C 87
BD009060	Immunosti	20	6	BD009060	66.3	12.6	C 88

92	12.6	66.3	21	6	AX104812	Sequence	165	12.2	64.2	48	6	AR494672	Sequence
93	12.6	66.3	21	6	AX105257	Sequence	c 166	12.2	64.2	50	6	CQ008444	Sequence
94	12.6	66.3	21	6	AX547855	Sequence	c 167	12.2	64.2	50	6	AX033084	Sequence
95	12.6	66.3	24	6	AX104326	Sequence	c 168	11.8	62.1	18	6	AR181702	Sequence
c 96	12.6	66.3	24	6	AX547379	Sequence	c 169	11.8	62.1	18	6	ARG29692	Sequence
c 97	12.6	66.3	25	6	AX463125	Sequence	c 170	11.8	62.1	20	6	AR137469	Sequence
c 98	12.6	66.3	26	6	BD078174	Modulator	c 171	11.8	62.1	20	6	CS012607	Sequence
c 99	12.6	66.3	26	6	BD078225	Modulator	c 172	11.8	62.1	20	6	AX664900	Sequence
c 100	12.6	66.3	30	6	E04679	Sequence	c 173	11.8	62.1	20	6	AX670947	Sequence
c 101	12.6	66.3	30	6	E04682	Sequence	c 174	11.8	62.1	21	6	CS081480	Sequence
c 102	12.6	66.3	30	6	AX105266	Sequence	c 175	11.8	62.1	21	6	AX117610	Sequence
c 103	12.6	66.3	30	6	AX351709	Sequence	c 176	11.8	62.1	22	6	CQ774347	Sequence
c 104	12.6	66.3	30	6	AX351712	Sequence	c 177	11.8	62.1	22	6	CQ779543	Sequence
c 105	12.6	66.3	30	6	AX351714	Sequence	c 178	11.8	62.1	24	6	A56967	Sequence
c 106	12.6	66.3	30	6	AX351714	Sequence	c 179	11.8	62.1	25	6	A92794	Sequence
c 107	12.6	66.3	44	6	AR410782	Sequence	c 180	11.8	62.1	25	6	BD238067	Sequence
c 108	12.6	66.3	44	6	AR439146	Sequence	c 181	11.8	62.1	25	6	AX023972	Sequence
c 109	12.6	66.3	44	6	AR473166	Sequence	c 182	11.8	62.1	25	6	AX609210	Sequence
c 110	12.6	66.3	44	6	AR527152	Sequence	c 183	11.8	62.1	30	6	AR090268	Sequence
c 111	12.6	66.3	44	6	AR566185	Sequence	c 184	11.8	62.1	30	6	AR197303	Sequence
c 112	12.6	66.3	44	6	AR592203	Sequence	c 185	11.8	62.1	30	6	AR259457	Sequence
c 113	12.6	66.3	44	6	AR604477	Sequence	c 186	11.8	62.1	31	6	BD233524	Formation
c 114	12.6	66.3	44	6	AR605063	Sequence	c 187	11.8	62.1	31	6	AR448494	Sequence
c 115	12.6	66.3	44	6	AR613728	Sequence	c 188	11.8	62.1	31	6	AX078480	Sequence
c 116	12.6	66.3	44	6	AR635899	Sequence	c 189	11.8	62.1	32	6	CS050648	Sequence
c 117	12.6	66.3	44	6	AR650628	Sequence	c 190	11.8	62.1	36	6	AR272252	Sequence
c 118	12.6	66.3	44	6	AR657569	Sequence	c 191	11.8	62.1	47	6	AR290405	Sequence
c 119	12.6	66.3	44	6	AR697634	Sequence	c 192	11.8	62.1	48	6	AX300111	Sequence
c 120	12.6	66.3	45	6	BD075553	Secretary	c 193	11.8	62.1	48	10	CR380691	Arabidops
c 121	12.6	66.3	45	6	BD172413	Secreted	c 194	11.6	61.1	18	6	AR7621	Sequence
c 122	12.6	66.3	45	6	BD172732	Secreted	c 195	11.6	61.1	18	6	BD104031	Kit and m
c 123	12.6	66.3	45	6	BD173051	Secreted	c 196	11.6	61.1	19	6	CQ753472	Sequence
c 124	12.6	66.3	45	6	BD173370	Secreted	c 197	11.6	61.1	19	6	CQ753473	Sequence
c 125	12.6	66.3	45	6	BD175404	Secretary	c 198	11.6	61.1	19	6	CQ888031	Sequence
c 126	12.4	65.3	47	6	AR583328	Sequence	c 199	11.6	61.1	19	6	CQ888032	Sequence
c 127	12.4	65.3	20	6	AX104334	Sequence	c 200	11.6	61.1	19	6	CQ888168	Sequence
c 128	12.4	65.3	20	6	AX104664	Sequence	c 201	11.6	61.1	19	6	CQ888169	Sequence
c 129	12.4	65.3	20	6	AX354978	Sequence	c 202	11.6	61.1	19	6	AX104785	Sequence
c 130	12.4	65.3	20	6	AX354979	Sequence	c 203	11.6	61.1	19	6	AX194446	Sequence
c 131	12.4	65.3	20	6	AX547387	Sequence	c 204	11.6	61.1	19	6	AX465396	Sequence
c 132	12.4	65.3	21	6	AX547717	Sequence	c 205	11.6	61.1	19	6	AX547838	Sequence
c 133	12.4	65.3	22	6	AX103724	Sequence	c 206	11.6	61.1	19	6	AX771751	Sequence
c 134	12.4	65.3	24	6	A69776	Sequence	c 207	11.6	61.1	19	6	AX771752	Sequence
c 135	12.4	65.3	24	6	AR209843	Sequence	c 208	11.6	61.1	19	11	CS000879	Sequence
c 136	12.4	65.3	24	6	AX924199	Sequence	c 209	11.6	61.1	21	6	AR299149	Sequence
c 137	12.4	65.3	41	6	AX520567	Sequence	c 210	11.6	61.1	22	6	AR011757	Sequence
c 138	12.4	65.3	41	6	AX520568	Sequence	c 211	11.6	61.1	22	6	BD226639	Methods f
c 139	12.4	65.3	48	6	AX555106	Sequence	c 212	11.6	61.1	22	6	CS021016	Sequence
c 140	12.2	64.2	17	6	A64836	Sequence	c 213	11.6	61.1	22	6	I15870	Sequence
c 141	12.2	64.2	21	6	CQ857995	Sequence	c 214	11.6	61.1	22	6	AR317236	Sequence
c 142	12.2	64.2	21	6	CQ890978	Sequence	c 215	11.6	61.1	22	6	AR453336	Sequence
c 143	12.2	64.2	22	6	AR043695	Sequence	c 216	11.6	61.1	22	6	AR454805	Sequence
c 144	12.2	64.2	22	6	AR043705	Sequence	c 217	11.6	61.1	23	6	I4766	Sequence
c 145	12.2	64.2	26	6	AR633199	Sequence	c 218	11.6	61.1	24	6	AR098538	Sequence
c 146	12.2	64.2	26	6	AR633200	Sequence	c 219	11.6	61.1	24	6	AR108883	Sequence
c 147	12.2	64.2	27	6	AR173103	Sequence	c 220	11.6	61.1	25	6	CQ865740	Sequence
c 148	12.2	64.2	27	6	BD106943	Method fo	c 221	11.6	61.1	25	6	AX463124	Sequence
c 149	12.2	64.2	27	6	BD139588	Arginine	c 222	11.6	61.1	26	6	AR050964	Sequence
c 150	12.2	64.2	33	6	AR636091	Sequence	c 223	11.6	61.1	26	6	I51765	Sequence
c 151	12.2	64.2	33	6	AR636092	Sequence	c 224	11.6	61.1	26	6	I84365	Sequence
c 152	12.2	64.2	42	9	S77070	T-cell rece	c 225	11.6	61.1	26	6	AR204573	Sequence
c 153	12.2	64.2	43	6	CS087286	Sequence	c 226	11.6	61.1	26	6	AR307255	Sequence
c 154	12.2	64.2	43	6	CS087287	Sequence	c 227	11.6	61.1	27	6	BD238542	Expressio
c 155	12.2	64.2	43	6	CS087289	Sequence	c 228	11.6	61.1	28	6	AR593306	Sequence
c 156	12.2	64.2	43	6	CS087292	Sequence	c 229	11.6	61.1	28	6	AX082658	Sequence
c 157	12.2	64.2	43	6	CS087330	Sequence	c 230	11.6	61.1	28	6	AX030300	Sequence
c 158	12.2	64.2	43	6	CS087331	Sequence	c 231	11.6	61.1	29	6	CQ786953	Sequence
c 159	12.2	64.2	45	6	BD169771	Transcrip	c 232	11.6	61.1	30	6	AR154128	Sequence
c 160	12.2	64.2	45	6	BD184729	Transcrip	c 233	11.6	61.1	30	6	AX611194	Sequence
c 161	12.2	64.2	47	6	AR140184	Sequence	c 234	11.6	61.1	31	6	AR411039	Sequence
c 162	12.2	64.2	47	6	CS087332	Sequence	c 235	11.6	61.1	33	6	AR215282	Sequence
c 163	12.2	64.2	47	6	CS087333	Sequence	c 236	11.6	61.1	33	6	AR308656	Sequence
c 164	12.2	64.2	48	6	AR369026	Sequence	c 237	11.6	61.1	36	6	AR077845	Sequence

238	11.6	61.1	36	6	AR077847	Sequence
239	11.6	61.1	36	6	AR077849	Sequence
240	11.6	61.1	36	8	HSJ5142	Homo sapi
c 241	11.6	61.1	39	6	CS055984	Sequence
242	11.6	61.1	39	6	CS055985	Sequence
243	11.6	61.1	41	6	AX516102	Sequence
c 244	11.6	61.1	41	6	AX517508	Sequence
245	11.6	61.1	42	6	A93596	Sequence
c 246	11.6	61.1	42	6	BD139665	A novel m
c 247	11.6	61.1	42	6	BD139666	A novel m
248	11.6	61.1	42	6	BD222933	Heteromim
c 249	11.6	61.1	42	6	BD222934	Heteromim
250	11.6	61.1	42	6	AX003756	Sequence
c 251	11.6	61.1	42	6	AX003757	Sequence
252	11.6	61.1	42	6	AX023357	Sequence
c 253	11.6	61.1	42	6	AX023358	Sequence
c 254	11.6	61.1	43	6	AX484631	Sequence
255	11.6	61.1	47	6	BD232083	Complex f
256	11.6	61.1	47	6	CS087334	Sequence
257	11.6	61.1	47	6	CS087336	Sequence
c 258	11.6	61.1	47	6	AR288368	Sequence
259	11.6	61.1	47	6	AR290478	Sequence
260	11.6	61.1	47	6	AR583333	Sequence
c 261	11.6	61.1	50	6	QQ05508	Sequence
262	11.6	61.1	50	6	QQ06009	Sequence
c 263	11.6	61.1	50	6	AX147170	Sequence
c 264	11.4	60.0	16	6	AX352071	Sequence
265	11.4	60.0	19	6	CS014898	Sequence
c 266	11.4	60.0	19	6	CS053312	Sequence
c 267	11.4	60.0	19	6	CS050306	Sequence
c 273	11.4	60.0	22	6	AR043704	Sequence
c 274	11.4	60.0	30	6	AR441814	Sequence
c 275	11.4	60.0	30	6	AX454811	Sequence
c 276	11.4	60.0	30	6	AX477003	Sequence
c 277	11.4	60.0	33	6	BD061423	Novel pol
278	11.4	60.0	34	6	Q8411175	Sequence
279	11.4	60.0	34	6	Q848896	Sequence
280	11.4	60.0	35	6	AR025462	Sequence
281	11.4	60.0	37	6	E13251	Oligonucleo
282	11.4	60.0	47	6	AR284483	Sequence
c 283	11.4	60.0	47	6	AR583119	Sequence
284	11.4	60.0	48	6	Q848225	Sequence
285	11.4	60.0	48	6	CS122612	Sequence
c 286	11.4	60.0	50	6	QQ08715	Sequence
c 287	11.4	60.0	50	6	QQ08716	Sequence
288	11.2	58.9	16	6	AX194461	Sequence
289	11.2	58.9	16	6	AX194463	Sequence
290	11.2	58.9	16	6	AX255819	Sequence
291	11.2	58.9	16	6	AX465411	Sequence
292	11.2	58.9	16	6	AX465413	Sequence
293	11.2	58.9	17	6	BD104484	Kit and m
c 294	11.2	58.9	17	6	AR286146	Sequence
c 295	11.2	58.9	17	6	AR398136	Sequence
c 296	11.2	58.9	18	6	AX116882	Sequence
c 297	11.2	58.9	19	6	CS093133	Sequence
298	11.2	58.9	19	6	CS093440	Sequence
c 299	11.2	58.9	20	6	AR118909	Sequence
300	11.2	58.9	20	6	BD196114	Antisense

ALIGNMENTS

RESULT 1  
AX103888  
LOCUS  
DEFINITION Sequence 80 from Patent WO0122972.  
ACCESSION AX103888

AX103888 19 bp DNA linear PAT 30-APR-2001

VERSION AX103888.1 GI:13920085  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.  
TITLE Immunostimulatory nucleic acids  
JOURNAL Patent: WO 0122972-A 80 05-APR-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical  
GmbH (DE)  
FEATURES Location/Qualifiers  
source 1..19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 100.0%; Score 19; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTCACGTTTCAGGGGG 19  
|||||  
Db 1 GGGGTACGTTTCAGGGGG 19  
|||||  
RESULT 2  
AX355419  
LOCUS AX355419 19 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 447 from Patent WO0197843.  
ACCESSION AX355419  
VERSION AX355419.1 GI:18620087  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Weiner,G. and Hartmann,G.  
TITLE Methods for enhancing antibody-induced cell lysis and treating  
cancer  
JOURNAL Patent: WO 0197843-A 447 27-DEC-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
FEATURES Location/Qualifiers  
source 1..19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic oligonucleotide  
chimeric phosphorothioate/phosphodiester backbone with  
phosphorothioate at 5' and 3' ends"  
ORIGIN  
Query Match 100.0%; Score 19; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTCACGTTTCAGGGGG 19  
|||||  
Db 1 GGGGTACGTTTCAGGGGG 19  
|||||  
RESULT 3  
AX546941  
LOCUS AX546941 19 bp DNA linear PAT 01-MAR-2003  
DEFINITION Sequence 80 from Patent WO02053141.  
ACCESSION AX546941  
VERSION AX546941.1 GI:25812085  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1

```
AUTHORS      Bratzler,R.L.
TITLE         Inhibition of angiogenesis by nucleic acids
JOURNAL       Patent: WO 02053141-A 80 11-JUL-2002;
              Coley Pharmaceutical Group, Inc. (US)
FEATURES      Location/Qualifiers
              source
                1..19
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthetic Sequence"
ORIGIN
  Query Match      100.0%; Score 19; DB 6; Length 19;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGGG 19
    ||||| ||||| ||||| |||||
Db 1 GGGGTGACGTTTCAGGGGGG 19
    ||||| ||||| ||||| |||||
RESULT 4
AX103890          AX103890          19 bp DNA linear PAT 30-APR-2001
LOCUS             Sequence 82 from Patent WO0122972.
DEFINITION        AX103890
ACCESSION          AX103890
VERSION            AX103890.1 GI:13920087
KEYWORDS           .
SOURCE             synthetic construct
ORGANISM           other sequences; artificial sequences.
REFERENCE          1
AUTHORS            Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE              Immunostimulatory nucleic acids
JOURNAL            Patent: WO 0122972-A 82 05-APR-2001;
                  UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
                  GmbH (DE)
FEATURES           Location/Qualifiers
              source
                1..19
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
ORIGIN
  Query Match      91.6%; Score 17.4; DB 6; Length 19;
  Best Local Similarity 94.7%; Pred. No. 8e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGGG 19
    ||||| ||||| ||||| |||||
Db 1 GGGGTGTCGTTTCAGGGGGG 19
    ||||| ||||| ||||| |||||
RESULT 5
AX355420          AX355420          19 bp DNA linear PAT 06-FEB-2002
LOCUS             Sequence 448 from Patent WO0197843.
DEFINITION        AX355420
ACCESSION          AX355420
VERSION            AX355420.1 GI:18620088
KEYWORDS           .
SOURCE             synthetic construct
ORGANISM           other sequences; artificial sequences.
REFERENCE          1
AUTHORS            Weiner,G. and Hartmann,G.
TITLE              Methods for enhancing antibody-induced cell lysis and treating
                  cancer
JOURNAL            Patent: WO 0197843-A 448 27-DEC-2001;
                  UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES           Location/Qualifiers
              source
                1..19
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
ORIGIN
  Query Match      91.6%; Score 17.4; DB 6; Length 19;
  Best Local Similarity 94.7%; Pred. No. 8e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGGG 19
    ||||| ||||| ||||| |||||
Db 1 GGGGTGTCGTTTCAGGGGGG 19
    ||||| ||||| ||||| |||||
RESULT 6
AX546943          AX546943          19 bp DNA linear PAT 01-MAR-2003
LOCUS             Sequence 82 from Patent WO02053141.
DEFINITION        AX546943
ACCESSION          AX546943
VERSION            AX546943.1 GI:25812087
KEYWORDS           .
SOURCE             synthetic construct
ORGANISM           other sequences; artificial sequences.
REFERENCE          1
AUTHORS            Bratzler,R.L.
TITLE              Inhibition of angiogenesis by nucleic acids
JOURNAL            Patent: WO 02053141-A 82 11-JUL-2002;
                  Coley Pharmaceutical Group, Inc. (US)
FEATURES           Location/Qualifiers
              source
                1..19
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthetic Sequence"
ORIGIN
  Query Match      91.6%; Score 17.4; DB 6; Length 19;
  Best Local Similarity 94.7%; Pred. No. 8e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGGG 19
    ||||| ||||| ||||| |||||
Db 1 GGGGTGTCGTTTCAGGGGGG 19
    ||||| ||||| ||||| |||||
RESULT 7
AR096686          AR096686          20 bp DNA linear PAT 08-SEP-2000
LOCUS             Sequence 1 from patent US 6008200.
DEFINITION        AR096686
ACCESSION          AR096686
VERSION            AR096686.1 GI:10025701
KEYWORDS           .
SOURCE             Unknown.
ORGANISM           Unclassified.
REFERENCE          1 (bases 1 to 20)
AUTHORS            Krieg,A.M.
TITLE              Immunomodulatory oligonucleotides
JOURNAL            Patent: US 6008200-A 1 28-DEC-1999;
                  Location/Qualifiers
FEATURES           Location/Qualifiers
              source
                1..20
                /organism="unknown"
                /mol_type="unassigned DNA"
ORIGIN
  Query Match      74.7%; Score 14.2; DB 6; Length 20;
  Best Local Similarity 84.2%; Pred. No. 3.2e+04;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGGG 19
    ||| ||||| ||||| ||||| |||||
```

Db 2 GGCTCAACGTTTCAGGGGG 20

RESULT 8  
LOCUS AR135030 20 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 1 from patent US 6194388.  
ACCESSION AR135030  
VERSION AR135030.1 GI:14123935  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Krieg, A.M., Klinman, D. and Steinberg, A.D.  
TITLE Immunomodulatory oligonucleotides  
JOURNAL Patent: US 6194388-A 1:27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 74.7%; Score 14.2; DB 6; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCGTGACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGCTCAACGTTTCAGGGGG 20

RESULT 11  
LOCUS AX104032 20 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 224 from Patent WO0122972.  
ACCESSION AX104032  
VERSION AX104032.1 GI:13920229  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.  
TITLE Immunostimulatory nucleic acids  
JOURNAL Patent: WO 0122972-A 224 05-APR-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical  
GmbH (DE)

FEATURES Location/Qualifiers  
source 1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 74.7%; Score 14.2; DB 6; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCGTGACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGCTCAACGTTTCAGGGGG 20

RESULT 12  
LOCUS AX342378 20 bp DNA linear PAT 12-JAN-2002  
DEFINITION Sequence 1 from Patent EP1187377.  
ACCESSION AX342378  
VERSION AX342378.1 GI:18151821  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Krieg, A.M.  
TITLE Immunomodulatory oligonucleotides  
JOURNAL Patent: EP 1187377-A 1 02-JAN-2002;  
THE UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
FEATURES Location/Qualifiers  
source 1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 74.7%; Score 14.2; DB 6; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCGTGACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGCTCAACGTTTCAGGGGG 20

RESULT 9  
LOCUS AR182891 20 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 63 from patent US 6339068.  
ACCESSION AR182891  
VERSION AR182891.1 GI:20226098  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Krieg, A.M., Davis, H.L., Wu, T. and Schorr, J.  
TITLE Vectors and methods for immunization or therapeutic protocols  
JOURNAL Patent: US 6339068-A 63 15-JAN-2002;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical  
GmbH (DE)

FEATURES Location/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 74.7%; Score 14.2; DB 6; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.2e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCGTGACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGCTCAACGTTTCAGGGGG 20

RESULT 10  
LOCUS AR607454 20 bp DNA linear PAT 15-DEC-2004  
DEFINITION Sequence 63 from patent US 6821957.  
ACCESSION AR607454  
VERSION AR607454.1 GI:56659871  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Krieg, A.M., Davis, H.L., Wu, T. and Joachim, S.

```
Best Local Similarity 84.2%; Pred. No. 3.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
   ||| ||||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 13
LOCUS AX342405
DEFINITION Sequence 1 from Patent EP1167379.
ACCESSION AX342405
VERSION AX342405.1 GI:18151848
KEYWORDS .
SOURCE .
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M.
TITLE Immunomodulatory oligonucleotides
JOURNAL Patent: EP 1167379-A 1 02-JAN-2002;
          UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source Location/Qualifiers
      1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
ORIGIN
Query Match 74.7%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
   ||| ||||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 14
LOCUS AX342438
DEFINITION Sequence 1 from Patent EP1167378.
ACCESSION AX342438
VERSION AX342438.1 GI:18151881
KEYWORDS .
SOURCE .
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M.
TITLE Immunomodulatory oligonucleotides
JOURNAL Patent: EP 1167378-A 1 02-JAN-2002;
          UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source Location/Qualifiers
      1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
ORIGIN
Query Match 74.7%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
   ||| ||||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 15
LOCUS AX355421
DEFINITION Sequence 449 from Patent WO0197843.
ACCESSION AX355421
VERSION AX355421.1 GI:18620089
KEYWORDS .
SOURCE .
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
          cancer
JOURNAL Patent: WO 0197843-A 449 27-DEC-2001;
          UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source Location/Qualifiers
      1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic oligonucleotide
            chimeric phosphorothioate/phosphodiester backbone with
            phosphorothioate at 5' and 3' ends"
ORIGIN
Query Match 74.7%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
   ||| ||||| ||||| |||||
Db 2 GGGTTGACGTTTTCAGGGGG 20

RESULT 16
LOCUS AX547085
DEFINITION Sequence 224 from Patent WO02053141.
ACCESSION AX547085
VERSION AX547085.1 GI:25812229
KEYWORDS .
SOURCE .
ORGANISM synthetic construct
          other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 224 11-JUL-2002;
          Coley Pharmaceutical Group, Inc. (US)
FEATURES
source Location/Qualifiers
      1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic Sequence"
ORIGIN
Query Match 74.7%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
   ||| ||||| ||||| |||||
Db 2 GGGTTGACGTTTTCAGGGGG 20

RESULT 17
LOCUS AR337615/c
DEFINITION Sequence 18 from patent US 6566500.
ACCESSION AR337615
VERSION AR337615.1 GI:33724021
KEYWORDS .
SOURCE .
ORGANISM Unknown.
          Unknown.
```



Unclassified.

REFERENCE 1 (bases 1 to 39)  
AUTHORS Vitetta,E.S., Ghetie,V.F., Smallshaw,J. and Baluna,R.G.  
TITLE Combinations and methods for modifying toxic effects of  
proteinaceous compounds  
JOURNAL Patent: US 656500-A 18 20-MAY-2003;  
Board of Regents, The University of Texas System; Austin, TX

FEATURES  
source  
1..39  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 73.7%; Score 14; DB 6; Length 39;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGG 16  
|||||

Db 26 GGTGACGTTTCAGG 13

RESULT 18  
AR137717  
LOCUS AR137717 22 bp DNA linear PAT 16-JUN-2001  
DEFINITION Sequence 5 from patent US 6197556.  
ACCESSION AR137717  
VERSION AR137717.1 GI:14479226  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Ulanovsky,L. and Raja,M.C.  
TITLE Nucleic acid amplification using modular branched primers  
JOURNAL Patent: US 6197556-A 5 06-MAR-2001;  
Metabolic Explorer (FR)

FEATURES  
source  
1..22  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 70.5%; Score 13.4; DB 6; Length 22;  
Best Local Similarity 93.3%; Pred. No. 8e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TGACGTTTCAGGGGG 19  
|||||

Db 2 TGACGTTTCAGGGGTG 16

RESULT 19  
AR137426  
LOCUS AR137426 30 bp DNA linear PAT 27-SEP-2004  
DEFINITION Sequence 21 from Patent WO2004076659.  
ACCESSION AR137426  
VERSION AR137426.1 GI:52747896  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Chateau,M., Gonzalez,B., Meynial-Salles,I., Soucaille,P.N. and  
Zink,O.  
TITLE Method for the production of evolved microorganisms which permit  
the generation or modification of metabolic pathways  
JOURNAL Patent: WO 2004076659-A 21 10-SEP-2004;  
Metabolic Explorer (FR)

FEATURES  
source  
1..30  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

Unclassified.

REFERENCE 1 (bases 1 to 39)  
AUTHORS Vitetta,E.S., Ghetie,V.F., Smallshaw,J. and Baluna,R.G.  
TITLE Combinations and methods for modifying toxic effects of  
proteinaceous compounds  
JOURNAL Patent: US 656500-A 18 20-MAY-2003;  
Board of Regents, The University of Texas System; Austin, TX

FEATURES  
source  
1..39  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 73.7%; Score 14; DB 6; Length 39;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGG 16  
|||||

Db 26 GGTGACGTTTCAGG 13

RESULT 18  
AR137717  
LOCUS AR137717 22 bp DNA linear PAT 16-JUN-2001  
DEFINITION Sequence 5 from patent US 6197556.  
ACCESSION AR137717  
VERSION AR137717.1 GI:14479226  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
UNCLASSIFIED.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Ulanovsky,L. and Raja,M.C.  
TITLE Nucleic acid amplification using modular branched primers  
JOURNAL Patent: US 6197556-A 5 06-MAR-2001;  
Metabolic Explorer (FR)

FEATURES  
source  
1..22  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 70.5%; Score 13.4; DB 6; Length 22;  
Best Local Similarity 93.3%; Pred. No. 8e+04;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 TGACGTTTCAGGGGG 19  
|||||

Db 2 TGACGTTTCAGGGGTG 16

RESULT 19  
AR137426  
LOCUS AR137426 30 bp DNA linear PAT 27-SEP-2004  
DEFINITION Sequence 21 from Patent WO2004076659.  
ACCESSION AR137426  
VERSION AR137426.1 GI:52747896  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Chateau,M., Gonzalez,B., Meynial-Salles,I., Soucaille,P.N. and  
Zink,O.  
TITLE Method for the production of evolved microorganisms which permit  
the generation or modification of metabolic pathways  
JOURNAL Patent: WO 2004076659-A 21 10-SEP-2004;  
Metabolic Explorer (FR)

FEATURES  
source  
1..30  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

```

QY      1 GGGGTGACGTTTCAGGGG 17
        |||||: |||||
Db      26 GGGTREGGTTTCAGGGG 10

RESULT 22
AX104329
LOCUS      AX104329          20 bp      DNA      linear      PAT 30-APR-2001
DEFINITION Sequence 521 from Patent WO0122972..
ACCESSION  AX104329
VERSION     AX104329.1  GI:13920526
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE       Immunostimulatory nucleic acids
JOURNAL     Patent: WO 0122972-A 521 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ;
            GmbH (DE)
FEATURES    Location/Qualifiers
             source
             1..20
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"

ORIGIN
Query Match      69.5%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGG 18
        |||||: |||||
Db      3 GGCATGACGTTTCGGGGG 20

RESULT 23
AX104332
LOCUS      AX104332          20 bp      DNA      linear      PAT 30-APR-2001
DEFINITION Sequence 524 from Patent WO0122972..
ACCESSION  AX104332
VERSION     AX104332.1  GI:13920529
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE       Immunostimulatory nucleic acids
JOURNAL     Patent: WO 0122972-A 524 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ;
            GmbH (DE)
FEATURES    Location/Qualifiers
             source
             1..20
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"

ORIGIN
Query Match      69.5%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGG 18
        |||||: |||||
Db      3 GGCATGACGTTTCGGGGG 20

RESULT 24
AX355395
LOCUS      AX355395          20 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 423 from Patent WO0197843..
ACCESSION  AX355395
VERSION     AX355395.1  GI:18620063
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Weiner,G. and Hartmann,G.
TITLE       Methods for enhancing antibody-induced cell lysis and treating
            cancer
JOURNAL     Patent: WO 0197843-A 423 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
            Location/Qualifiers
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic oligonucleotide
            phosphorodithioate backbone"

ORIGIN
Query Match      69.5%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGG 18
        |||||: |||||
Db      3 GGCATGACGTTTCGGGGG 20

RESULT 25
AX355396
LOCUS      AX355396          20 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 424 from Patent WO0197843..
ACCESSION  AX355396
VERSION     AX355396.1  GI:18620064
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Weiner,G. and Hartmann,G.
TITLE       Methods for enhancing antibody-induced cell lysis and treating
            cancer
JOURNAL     Patent: WO 0197843-A 424 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
            Location/Qualifiers
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic oligonucleotide
            chimeric phosphorothioate/phosphodiester backbone with
            phosphorothioate at 5' and 3' ends"

ORIGIN
Query Match      69.5%; Score 13.2; DB 6; Length 20;
Best Local Similarity 83.3%; Pred. No. 1e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGG 18
        |||||: |||||
Db      3 GGCATGACGTTTCGGGGG 20

RESULT 26
AX547382
LOCUS      AX547382          20 bp      DNA      linear      PAT 01-MAR-2003
DEFINITION Sequence 521 from Patent WO02053141..
ACCESSION  AX547382
VERSION     AX547382.1  GI:25812526
KEYWORDS   .
SOURCE      synthetic construct

```

Query Match      69.5%;    Score 13.2;    DB 6;    Length 47;

```

Best Local Similarity 83.3%; Pred. No. 9.9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 18
    |||||
Db 26 GGGGTGACGGCAGGGAG 43

RESULT 31
CS087338
LOCUS CS087338 47 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 466 from Patent WO2005042743.
ACCESSION CS087338
VERSION CS087338.1 GI:66712787
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Dall-Acqua,W., Damschroder,M. and Wu,H.
TITLE Humanization of antibodies
JOURNAL Patent: WO 2005042743-A 466 12-MAY-2005;
MedImmune, Inc. (US)
FEATURES
source
1..47
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primers"

ORIGIN
Query Match 69.5%; Score 13.2; DB 6; Length 47;
Best Local Similarity 83.3%; Pred. No. 9.9e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 18
    |||||
Db 26 GGGGTGACGGCAGGGAG 43

RESULT 34
AX455113/c
LOCUS AX455113 20 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 180 from Patent WO0208453.
ACCESSION AX455113
VERSION AX455113.1 GI:21714298
KEYWORDS .
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1
AUTHORS Farr,S.B., Pickett,G.G., Neft,R.E. and Dunn,R.T.
TITLE Canine toxicity genes
JOURNAL Patent: WO 0208453-A 180 31-JAN-2002;
Phase-1 Molecular Toxicology (US)
FEATURES
source
1..20
/organism="Canis familiaris"
/mol_type="unassigned DNA"
/db_xref="taxon:9615"

ORIGIN
Query Match 68.4%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGG 15
    |||||
Db 18 GGTGACGTTTCAGG 6

RESULT 35
CQ827797
LOCUS CQ827797 19 bp DNA linear PAT 29-JUN-2004
DEFINITION Sequence 20 from Patent WO2004051269.
ACCESSION CQ827797
VERSION CQ827797.1 GI:49456213
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct

```

2017

```
QY      3  GGTGACGTTTCAGGGGG 18
Db      21 GGTGACGCTCTGGGGG 6

RESULT 40
LOCUS   CQ760697/c
DEFINITION Sequence 139 from Patent WO2004003229.
ACCESSION CQ760697
VERSION   CQ760697.1 GI:44904200
KEYWORDS .
SOURCE   synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS  Nex,B.R., Vogel,U., Rockenbauer,E. and Bukowy,Z.K.
TITLE    Disease risk estimating method using sequence polymorphisms in a
JOURNAL  specific region of chromosome 19
PATENT:  WO 2004003229-A 139 08-JAN-2004;
Aarhus University (DK) ; Arbejdsmilj Institutttet (National
Institute of Occupational Health) (DK)
FEATURES
source 1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32830"
/note="Probe"

ORIGIN
Query Match 67.4%; Score 12.8; DB 6; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3  GGTGACGTTTCAGGGGG 18
Db      21 GGTGACGCTCTGGGGG 6

RESULT 41
AX249619/c
LOCUS   AX249619
DEFINITION Sequence 1698 from Patent WO0166800.
ACCESSION AX249619
VERSION   AX249619.1 GI:15864242
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS  Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE    Human single nucleotide polymorphisms
JOURNAL  Patent: WO 0166800-A 1698 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
source 1..31
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 67.4%; Score 12.8; DB 6; Length 31;
Best Local Similarity 77.8%; Pred. No. 1.6e+05;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2  GGTGACGTTTCAGGGGG 19
Db      29 GGGAGACAGTCAGKGGGG 12

RESULT 42
AX249619/c
LOCUS   AX249619
DEFINITION Sequence 1698 from Patent WO0166800.
ACCESSION AX249619
VERSION   AX249619.1 GI:15864242
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS  Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE    Human single nucleotide polymorphisms
JOURNAL  Patent: WO 0166800-A 1698 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
source 1..31
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 67.4%; Score 12.8; DB 6; Length 31;
Best Local Similarity 77.8%; Pred. No. 1.6e+05;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2  GGTGACGTTTCAGGGGG 19
Db      29 GGGAGACAGTCAGKGGGG 12

RESULT 43
AR029533/c
LOCUS   AR029533
DEFINITION Sequence 43 from patent US 5859336.
ACCESSION AR029533
VERSION   AR029533.1 GI:5941506
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS  Koziel,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Evola,S.V.,
Crossland,L.D., Wright,M.S., Merlin,E.J., Launis,K.L., Bowman,C.G.,
Dawson,J.L., Dunder,E.M., Pace,G.M. and Suttie,J.L.
TITLE    Synthetic DNA sequence having enhanced activity in maize
JOURNAL  Patent: US 5859336-A 43 12-JAN-1999;
FEATURES
source 1..32
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 67.4%; Score 12.8; DB 6; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3  GGTGACGTTTCAGGGGG 18
Db      18 GGTGCCGTACAGGGGG 3

RESULT 43
AR098486/c
LOCUS   AR098486
DEFINITION Sequence 43 from patent US 6075185.
ACCESSION AR098486
VERSION   AR098486.1 GI:12807743
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
AUTHORS  Koziel,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Evola,S.V.,
Wright,M.S., Launis,K.L., Rothstein,S.J., Bowman,C.G., Dawson,J.L.,
Dunder,E.M., Pace,G.M. and Suttie,J.L.
TITLE    Synthetic DNA sequence having enhanced insecticidal activity in
JOURNAL  maize
FEATURES
source Patent: US 6075185-A 43 13-JUN-2000;
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 67.4%; Score 12.8; DB 6; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.6e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3  GGTGACGTTTCAGGGGG 18
Db      18 GGTGCCGTACAGGGGG 3

RESULT 44
I41446/c
LOCUS   I41446
DEFINITION Sequence 43 from patent US 5625136.
ACCESSION I41446
VERSION   I41446.1 GI:2082036
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 32)
```

AUTHORS Koziel, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W.,  
Evola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launis, K.L.,  
Rothstein, S.J., Bowman, C.G., Dawson, J.L., Dunder, E.M., Pace, G.M.  
and Suttie, J.L.

TITLE Synthetic DNA sequence having enhanced insecticidal activity in  
maize

JOURNAL Patent: US 5625136-A 43 29-APR-1997;  
FEATURES Location/Qualifiers

source 1. .32  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 67.4%; Score 12.8; DB 6; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGG 18  
||||| ||||| ||||| ||||| |||||  
Db 18 GGTGCCGTACAGGGG 3

RESULT 45  
AR494995/c  
LOCUS AR494995 32 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 43 from patent US 6720488.  
ACCESSION AR494995  
VERSION AR494995.1 GI:47270365  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 32)  
AUTHORS Koziel, M., Desai, N., Pace, G.M., Suttie, J., Carozzi, N., Boyce, C.,  
Dawson, J.L., Dunder, E., Wright, M., Launis, K., Rothstein, S.J.,  
Lewis, K., Warren, G. and Evola, S.  
TITLE Transgenic maize seed and method for controlling insect pests  
JOURNAL Patent: US 6720488-A 43 13-APR-2004;  
FEATURES Syngenta Investment Corporation; Wilmington, DE  
source Location/Qualifiers

1. .32  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 67.4%; Score 12.8; DB 6; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGG 18  
||||| ||||| ||||| ||||| |||||  
Db 18 GGTGCCGTACAGGGG 3

RESULT 46  
AX441412/c  
LOCUS AX441412 32 bp DNA linear PAT 03-JUL-2002  
DEFINITION Sequence 43 from Patent EP1209237.  
ACCESSION AX441412  
VERSION AX441412.1 GI:21690393  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Koziel, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W.,  
Evola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launis, K.L.  
and Rothstein, S.J.  
TITLE Synthetic dna sequence having enhanced insecticidal activity in  
maize  
JOURNAL Patent: EP 1209237-A 43 29-MAY-2002;  
FEATURES Syngenta Participations AG (CH)  
source Location/Qualifiers

source 1. .32  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="primer P5(a)"

ORIGIN

Query Match 67.4%; Score 12.8; DB 6; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGG 18  
||||| ||||| ||||| ||||| |||||  
Db 18 GGTGCCGTACAGGGG 3

RESULT 47  
AX453908/c  
LOCUS AX453908 32 bp DNA linear PAT 06-JUL-2002  
DEFINITION Sequence 43 from Patent EP1213356.  
ACCESSION AX453908  
VERSION AX453908.1 GI:21713566  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Koziel, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W.,  
Evola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launis, K.L.  
and Rothstein, S.J.  
TITLE Synthetic dna sequence having enhanced insecticidal activity in  
maize  
JOURNAL Patent: EP 1213356-A 43 12-JUN-2002;  
FEATURES Syngenta Participations AG (CH)  
source Location/Qualifiers

1. .32  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="primer P5(a)"

ORIGIN

Query Match 67.4%; Score 12.8; DB 6; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.6e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGG 18  
||||| ||||| ||||| ||||| |||||  
Db 18 GGTGCCGTACAGGGG 3

RESULT 48  
AX514624/c  
LOCUS AX514624 41 bp DNA linear PAT 05-OCT-2002  
DEFINITION Sequence 822 from Patent WO20252044.  
ACCESSION AX514624  
VERSION AX514624.1 GI:23561182  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.  
TITLE Detection of genetic polymorphisms  
JOURNAL Patent: WO 02052044-A 822 04-JUL-2002;  
FEATURES Riken (JP)  
source Location/Qualifiers

1. .41  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"





GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:25:23 ; Search time 143.207 Seconds  
(without alignments)  
884.241 Million cell updates/sec

Title: US-09-669-187A-80

Perfect score: 19

Sequence: 1 999gtgacgttcagggggg 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

N\_Geneseq\_21.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	4	Aaf98955 Immunosti
2	19	100.0	19	6	Abz77596 Angiogene
3	19	100.0	19	6	Abz77596 Angiogene
4	19	100.0	19	9	Abz77596 Angiogene
5	19	100.0	19	9	Abz77596 Angiogene
6	19	100.0	19	13	Abz77596 Angiogene
7	17.4	91.6	19	4	Aaf98955 Immunosti
8	17.4	91.6	19	6	Abz77596 Angiogene
9	17.4	91.6	19	6	Abz77596 Angiogene
10	17.4	91.6	19	9	Abz77596 Angiogene
11	17.4	91.6	19	9	Abz77596 Angiogene
12	17.4	91.6	19	13	Abz77596 Angiogene
13	14.4	75.8	40	3	Aaz295948 Polynucle
14	14.2	74.7	20	2	Aav27677 Immunosti
15	14.2	74.7	20	2	Aav74249 CpG-N mot
16	14.2	74.7	20	3	Aaz48834 B-cell sc
17	14.2	74.7	20	4	Aad02961 Immunosti
18	14.2	74.7	20	4	Aaf99097 Immunosti
19	14.2	74.7	20	6	Abz77740 Angiogene

20	14.2	74.7	20	6	ABL39045	Immunost	
21	14.2	74.7	20	9	ACD91359	B-cell st	
22	14.2	74.7	20	9	ACD99530	Immunost	
23	14.2	74.7	20	9	ACA62324	Lymphocyt	
24	14.2	74.7	20	9	ADB36599	Immunost	
25	14.2	74.7	20	12	AD058881	Mitogeni	
26	14.2	74.7	20	12	ADQ36558	B-cell s	
27	14.2	74.7	20	12	ADQ36584	Unmethy	
28	14.2	74.7	20	13	ADR20014	B-cell s	
29	14.2	74.7	20	13	ADR28877	CpG-cont	
30	14.2	74.7	20	13	ADR44692	Mitogeni	
31	14.2	74.7	20	13	ADR45002	CpG oilg	
32	14.2	74.7	20	13	ADR88228	CpG immu	
33	14.2	74.7	20	13	ADSI7223	ODN1, ol	
34	14.2	74.7	20	13	ADU89540	Allergic	
35	14.2	74.7	20	14	ADW28066	Mitogeno	
36	14.2	74.7	20	14	ADV97282	Immunost	
37	14.2	74.7	20	14	ADX87198	B cell1-s	
38	14.2	74.7	20	14	ADX84981	CpG olig	
C	39	14	73.7	39	ADC24305	Primer,	
C	40	13.8	72.6	30	ACA89992	Rabbit ti	
C	41	13.8	72.6	41	ABZ43529	Human SUL	
C	42	13.8	72.6	41	ABZ49680	Human SUL	
43	13.4	70.5	22	4	AAO7150	PCR prime	
44	13.4	70.5	22	4	AAF74944	Bacteriop	
C	45	13.2	69.5	30	ADR99754	Nucleic	
C	46	13.2	69.5	19	ADW46519	Human su	
C	47	13.2	69.5	19	ADW46518	Human su	
48	13.2	69.5	20	4	AAF99395	Immunost	
49	13.2	69.5	20	4	AAF99392	Immunost	
50	13.2	69.5	20	6	ABS78040	Angiogene	
51	13.2	69.5	20	6	ABS78037	Angiogene	
52	13.2	69.5	20	6	ABL39019	Immunost	
53	13.2	69.5	20	6	ABL39020	Immunost	
54	13.2	69.5	20	9	ACD99815	Immunost	
55	13.2	69.5	20	9	ACD99812	Immunost	
56	13.2	69.5	20	9	ACA62351	Lymphocyt	
57	13.2	69.5	20	9	ADB36897	Immunost	
58	13.2	69.5	20	9	ADB36894	Immunost	
59	13.2	69.5	20	13	ADU89837	Allergic	
60	13.2	69.5	20	13	ADU89840	Allergic	
61	13.2	69.5	20	14	ADW46375	Human su	
C	62	13.2	69.5	20	14	ADW46374	Human su
C	63	13.2	69.5	25	9	ACK07484	Human mic
C	64	13.2	69.5	31	AAI31210	Human sin	
C	65	13.2	69.5	32	10	ADJ76931	Anti-IGF
66	13.2	69.5	32	14	ADZ67101	Humanize	
C	67	13.2	69.5	33	6	ABZ56947	Alpha-1 i
C	68	13.2	69.5	39	10	ACC49874	Human mu
C	69	13.2	69.5	41	6	ABZ56949	Alpha-1 i
C	70	13.2	69.5	47	14	ADY35036	Kappa VL
71	13.2	69.5	47	14	ADY35075	Kappa VL	
72	13.2	69.5	47	14	ADY35033	Kappa VL	
73	13.2	69.5	47	14	ADY35074	Kappa VL	
74	13.2	69.5	50	6	ABZ03672	Human leu	
C	75	13	68.4	20	6	ABL99541	Canine su
C	76	13	68.4	30	10	ABZ283722	Human mu
C	77	13	68.4	42	14	ADZ51509	HB PCR p
C	78	12.8	67.4	19	12	ADNI11956	Primer o
79	12.8	67.4	19	12	ADP83591	Human Ci	
C	80	12.8	67.4	20	2	AAQ91247	EAAS rece
C	81	12.8	67.4	20	3	AAQ95526	Primer 1
C	82	12.8	67.4	20	4	AAAC62057	PCR prime
C	83	12.8	67.4	20	10	ADH93300	Human ge
84	12.8	67.4	20	10	ABZ284854	Human ol	
85	12.8	67.4	20	11	ABD21084	Human tr	
86	12.8	67.4	20	12	ADO15471	Human CD	
C	87	12.8	67.4	21	ADK41381	Human ch	
C	88	12.8	67.4	21	ADK41299	Human ch	
C	89	12.8	67.4	25	9	ACI02236	Human mic
C	90	12.8	67.4	26	14	AEB79114	Mouse lat
C	91	12.8	67.4	32	2	AAQ38984	Synthetic
92	12.8	67.4	50	4	AAH90432	Human clo	

c	93	12.8	67.4	50	6	AB204742	Abz04742 Human leu	166	12.6	66.3	20	13	ADU90284	Adu90284 Allergic	
	94	12.6	66.3	19	4	AAF98757	Aaf98757 Human IFN	167	12.6	66.3	20	14	ADW29187	Adw29187 Immunosti	
	95	12.6	66.3	19	4	AAF99840	Aaf99840 Immunosti	168	12.6	66.3	20	14	ADY53603	Ady53603 Anti-canc	
	96	12.6	66.3	19	4	AAF99771	Aaf99771 Immunosti	169	12.6	66.3	20	14	ADY39617	Ady39617 Phosphoro	
	97	12.6	66.3	19	6	ABS78492	Abs78492 Angiogene	170	12.6	66.3	20	14	ADZ88500	Adz88500 CpG ODNI	
	98	12.6	66.3	19	6	ABS78562	Abs78562 Angiogene	171	12.6	66.3	20	14	AEA16606	Aea16606 CpG immun	
	99	12.6	66.3	19	9	ACH03295	Ach03295 Immunosti	172	12.6	66.3	20	14	ABE07462	Aeb07462 Novel vir	
	100	12.6	66.3	19	9	ADB37342	Adb37342 Immunosti	173	12.6	66.3	20	14	ABE16203	Aec16203 NK activi	
	101	12.6	66.3	19	9	ADB37273	Adb37273 Immunosti	174	12.6	66.3	21	4	AAF98875	Aaf98875 Immunosti	
	102	12.6	66.3	19	13	ADU90362	Adu90362 Allergic	175	12.6	66.3	21	4	AAF99798	Aaf99798 Immunosti	
	103	12.6	66.3	19	13	ADU90292	Adu90292 Allergic	176	12.6	66.3	21	6	ABS78520	Abs78520 Angiogene	
	104	12.6	66.3	20	2	AAI16894	Aat16894 Immunomod	177	12.6	66.3	21	8	ABZ80185	Abz80185 Immunosti	
	105	12.6	66.3	20	2	AAV47684	Aav47684 Urmethyla	178	12.6	66.3	21	9	ACH03322	Ach03322 Immunosti	
	106	12.6	66.3	20	2	AAV27654	Aav27654 Immunosti	179	12.6	66.3	21	9	ADB37300	Adb37300 Immunosti	
	107	12.6	66.3	20	2	AAV74238	Aav74238 CpG-N mot	180	12.6	66.3	21	13	ADU90320	Adu90320 Allergic	
	108	12.6	66.3	20	2	AAV74245	Aav74245 CpG-N mot	181	12.6	66.3	24	4	AAF99389	Aaf99389 Immunosti	
	109	12.6	66.3	20	3	AAA90449	Aaa90449 CpG adjuv	182	12.6	66.3	24	6	ABS78034	Abs78034 Angiogene	
	110	12.6	66.3	20	4	AAH20394	Aah20394 CpG motif	183	12.6	66.3	24	9	ACD99809	Acd99809 Immunosti	
	111	12.6	66.3	20	4	AAH50658	Aah50658 Immune re	184	12.6	66.3	24	9	ADB36891	Adb36891 Immunosti	
	112	12.6	66.3	20	4	AAH19262	Aah19262 Oligonucl	185	12.6	66.3	24	13	ADU89834	Adu89834 Allergic	
	113	12.6	66.3	20	4	AAF98854	Aaf98854 Poly-G im	c	186	12.6	66.3	25	6	ABL59183	Abi59183 Oligonucl
	114	12.6	66.3	20	4	AAF98731	Aaf98731 Human IFN	187	12.6	66.3	25	9	ACT09013	Act09013 Human mic	
	115	12.6	66.3	20	4	AAF98855	Aaf98855 Poly-G im	188	12.6	66.3	25	14	ADX83315	Adx83315 Human tEG	
	116	12.6	66.3	20	4	AAF98735	Aaf98735 Human IFN	189	12.6	66.3	26	2	AAx40773	Aax40773 Oligonucl	
	117	12.6	66.3	20	4	AAc80669	Aac80669 Immunogen	c	190	12.6	66.3	26	2	AAx40824	Aax40824 Genomic s
	118	12.6	66.3	20	4	AAE59504	Aae59504 Immunosti	191	12.6	66.3	26	12	ADO55232	Ado55232 Immune mo	
	119	12.6	66.3	20	4	AAE99567	Aae99567 Immunosti	192	12.6	66.3	26	12	ADO55229	Ado55229 Immune mo	
	120	12.6	66.3	20	4	AAE99704	Aae99704 Immunosti	c	193	12.6	66.3	30	2	AAQ20873	Aaq20873 Immunosti
	121	12.6	66.3	20	4	AAE99764	Aae99764 Immunosti	194	12.6	66.3	30	2	AAQ20870	Aaq20870 Immunosti	
	122	12.6	66.3	20	4	AAE99390	Aae99390 Immunosti	c	195	12.6	66.3	30	3	AAQ05777	Aaa05777 Streptavi
	123	12.6	66.3	20	4	AAE99763	Aae99763 Immunosti	196	12.6	66.3	30	4	AAF98884	Aaf98884 IFN-1 ind	
	124	12.6	66.3	20	4	AAE92361	Aae92361 CG motif	197	12.6	66.3	30	6	ABL35104	Abi35104 Phosphoro	
	125	12.6	66.3	20	4	AAE99639	Aae99639 Immunorea	198	12.6	66.3	30	6	ABL35099	Abi35099 Phosphoro	
	126	12.6	66.3	20	5	AAE27750	Aae27750 P. falcip	199	12.6	66.3	30	6	ABL35102	Abi35102 Phosphoro	
	127	12.6	66.3	20	6	ABS78484	Abs78484 Angiogene	200	12.6	66.3	30	13	ADU70018	Adu70018 Immunosti	
	128	12.6	66.3	20	6	ABS78485	Abs78485 Angiogene	c	201	12.6	66.3	31	14	ADU70016	Adu70016 Immunosti
	129	12.6	66.3	20	6	ABS78283	Abs78283 Angiogene	202	12.6	66.3	31	14	ADU92126	Adu92126 Leuconost	
	130	12.6	66.3	20	6	ABS78035	Abs78035 Angiogene	203	12.6	66.3	33	10	ADB61582	Adb61582 Hepatocyt	
	131	12.6	66.3	20	6	ABS78425	Abs78425 Angiogene	c	204	12.6	66.3	44	8	ACA60185	Aca60185 Human sec
	132	12.6	66.3	20	6	ABL39032	Abi39032 Immunosti	c	205	12.6	66.3	44	8	ACD07585	Acd07585 Novel hum
	133	12.6	66.3	20	6	ABL39033	Abi39033 Immunosti	c	206	12.6	66.3	44	8	ABX71633	Abx71633 Human sec
	134	12.6	66.3	20	6	ABL39039	Abi39039 Immunosti	c	207	12.6	66.3	44	8	ACH06965	Ach06965 Human sec
	135	12.6	66.3	20	6	ABK46517	Abk46517 Immunosti	c	208	12.6	66.3	44	8	ABX96202	Abx96202 Human sec
	136	12.6	66.3	20	6	AAI44488	Aai44488 CpG motif	c	209	12.6	66.3	44	8	ACA05523	Aca05523 Human sec
	137	12.6	66.3	20	6	ABS70558	Abs70558 Dendritic	c	210	12.6	66.3	44	8	ACD20190	Acd20190 Human sec
	138	12.6	66.3	20	8	ACC48308	Acc48308 CpG oligo	c	211	12.6	66.3	44	8	ACA54993	Aca54993 Novel sec
	139	12.6	66.3	20	8	ABZ80163	Abz80163 Immunosti	c	212	12.6	66.3	44	9	ACD19828	Acd19828 Human sec
	140	12.6	66.3	20	9	ACH03113	Ach03113 D class C	c	213	12.6	66.3	44	9	ADB29430	Adb29430 Human sec
	141	12.6	66.3	20	9	ACH03243	Ach03243 Immunosti	c	214	12.6	66.3	44	9	ADA18286	Ada18286 Human sec
	142	12.6	66.3	20	9	ACH09910	Ach09910 Immunosti	c	215	12.6	66.3	44	9	ACD66975	Acd66975 Human sec
	143	12.6	66.3	20	9	ACH03405	Ach03405 Immunosti	c	216	12.6	66.3	44	9	ACD83136	Acd83136 Human PRO
	144	12.6	66.3	20	9	ACH03105	Ach03105 Immunosti	c	217	12.6	66.3	44	9	ADA16261	Ada16261 Human sec
	145	12.6	66.3	20	9	ACH03288	Ach03288 Immunosti	c	218	12.6	66.3	44	9	ADA42406	Ada42406 Human sec
	146	12.6	66.3	20	9	ADB37069	Adb37069 Immunosti	c	219	12.6	66.3	44	9	ACD23314	Acd23314 Human PRO
	147	12.6	66.3	20	9	ADB37266	Adb37266 Immunosti	c	220	12.6	66.3	44	9	ADA16685	Ada16685 Human sec
	148	12.6	66.3	20	9	ADB36892	Adb36892 Immunosti	c	221	12.6	66.3	44	9	ADA13114	Ada13114 Human sec
	149	12.6	66.3	20	9	ADB37206	Adb37206 Immunosti	c	222	12.6	66.3	44	9	ADA41982	Ada41982 Human sec
	150	12.6	66.3	20	9	ADB37265	Adb37265 Immunosti	c	223	12.6	66.3	44	9	ADA17329	Ada17329 Human sec
	151	12.6	66.3	20	10	AAE60208	Aae60208 Oligonucl	c	224	12.6	66.3	44	9	ADA42832	Ada42832 Human sec
	152	12.6	66.3	20	10	ADG68114	Adg68114 Urmethyla	c	225	12.6	66.3	44	9	ACD23676	Acd23676 Human PRO
	153	12.6	66.3	20	12	ADI01054	Adi01054 Immunosti	c	226	12.6	66.3	44	10	ADB77751	Adb77751 Human sec
	154	12.6	66.3	20	12	ACA63219	Aca63219 Toll-like	c	227	12.6	66.3	44	10	ADB74887	Adb74887 Human sec
	155	12.6	66.3	20	12	ADM99023	Adm99023 Immunosti	c	228	12.6	66.3	44	10	ADC28533	Adc28533 Human sec
	156	12.6	66.3	20	12	ADO04739	Ado04739 CpG oligo	c	229	12.6	66.3	44	10	ADC39733	Adc39733 Human sec
	157	12.6	66.3	20	13	ADR28904	Adr28904 CpG-conta	c	230	12.6	66.3	44	10	ADC40247	Adc40247 Human sec
	158	12.6	66.3	20	13	ADR69222	Adr69222 CpG immun	c	231	12.6	66.3	44	10	ADC19071	Adc19071 Human sec
	159	12.6	66.3	20	13	ADT61920	Adt61920 Mitogenic	c	232	12.6	66.3	44	10	ADC34371	Adc34371 Human sec
	160	12.6	66.3	20	13	ADU70246	Adu70246 Immunosti	c	233	12.6	66.3	44	10	ADC29426	Adc29426 Human sec
	161	12.6	66.3	20	13	ADU70022	Adu70022 Immunosti	c	234	12.6	66.3	44	10	ADC28957	Adc28957 Human sec
	162	12.6	66.3	20	13	ADU90225	Adu90225 Allergic	c	235	12.6	66.3	44	10	ADC40842	Adc40842 Human sec
	163	12.6	66.3	20	13	ADU90285	Adu90285 Allergic	c	236	12.6	66.3	44	10	ADC19499	Adc19499 Human sec
	164	12.6	66.3	20	13	ADU90083	Adu90083 Allergic	c	237	12.6	66.3	44	10	ADC33947	Adc33947 Human sec
	165	12.6	66.3	20	13	ADU89835	Adu89835 Allergic	c	238	12.6	66.3	44	10	ADC13017	Adc13017 Human sec

C 239 12.6 66.3 44 10 ADC12469 Human sec  
C 240 12.6 66.3 44 10 ADD05024 Human sec  
C 241 12.6 66.3 44 10 ADD04030 Human sec  
C 242 12.6 66.3 44 10 ADD03606 Human sec  
C 243 12.6 66.3 44 10 ADP34858 Human sec  
C 244 12.6 66.3 44 10 ADH59341 Human sec  
C 245 12.6 66.3 44 10 ADH59341 Human sec  
C 246 12.6 66.3 44 10 ADH59341 Human sec  
C 247 12.6 66.3 44 10 ADH59341 Human sec  
C 248 12.6 66.3 44 10 ADH59341 Human sec  
C 249 12.6 66.3 44 10 ADH59341 Human sec  
C 250 12.6 66.3 44 10 ADH59341 Human sec  
C 251 12.6 66.3 44 10 ADH59341 Human sec  
C 252 12.6 66.3 44 10 ADH59341 Human sec  
C 253 12.6 66.3 44 10 ADH59341 Human sec  
C 254 12.6 66.3 44 10 ADH59341 Human sec  
C 255 12.6 66.3 44 10 ADH59341 Human sec  
C 256 12.6 66.3 44 10 ADH59341 Human sec  
C 257 12.6 66.3 44 10 ADH59341 Human sec  
C 258 12.6 66.3 44 10 ADH59341 Human sec  
C 259 12.6 66.3 44 10 ADH59341 Human sec  
C 260 12.6 66.3 44 10 ADH59341 Human sec  
C 261 12.6 66.3 44 10 ADH59341 Human sec  
C 262 12.6 66.3 44 10 ADH59341 Human sec  
C 263 12.6 66.3 44 10 ADH59341 Human sec  
C 264 12.6 66.3 44 10 ADH59341 Human sec  
C 265 12.6 66.3 44 10 ADH59341 Human sec  
C 266 12.6 66.3 44 10 ADH59341 Human sec  
C 267 12.6 66.3 44 10 ADH59341 Human sec  
C 268 12.6 66.3 44 10 ADH59341 Human sec  
C 269 12.6 66.3 44 10 ADH59341 Human sec  
C 270 12.6 66.3 44 10 ADH59341 Human sec  
C 271 12.6 66.3 44 10 ADH59341 Human sec  
C 272 12.6 66.3 44 10 ADH59341 Human sec  
C 273 12.6 66.3 44 10 ADH59341 Human sec  
C 274 12.6 66.3 44 10 ADH59341 Human sec  
C 275 12.6 66.3 44 10 ADH59341 Human sec  
C 276 12.6 66.3 44 10 ADH59341 Human sec  
C 277 12.6 66.3 44 10 ADH59341 Human sec  
C 278 12.6 66.3 44 10 ADH59341 Human sec  
C 279 12.6 66.3 44 10 ADH59341 Human sec  
C 280 12.6 66.3 44 10 ADH59341 Human sec  
C 281 12.6 66.3 44 10 ADH59341 Human sec  
C 282 12.6 66.3 44 10 ADH59341 Human sec  
C 283 12.6 66.3 44 10 ADH59341 Human sec  
C 284 12.6 66.3 44 10 ADH59341 Human sec  
C 285 12.6 66.3 44 10 ADH59341 Human sec  
C 286 12.6 66.3 44 10 ADH59341 Human sec  
C 287 12.6 66.3 44 10 ADH59341 Human sec  
C 288 12.6 66.3 44 10 ADH59341 Human sec  
C 289 12.6 66.3 44 10 ADH59341 Human sec  
C 290 12.6 66.3 44 10 ADH59341 Human sec  
C 291 12.6 66.3 44 10 ADH59341 Human sec  
C 292 12.6 66.3 44 10 ADH59341 Human sec  
C 293 12.6 66.3 44 10 ADH59341 Human sec  
C 294 12.6 66.3 44 10 ADH59341 Human sec  
C 295 12.6 66.3 44 10 ADH59341 Human sec  
C 296 12.6 66.3 44 10 ADH59341 Human sec  
C 297 12.6 66.3 44 10 ADH59341 Human sec  
C 298 12.6 66.3 44 10 ADH59341 Human sec  
C 299 12.6 66.3 44 10 ADH59341 Human sec  
C 300 12.6 66.3 44 10 ADH59341 Human sec

## ALIGNMENTS

RESULT 1  
AAF98955  
ID AAF98955 standard; DNA; 19 BP.  
XX  
AC AAF98955;  
XX

DT 12-JUN-2001 (first entry)  
XX Immunostimulatory nucleic acid #71.  
DE Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
XX immunostimulatory; tumour; viral infection; bacterial infection;  
KW fungal infection; parasitic infection; cancer; asthma;  
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
OS Synthetic.  
XX WO200122972-A2.  
PN 05-APR-2001.  
XX 25-SEP-2000; 2000WO-US026383.  
PD 25-SEP-1999; 99US-0156113P.  
PF 27-SEP-1999; 99US-0156135P.  
XX 23-AUG-2000; 2000US-0227436P.  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA (COLE-) COLEY PHARM GMBH.  
XX Krieg AM, Schetter C, Vollmer J;  
PI WPI; 2001-273485/28.  
XX Vaccinating against tumors, infectious diseases, allergies and asthma  
DR using immunostimulatory Py-rich and TG nucleic acids.  
XX Disclosure; Page 40; 338pp; English.  
PT The present invention relates to a method for stimulating an immune  
CC response. The method comprises administering an immunostimulatory nucleic  
CC acid to a non-rodent subject in sufficient quantity to stimulate an  
CC immune response. The present sequence is one such immunostimulatory  
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
CC also useful for preventing cancer, asthma, infectious disease, allergy or  
CC immune deficiency. The present sequence can also be used to redirect a  
CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
CC present sequence may have a phosphorothioate backbone  
XX  
SQ Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 19; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGACCTTCAGGGGG 19  
Db 1 GGGGTGACCTTCAGGGGG 19  
RESULT 2  
ABS77596  
ID ABS77596 standard; DNA; 19 BP.  
XX  
AC ABS77596;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Angiogenesis inhibitory oligonucleotide #80.  
XX  
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX Synthetic.  
OS  
XX  
PN WO200253141-A2.  
XX  
XX  
PD 11-JUL-2002.  
XX  
PF 14-DEC-2001; 2001WO-US048458.  
XX  
XX 14-DEC-2000; 2000US-0255534P.  
XX  
XX (COLE-) COLEY PHARM GROUP INC.  
PA  
XX Bratzler RL;  
PI  
XX  
DR WPI; 2002-566690/60.  
XX  
XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.  
PT  
XX  
XX Claim 2; Page 21; 276pp; English.  
XX  
XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX  
SQ Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 19; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGGG 19  
Db 1 GGGGTGACGTTTCAGGGGGG 19  
RESULT 3  
ABL39043  
ID ABL39043 standard; DNA; 19 BP.  
XX  
XX ABL39043;  
AC  
XX  
DT 16-APR-2002 (first entry)  
XX  
DE Immunostimulatory nucleic acid SEQ ID NO: 447.  
XX  
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; ss.  
XX Synthetic.  
OS  
XX WO200197843-A2.  
PN  
XX 27-DEC-2001.  
PD  
XX 22-JUN-2001; 2001WO-US020154.  
PF  
XX

PR 22-JUN-2000; 2000US-0213346P.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA  
XX Weiner G, Hartmann G;  
PI  
XX WPI; 2002-154611/20.  
DR  
XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer.  
XX  
XX Disclosure; Page 208; 312pp; English.  
PS  
XX The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention  
XX  
SQ Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 19; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGGG 19  
Db 1 GGGGTGACGTTTCAGGGGGG 19  
RESULT 4  
ACD9388  
ID ACD9388 standard; DNA; 19 BP.  
XX  
XX ACD9388;  
AC  
XX  
DT 25-SEP-2003 (first entry)  
XX  
XX Immunostimulatory nucleic acid #74.  
DE  
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX Synthetic.  
OS  
XX US2003050268-A1.  
PN  
XX 13-MAR-2003.  
PD  
XX 29-MAR-2002; 2002US-00112653.  
PF  
XX 29-MAR-2001; 2001US-0279642P.  
PR  
XX (KRIE/) KRIEG A M.  
PA (BERG/) BERG D J.  
XX  
XX Krieg AM, Berg DJ;  
PI  
XX WPI; 2003-521815/49.  
DR  
XX

PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
XX disease by administering an immunostimulatory nucleic acid.  
XX  
PS Disclosure; Page 10; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
XX This sequence represents an immunostimulatory nucleic acid  
XX  
SQ Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
Db 1 GGGGTGACGTTTCAGGGGG 19

RESULT 5  
ADB36457  
ID ADB36457 standard; DNA; 19 BP.

XX  
AC ADB36457;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Immunostimulatory nucleic acid #71.

XX de; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
XX hypo-responsive subject; immunostimulatory.

OS Synthetic.

XX US2003087848-A1.

XX 08-MAY-2003.

XX 02-FEB-2001; 2001US-00776479.

XX 03-FEB-2000; 2000US-0179991P.

XX (BRAT/) BRATZLER R L.

XX (PETE/) PETERSEN D M.

XX (FOUR/) FOURON Y.

XX Bratzler RL, Petersen DM, Fouron Y;

XX WPI; 2003-657977/62.

XX Treating and/or preventing allergy or asthma using an immunostimulatory  
XX nucleic acid alone or in combination with an asthma/allergy medicament.

PS Disclosure; Page 6; 221pp; English.

XX The invention relates to a method of treating or preventing allergy or  
XX asthma which comprises administering to a subject a poly-G nucleic acid  
XX in an aerosol formulation. The methods and compositions of the present  
XX invention are useful for diagnosing and/or treating asthma and allergy  
XX especially in a hypo-responsive subject. The present sequence represents  
XX an immunostimulatory nucleic acid of the invention.

XX Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 18;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGTGACGTTTCAGGGGG 19  
Db 1 GGGGTGACGTTTCAGGGGG 19

RESULT 6

ADU89396

ID ADU89396 standard; DNA; 19 BP.

XX  
AC ADU89396;

XX  
DT 10-FEB-2005 (first entry)

XX Allergic response suppressor oligonucleotide #80.

XX ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;  
XX antibacterial; virucide; immunoglobulin E antagonist; allergy;  
XX immunostimulator; asthma; rhinitis; urticaria; dermatitis;  
XX bacterial infection; viral infection.

OS Synthetic.

XX US2004235774-A1.

XX 25-NOV-2004.

XX 23-APR-2004; 2004US-00831778.

XX 03-FEB-2000; 2000US-0179991P.

XX 02-FEB-2001; 2001US-00776479.

XX (BRAT/) BRATZLER R L.

XX (PETE/) PETERSEN D M.

XX (FOUR/) FOURON Y.

XX Bratzler RL, Petersen DM, Fouron Y;

XX WPI; 2004-833006/82.

XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
XX dermatitis, in a subject, comprises administering a first and second dose  
XX of an immunostimulatory nucleic acid.

XX Disclosure; SEQ ID NO 80; 235pp; English.

XX The invention relates to a method of suppressing a symptom of an allergic  
XX response in a subject by administering a first and second dose of an  
XX immunostimulatory nucleic acid that comprises a nucleotide sequence  
XX comprising 5'-cg-3', and where the second dose is administered from 1 day  
XX to 8 weeks after the first dose. The methods and compositions of the  
XX present invention are useful for the treatment or prevention of asthma  
XX and allergy, including rhinitis, urticaria and atopic dermatitis, using  
XX an immunostimulatory nucleic acid alone or in combination with other  
XX medicaments. They can also be used in preventing bacterial and viral  
XX infections. This sequence represents an oligonucleotide used in the  
XX method of the invention.

XX Sequence 19 BP; 2 A; 2 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 13; Length 19;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19

Db 1 GGGGTGACGTTTCAGGGGG 19

RESULT 7

AAF98957

ID AAF98957 standard; DNA; 19 BP.

```
XX AAF98957;
AC
XX 12-JUN-2001 (first entry)
DT
XX Immunostimulatory nucleic acid #73.
DE
XX
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
XX Synthetic.
OS
XX WO200122972-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 25-SEP-2000; 2000WO-US026383.
PF
XX
XX 25-SEP-1999; 99US-0156113P.
PR
XX
XX 27-SEP-1999; 99US-0156135P.
PR
XX
XX 23-AUG-2000; 2000US-0227436P.
PR
XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA
XX (COLE-) COLEY PHARM GMBH.
PA
XX Krieg AM, Schetter C, Vollmer J;
PI
XX
XX WPI; 2001-273485/28.
DR
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
PT
XX
XX Disclosure; Page 40; 338pp; English.
PS
XX
XX The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
XX Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;
SQ
Query Match 91.6%; Score 17.4; DB 4; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGG 19
Db ||||| ||||| ||||| |||||
1 GGGGTGTCGTTTCAGGGGG 19
RESULT 8
AB877598
ID AB877598 standard; DNA; 19 BP.
XX
XX AB877598;
AC
XX
XX 13-DEC-2002 (first entry)
DT
XX
XX Angiogenesis inhibitory oligonucleotide #82.
DE
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW
```

```
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubrosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophilic joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
XX Synthetic.
OS
XX WO200253141-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 14-DEC-2001; 2001WO-US048458.
PF
XX
XX 14-DEC-2000; 2000US-0255534P.
PR
XX
XX (COLE-) COLEY PHARM GROUP INC.
PA
XX Bratzler RL;
PI
XX
XX WPI; 2002-566690/60.
DR
XX
XX Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
PT
XX
XX Claim 2; Page 21; 276pp; English.
PS
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubrosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
XX Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;
SQ
Query Match 91.6%; Score 17.4; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGG 19
Db ||||| ||||| ||||| |||||
1 GGGGTGTCGTTTCAGGGGG 19
RESULT 9
ABL39044
ID ABL39044 standard; DNA; 19 BP.
XX
XX ABL39044;
AC
XX
XX 16-APR-2002 (first entry)
DT
XX
XX Immunostimulatory nucleic acid SEQ ID NO: 448.
DE
XX
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
XX Synthetic.
OS
XX WO200197843-A2.
PN
XX
XX 27-DEC-2001.
PD
```

XX PF 22-JUN-2001; 2001WO-US020154.  
XX PR 23-JUN-2000; 2000US-0213346P.  
XX PA (IOWA ) UNIV IOWA RES FOUND.  
XX PI Weiner G, Hartmann G;  
XX WPI; 2002-154611/20.  
XX PT Treating or preventing cancer, such as basal cell carcinoma, comprises  
XX administering immunostimulatory nucleic acids that induce expression of  
XX cell surface antigens and antibodies to a subject having or at risk of  
XX developing cancer.  
XX PS Disclosure; Page 209; 312pp; English.  
XX CC The present invention relates to methods for treating or preventing  
XX cancer, involving administering to a subject having or at risk of  
XX developing cancer immunostimulatory nucleic acids that induce expression  
XX of cell surface antigens and antibodies. The methods are useful for  
XX treating or preventing cancer such as basal cell carcinoma, bladder  
XX cancer, bone cancer, brain and central nervous system (CNS) cancer,  
XX breast cancer, cervical cancer, colon and rectum cancer, connective  
XX tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
XX cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
XX Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
XX cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
XX cancer, stomach cancer, testicular cancer, and uterine cancer. The  
XX present sequence is an immunostimulatory oligonucleotide described in the  
XX exemplification of the invention  
XX CC Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 91.6%; Score 17.4; DB 6; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGGG 19  
DB 1 GGGGTGTCGTTTCAGGGGGG 19  
RESULT 10  
ACD99390  
ID ACD99390 standard; DNA; 19 BP.  
XX AC ACD99390;  
XX DT 25-SBP-2003 (first entry)  
XX DE Immunostimulatory nucleic acid #76.  
XX KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
XX antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
XX psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX OS Synthetic.  
XX US2003050268-A1.  
XX PN 13-MAR-2003.  
XX PD 29-MAR-2002; 2002US-00112653.  
XX PR 29-MAR-2001; 2001US-0279642P.  
XX PA (KRIE/) KRIEG A M.  
XX PA (BERG/) BERG D J.  
XX PI Krieg AM, Berg DJ;

XX WPI; 2003-521815/49.  
XX PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
XX allergic contact dermatitis, latex dermatitis or inflammatory bowel  
XX disease by administering an immunostimulatory nucleic acid.  
XX PS Disclosure; Page 10; 229pp; English.  
XX CC The invention describes a method of treating non-allergic inflammatory  
XX disease comprising administering to a subject having or at risk of  
XX developing a non-allergic inflammatory disease an immunostimulatory  
XX nucleic acid for prevention or treatment of the disease. The method is  
XX useful for treating non-allergic inflammatory diseases, such as  
XX psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
XX inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
XX CC This sequence represents an immunostimulatory nucleic acid  
XX  
XX CC Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 91.6%; Score 17.4; DB 9; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGGG 19  
DB 1 GGGGTGTCGTTTCAGGGGGG 19  
RESULT 11  
ADB36459  
ID ADB36459 standard; DNA; 19 BP.  
XX AC ADB36459;  
XX DT 04-DEC-2003 (first entry)  
XX DE Immunostimulatory nucleic acid #73.  
XX KW de; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
XX hypo-responsive subject; immunostimulatory.  
XX OS Synthetic.  
XX US2003087848-A1.  
XX PN 08-MAY-2003.  
XX PD 02-FEB-2001; 2001US-00776479.  
XX PF 03-FEB-2000; 2000US-0179991P.  
XX PR (BRAT/) BRATZLER R L.  
XX PA (PETE/) PETERSEN D M.  
XX PA (FOUR/) FOURON Y.  
XX PI Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
XX PT Treating and/or preventing allergy or asthma using an immunostimulatory  
XX nucleic acid alone or in combination with an asthma/allergy medicament.  
XX PS Disclosure; Page 6; 221pp; English.  
XX CC The invention relates to a method of treating or preventing allergy or  
XX asthma which comprises administering to a subject a poly-G nucleic acid  
XX in an aerosol formulation. The methods and compositions of the present  
XX invention are useful for diagnosing and/or treating asthma and allergy  
XX especially in a hypo-responsive subject. The present sequence represents  
XX an immunostimulatory nucleic acid of the invention.  
XX CC Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 91.6%; Score 17.4; DB 9; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19  
 ||||| ||||| ||||| |||||  
 Db 1 GGGGTGTCGTTTCAGGGGGG 19

RESULT 12  
 ADU89398  
 ID ADU89398 standard; DNA; 19 BP.  
 XX  
 AC ADU89398;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE Allergic response suppressor oligonucleotide #82.  
 XX ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;  
 KW antibacterial; virucide; immunoglobulin E antagonist; allergy;  
 KW immunostimulatory; asthma; rhinitis; urticaria; dermatitis;  
 KW bacterial infection; viral infection.  
 XX  
 OS Synthetic.  
 XX  
 PN US2004235774-A1.  
 XX  
 PD 25-NOV-2004.  
 XX  
 PF 23-APR-2004; 2004US-00831778.  
 XX  
 PR 03-FEB-2000; 2000US-0179991P.  
 PR 02-FEB-2001; 2001US-00776479.  
 XX  
 PA (BRAT/) BRATZLER R L.  
 PA (PETE/) PETERSEN D M.  
 PA (FOUR/) FOURON Y.  
 XX  
 PI Bratzler RL, Petersen DM, Fouron Y;  
 XX WPI; 2004-833006/82.  
 XX  
 DR Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
 PT dermatitis, in a subject, comprises administering a first and second dose  
 PT of an immunostimulatory nucleic acid.  
 XX  
 PS Disclosure; SEQ ID NO 82; 235pp; English.  
 XX  
 CC The invention relates to a method of suppressing a symptom of an allergic  
 CC response in a subject by administering a first and second dose of an  
 CC immunostimulatory nucleic acid that comprises a nucleotide sequence  
 CC comprising 5'-cg-3', and where the second dose is administered from 1 day  
 CC to 8 weeks after the first dose. The methods and compositions of the  
 CC present invention are useful for the treatment or prevention of asthma  
 CC and allergy, including rhinitis, urticaria and atopic dermatitis, using  
 CC an immunostimulatory nucleic acid alone or in combination with other  
 CC medicaments. They can also be used in preventing bacterial and viral  
 CC infections. This sequence represents an oligonucleotide used in the  
 CC method of the invention.  
 XX  
 SQ Sequence 19 BP; 1 A; 2 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 91.6%; Score 17.4; DB 13; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19  
 ||||| ||||| ||||| |||||  
 Db 1 GGGGTGTCGTTTCAGGGGGG 19

RESULT 13  
 AAZ95948  
 ID AAZ95948 standard; DNA; 40 BP.  
 XX  
 AC AAZ95948;  
 XX  
 DT 10-APR-2000 (first entry)  
 XX  
 DE Polynucleotide sequence including binding site for BamHI.  
 XX  
 KW Ligand binding; restriction enzyme; nucleic acid determination;  
 KW pharmaceutical; BamHI; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9963077-A2.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 04-JUN-1999; 99WO-US012516.  
 XX  
 PR 04-JUN-1998; 98US-0087905P.  
 PR 03-JUN-1999; 99US-00324672.  
 XX  
 PA (TMTE-) TM TECHNOLOGIES INC.  
 XX  
 PI Lane MJ, Benight AS, Faldasz BD;  
 XX WPI; 2000-116369/10.  
 DR Modulating polynucleotide ligand binding site affinity using  
 PT determination of the flanking duplex sequences.  
 XX  
 PS Example 1; Page 40; 62pp; English.  
 XX  
 CC The invention provides a method for determining the sequence of  
 CC polynucleotide flanking regions that modulate ligand binding  
 CC characteristics of an adjacent binding site. The method comprises: (i)  
 CC providing a number of different duplex polynucleotides, each having the  
 CC same polynucleotide ligand binding site and a randomly synthesised  
 CC sequence flanking the binding site; (ii) exposing the duplex to a ligand  
 CC selective for the binding site; (iii) isolating duplexes which bind or do  
 CC not bind the ligand, and (iv) determining the nucleotide composition of  
 CC the flanking duplex sequence by sequencing the duplex sequence adjacent  
 CC to the binding site. The invention is used to modulate the ligand-binding  
 CC characteristics of any nucleotide sequence. The invention is less costly  
 CC and more efficient than prior art techniques that moderate ligand binding  
 CC using small molecule pharmaceuticals. Sequences AAZ95948-296170 represent  
 CC polynucleotide sequences including the binding site for the restriction  
 CC enzyme BamHI and used in the course of the invention  
 XX  
 SQ Sequence 40 BP; 9 A; 9 C; 15 G; 7 T; 0 U; 0 Other;

Query Match 75.8%; Score 14.4; DB 3; Length 40;  
 Best Local Similarity 93.8%; Pred. No. 3.1e+03;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTGAGCTTCAGGGGGG 19  
 ||||| ||||| ||||| |||||  
 Db 9 GTGGGCTTCAGGGGGG 24

RESULT 14  
 AAV27677  
 ID AAV27677 standard; DNA; 20 BP.  
 XX  
 AC AAV27677;  
 XX  
 DT 01-OCT-1998 (first entry)  
 XX  
 DE Immunostimulatory oligodeoxyribonucleotide of the invention.  
 XX Immunostimulatory; oligodeoxyribonucleotide; ODN;  
 KW





```

XX PD 28-DEC-1999.
XX PF 07-FEB-1995; 95US-00386063.
XX PR 15-JUL-1994; 94US-00276358.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PI Krieg AM;
XX DR WPI; 2000-086224/07.
XX PT Immunostimulatory oligonucleotides which enhance B cell activation useful
XX PT for treating an immune system deficiency e.g. cancer.
XX PS Claim 10; Col 10; 19pp; English.
XX CC This sequence represents a B cell stimulatory oligonucleotide. The
XX CC invention relates to compositions comprising an oligonucleotide (I) with
XX CC unethylated guanine and cytosine nucleotides and an antigen in a
XX CC carrier. The oligonucleotides can be administered to a subject in a
XX CC composition with an antigen in a carrier to enhance an immune response by
XX CC enhancing B cell activation. The oligonucleotides are immunostimulatory
XX CC and can be used to treat, prevent or ameliorate an immune system
XX CC deficiency e.g. cancer or a viral, fungal, bacterial or parasitic
XX CC infection. They can also be administered as a vaccine adjuvant to
XX CC stimulate the response of a host to a vaccine. The compositions can be
XX CC used to treat humans or vertebrate animals including dogs, cats, sheep
XX CC pigs, cows, goats, chickens, mice and monkeys. Preceding chemotherapy
XX CC with the immunostimulatory oligonucleotides should be useful for
XX CC increasing the responsiveness of malignant cells to subsequent
XX CC chemotherapy. The 8-40 nucleotide size of the oligonucleotides
XX CC facilitates uptake into cells
XX SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 74.7%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db ||| ||||| ||||| |||||
2 GGGTCAACGTTTCAGGGGG 20

RESULT 17
AAD02961
ID AAD02961 standard; DNA; 20 BP.
XX AC AAD02961;
XX DT 31-MAY-2001 (first entry)
XX DE Immunostimulatory oligodeoxyribonucleotide (ODN) 1585.
XX KW oligodeoxyribonucleotide; ODN; cytosine-guanine dinucleotide; CpG;
XX KW immunostimulatory; therapy; immune system deficiency; tumour; cancer;
XX KW antibacterial; antiparasitic; fungicide; antiviral; cytostatic;
XX KW leukaemia; systemic lupus erythematosus; sepsis; autoimmune disease;
XX KW immunoinhibitory; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..2
FT /*tag= a
FT /mod_base= OTHER
FT /*note= "Phosphorothioate backbone"
FT modified_base 15..20
FT /*tag= b
FT /mod_base= OTHER
FT /*note= "Phosphorothioate backbone"

```

```

XX PN US6194388-B1.
XX PD 27-FEB-2001.
XX PF 07-FEB-1995; 95US-00386063.
XX PR 15-JUL-1994; 94US-00276358.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PI (COLE-) COLEY PHARM GROUP.
XX DR Krieg AM, Klinman D, Steinberg AD;
XX DR WPI; 2001-217934/22.
XX PT Immunostimulatory composition useful for stimulating immune response in a
XX PT subject, comprises antigen and immunostimulatory nucleic acid comprising
XX PT oligonucleotides having unethylated cytosine-guanine dinucleotides.
XX PS Claim 10; Col 10; 20pp; English.
XX CC The present invention relates to immunomodulatory
XX CC oligodeoxyribonucleotides (ODNs) containing methylated or unmethylated
XX CC cytosine-guanine (CpG) dinucleotides. Immunostimulatory ODN compositions
XX CC having unmethylated CpG dinucleotides are useful for activating
XX CC lymphocytes and for treating, preventing or ameliorating an immune system
XX CC deficiency e.g. tumour or cancer or viral, fungal, bacterial or parasitic
XX CC infection and leukaemia. Neural ODN that contains a methylated CpG
XX CC dinucleotide are useful for treating diseases such as systemic lupus
XX CC erythematosus, sepsis and autoimmune diseases. Immunoinhibitory ODN
XX CC containing CpG dinucleotides that are not in the stimulatory motif and
XX CC GCG trinucleotide sequences at or near both termini have antiviral
XX CC activity. The present sequence is an immunostimulatory
XX CC oligodeoxyribonucleotide (ODN) 1585
XX SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 74.7%; Score 14.2; DB 4; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db ||| ||||| ||||| |||||
2 GGGTCAACGTTTCAGGGGG 20

RESULT 18
AAF99097
ID AAF99097 standard; DNA; 20 BP.
XX AC AAF99097;
XX DT 12-JUN-2001 (first entry)
XX DE Immunostimulatory nucleic acid #213.
XX KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX KW immunostimulatory; tumour; viral infection; bacterial infection;
XX KW fungal infection; parasitic infection; cancer; asthma;
XX KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX OS Synthetic.
XX PN WO200122972-A2.
XX PD 05-APR-2001.
XX PF 25-SEP-2000; 2000WO-US026383.
XX PR 25-SEP-1999; 99US-0156113P.
XX PR 27-SEP-1999; 99US-0156135P.
XX PR 23-AUG-2000; 2000US-0227436P.

```

```

XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GMBH.
XX PI Krieg AM, Schetter C, Vollmer J;
XX XX WPI; 2001-273485/28.
XX DR Vaccinating against tumors, infectious diseases, allergies and asthma
XX PT using immunostimulatory Py-rich and TG nucleic acids.
XX PT Claim 101; Page 42; 338pp; English.
XX PS The present invention relates to a method for stimulating an immune
XX CC response. The method comprises administering an immunostimulatory nucleic
XX CC acid to a non-todent subject in sufficient quantity to stimulate an
XX CC immune response. The present sequence is one such immunostimulatory
XX CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX CC also useful for preventing cancer, asthma, infectious disease, allergy or
XX CC immune deficiency. The present sequence can also be used to redirect a
XX CC Th2 to a Th1 immune response and to activate immune cells. Note: the
XX CC present sequence may have a phosphorothioate backbone
XX XX Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
SQ Query Match 74.7%; Score 14.2; DB 4; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db ||||| ||||| |||||
2 GGGTTGACGTTTGGGGGG 20

RESULT 19
ABST7740
ID ABS77740 standard; DNA; 20 BP.
XX AC ABS77740;
XX DT 13-DEC-2002 (first entry)
XX DE Angiogenesis inhibitory oligonucleotide #224.
XX KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
XX KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
XX KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
XX KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
XX KW plaque neovascularisation; telangiectasia; haemophiliac joint;
XX KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
XX KW scleroderma; hypertrophic scar.
XX OS Synthetic.
XX XX WO200253141-A2.
XX PN 11-JUL-2002.
XX PD 14-DEC-2001; 2001WO-US048458.
XX PF 14-DEC-2000; 2000US-0255534P.
XX PR (COLE-) COLEY PHARM GROUP INC.
XX PA Bratzler RL;
XX PI WPI; 2002-566690/60.
XX DR

XX XX The invention relates to inhibiting angiogenesis in a subject, comprising
XX CC administering at least one antiangiogenic nucleic acid molecule. Also
XX CC included is a kit comprising a first container housing the antiangiogenic
XX CC nucleic acids, and instructions for administering them to a subject
XX CC having a condition characterised by unwanted angiogenesis. The method is
XX CC useful for inhibiting angiogenesis associated with solid tumour growth,
XX CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
XX CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
XX CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
XX CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
XX CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
XX CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma, and
XX CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
XX CC acid of the invention
XX SQ Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;
SQ Query Match 74.7%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db ||||| ||||| |||||
2 GGGTTGACGTTTGGGGGG 20

RESULT 20
ABL39045
ID ABL39045 standard; DNA; 20 BP.
XX AC ABL39045;
XX DT 16-APR-2002 (first entry)
XX DE Immunostimulatory nucleic acid SEQ ID NO: 449.
XX XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
XX KW angiogenesis; metastasis; cytostatic; ss.
XX OS Synthetic.
XX XX WO200197843-A2.
XX PN 27-DEC-2001.
XX PD 22-JUN-2001; 2001WO-US020154.
XX PF 22-JUN-2000; 2000US-0213346P.
XX PR (IOWA ) UNIV IOWA RES FOUND.
XX PA Weiner G, Hartmann G;
XX PI WPI; 2002-154611/20.
XX DR Treating or preventing cancer, such as basal cell carcinoma, comprises
XX PT administering immunostimulatory nucleic acids that induce expression of
XX PT cell surface antigens and antibodies to a subject having or at risk of
XX PT developing cancer.
XX XX Disclosure; Page 209; 312pp; English.
XX PS The present invention relates to methods for treating or preventing
XX CC cancer, involving administering to a subject having or at risk of
XX CC developing cancer immunostimulatory nucleic acids that induce expression
XX CC of cell surface antigens and antibodies. The methods are useful for
XX CC treating or preventing cancer such as basal cell carcinoma, bladder

```

```
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;

Query Match          74.7%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTTGACGTTTGGGGGG 20

RESULT 21
ACD91359
ID ACD91359 standard; DNA; 20 BP.
XX
AC ACD91359;
XX
DT 22-SEP-2003 (first entry)
XX
DE B-cell stimulatory, CpG containing oligonucleotide #1.
XX
KW CpG island; ss; HIV infection; gene therapy; vaccine; B-cell;
KW immunostimulatory; adjuvant.
XX
OS Synthetic.
XX
PN US2003050263-A1.
XX
PD 13-MAR-2003.
XX
PF 16-AUG-2001; 2001US-00931583.
XX
PR 15-JUL-1994; 94US-00276358.
PR 07-FEB-1995; 95US-00386063.
PR 08-OCT-1999; 99US-00415142.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Klinman D, Steinberg AD;
XX
DR WPI; 2003-512356/48.
XX
PT Treating a subject infected with HIV by administering a CpG nucleic acid.
XX
PS Disclosure; Page 10; 22pp; English.
XX
CC The invention relates to treating a subject infected with HIV comprising
CC administering a CpG nucleic acid (e.g. an adjuvant type CpG
CC oligonucleotide, an immunostimulatory CpG oligonucleotide or a B cell
CC stimulatory CpG oligonucleotide). The CpG are used as gene therapy
CC vaccines to treat a subject infected with HIV. The present sequence is a
CC B-cell stimulatory CpG oligonucleotide
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match          74.7%; Score 14.2; DB 9; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGG 20
```

```
RESULT 22
ACD99530
ID ACD99530 standard; DNA; 20 BP.
XX
AC ACD99530;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #216.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 14; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;

Query Match          74.7%; Score 14.2; DB 9; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTTGACGTTTGGGGGG 20

RESULT 23
ACA62324
ID ACA62324 standard; DNA; 20 BP.
XX
AC ACA62324;
XX
DT 13-AUG-2003 (first entry)
XX
DE Lymphocyte (B cell) activating oligonucleotide #1.
XX
KW Immunostimulatory oligonucleotide; unmethylated CpG dinucleotide;
KW immunoinhibitory oligonucleotide; cellular transcription factor;
KW viral activity; lymphocyte activation; B cell; natural killer cell; NK;
KW immune system deficiency; viral infection; immune disease; SLE;
```

KW systemic lupus erythematosus; sepsis; cancer; immunomodulatory;  
KW immunostimulant; dermatological; antiinflammatory; cytostatic;  
KW antibacterial; virucide; ss.  
XX Synthetic.  
XX  
XX US2003026782-A1.  
XX  
XX 06-FEB-2003.  
XX  
XX 08-OCT-1999; 99US-00415142.  
XX  
XX 07-FEB-1995; 95US-00386063.  
XX  
XX (KRIE/) KRIEG A M.  
XX  
XX Krieg AM;  
XX  
XX WPI; 2003-466135/44.  
XX  
XX Novel immunostimulatory oligonucleotide comprising 2-100 nucleotides and  
PT containing at least one unmethylated CpG dinucleotide, useful for  
PT activating a subject's B cells or natural killer cells.  
XX  
XX Disclosure; Page 13; 19pp; English.  
XX  
XX The present invention relates to immunostimulatory oligonucleotides  
CC containing at least one unmethylated CpG dinucleotide, and  
CC immunoinhibitory oligonucleotides which are capable of interfering with  
CC the activity of viral or cellular transcription factors. The  
CC immunostimulatory oligonucleotides are useful for activating a subject's  
CC lymphocytes (B cells or natural killer (NK) cells). They are useful for  
CC treating, preventing or ameliorating an immune system deficiency. The  
CC immunoinhibitory oligonucleotides are useful for treating or preventing a  
CC viral infection in a subject. They are also useful for treating or  
CC preventing or ameliorating an immune system deficiency in a subject. The  
CC immunoinhibitory oligonucleotides can be used in a pharmaceutical  
CC composition which may be used for vaccinating a subject. The  
CC oligonucleotides may be used for treating an immune disease such as  
CC systemic lupus erythematosus (SLE), sepsis, or cancer. The  
CC oligonucleotides are safe to use since they do not initiate an immune  
CC reaction when administered to a subject in vivo. ACA62324-ACA62352  
CC represent the immunomodulatory oligonucleotides of the invention. Note:  
CC The present sequence given as SEQ ID No:1 in the Sequence listing differs  
CC from that given on page 6 (ACA62351) and page 17 (ACA62352) of the  
CC specification  
XX  
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
SQ  
  
Query Match 74.7%; Score 14.2; DB 9; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GGGGTACGTTTCAGGGGGG 19  
Db |||||  
2 GGGTCAACGTTTCAGGGGGG 20  
  
RESULT 24  
ADB36599  
ID ADB36599 standard; DNA; 20 BP.  
XX  
XX ADB36599;  
XX  
XX 04-DEC-2003 (first entry)  
DT  
XX  
DE Immunostimulatory nucleic acid #213.  
XX  
XX de; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX  
XX Synthetic.  
XX

PN US2003087848-A1.  
XX  
XX 08-MAY-2003.  
XX  
XX 02-FEB-2001; 2001US-00776479.  
XX  
XX 03-FEB-2000; 2000US-0179991P.  
XX  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
PI  
XX WPI; 2003-657977/62.  
DR  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
PT  
XX Disclosure; Page 9; 221pp; English.  
PS  
XX The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX  
XX Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;  
SQ  
  
Query Match 74.7%; Score 14.2; DB 9; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 GGGGTACGTTTCAGGGGGG 19  
Db |||||  
2 GGGTCAACGTTTCAGGGGGG 20  
  
RESULT 25  
ADO58881  
ID ADO58881 standard; DNA; 20 BP.  
XX  
XX ADO58881;  
XX  
XX 29-JUL-2004 (first entry)  
DT  
XX  
XX Mitogenic oligonucleotide ODN1585 used in B-cell stimulation.  
DE  
XX  
XX Lymphocyte; B cell; natural killer cell; immune response;  
KW systemic lupus erythematosus; sepsis; viral infection; immunosuppressive;  
KW immunostimulating; immunomodulating; antibacterial; antiinflammatory;  
KW dermatological; virucide; phosphorothioate backbone; ss.  
XX  
XX Unidentified.  
OS  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..2  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
FT modified\_base 16..20  
FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
XX  
XX US2004087534-A1.  
PN  
XX  
XX 06-MAY-2004.  
XX  
XX 30-JUL-2003; 2003US-00631676.  
XX  
XX 15-JUL-1994; 94US-00276358.  
XX

```

PR 07-FEB-1995; 95US-00386063.
PR 08-OCT-1999; 99US-00415142.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (COLE-) COLEY PHARM GROUP INC.
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.
XX
XX Krieg AM, Klinman D, Steinberg AD;
PI
XX
XX WPI; 2004-356245/33.
DR
XX
XX New immunomodulatory oligonucleotides containing at least one
PT unmethylated CpG dinucleotide, useful for treating diseases including
PT systemic lupus erythematosus and sepsis.
XX
XX Claim 5; SEQ ID NO 1; 19pp; English.
XX
XX The present invention provides oligonucleotides comprising unmethylated
CC CpG dinucleotides. The invention is useful to activate lymphocytes
CC specifically to activate B cells and natural killer cells, for treating
CC diseases associated with an immune system activation such as systemic
CC lupus erythematosus, sepsis and viral infections. The invention is useful
CC as an immunosuppressive, immunostimulating, immunomodulating,
CC antibacterial, antiinflammatory, dermatological and virucidal agent. The
CC present sequence is a mitogenic oligonucleotide used in the stimulation
CC of B-cells. This sequence is used in the invention.
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
SQ
Query Match 74.7%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred No. 3 7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 26
ADQ36558
ID ADQ36558 standard; DNA; 20 BP.
XX
AC ADQ36558;
XX
XX 07-OCT-2004 (first entry)
XX
XX B-cell stimulatory CpG oligonucleotide ODN1585.
XX
XX B-cell stimulation; CpG island; ss; viral transcription factor;
KW cellular transcription factor; immunoinhibitor; immune system deficiency;
KW systemic lupus erythematosus; sepsis; tumour; cancer; viral infection;
KW fungal infection; bacterial infection; parasitic infection; vaccine;
KW antisense gene therapy.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..2
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkage"
FT misc_feature 9..10
FT /*tag= b
FT /note= "CpG island"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkage"
XX
XX US2004143112-A1.
XX
XX 22-JUL-2004.

```

---

```

XX 21-OCT-2003; 2003US-00690495.
PF
XX
XX 15-JUL-1994; 94US-00276358.
PR
XX 07-FEB-1995; 95US-00386063.
PR
XX 08-OCT-1999; 99US-00415142.
XX
XX (KRIE/) KRIEG A M.
PA
XX (KLIN/) KLINMAN D.
PA
XX (STEI/) STEINBERG A D.
XX
XX Krieg AM, Klinman D, Steinberg AD;
PI
XX
XX WPI; 2004-552597/53.
DR
XX
XX New oligonucleotides containing unmethylated CpG dinucleotide, useful for
PT treating, preventing or ameliorating an immune system deficiency, e.g.
PT tumor, cancer, or viral, fungal, bacterial or parasitic infection.
XX
XX Claim 5; SEQ ID NO 1; 14pp; English.
XX
XX The invention relates to a new oligonucleotide which: (a) comprises about
XX 2-100 nucleotides and containing at least one unmethylated CpG
CC dinucleotide; or (b) is capable of interfering with the activity of viral
CC or cellular transcription factors and containing a consensus
CC immunoinhibitor CpG motif represented by the formula (I): 5'GCGXnGCG3'
CC where X a nucleotide and n 0-50. Also included are an oligonucleotide
CC delivery complex (comprising the oligonucleotide, and a targeting means),
CC a pharmaceutical composition comprising the oligonucleotide and a
CC pharmaceutical carrier, activating a subject's B cells or natural killer
CC cells (by contacting the cells with the oligonucleotide) treating,
CC (preventing or ameliorating) an immune system deficiency in a subject,
CC vaccinating a subject by administering the composition in conjunction
CC with a vaccine, treating a disease associated with an immune system
CC activation in a subject (by administering a neutral oligonucleotide alone
CC or in conjunction with a pharmaceutical carrier), an improved method for
CC performing antisense therapy (comprising methylating CpG containing
CC oligonucleotides prior to administration to a subject), an improved
CC method for in vivo diagnoses using oligonucleotide probes comprising
CC methylating CpG containing oligonucleotides prior to administration to a
CC subject and treating or preventing a viral infection in a subject by
CC administering the immunoinhibitory oligonucleotide defined above. The
CC oligonucleotide is useful for treating, preventing or ameliorating an
CC immune system deficiency, such as systemic lupus erythematosus, sepsis,
CC tumour, cancer, or viral, fungal, bacterial or parasitic infection.
CC Compositions comprising the oligonucleotide are useful for activating a
CC subject's B cells or natural killer cells, for treating, preventing or
CC ameliorating an immune system deficiency or for vaccinating a subject.
CC The immunoinhibitory oligonucleotide is useful for treating or preventing
CC a viral infection in a subject. The oligonucleotides may also be used in
CC conjunction with a vaccine to boost a subject's immune system to effect a
CC better response from the vaccine, or for increasing the responsiveness of
CC the malignant cells to subsequent chemotherapy. The present sequence is a
CC B-cell stimulatory CpG oligonucleotide of the invention.
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
SQ
Query Match 74.7%; Score 14.2; DB 12; Length 20;
Best Local Similarity 84.2%; Pred No. 3 7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 27
ADQ36584
ID ADQ36584 standard; DNA; 20 BP.
XX
XX ADQ36584;
XX
XX 07-OCT-2004 (first entry)

```

XX Unmethylated CpG dinucleotide #1.  
 DE Unmethylated CpG dinucleotide; B cell; natural killer cell;  
 XX immune system deficiency; immune system activation;  
 KW systemic lupus erythematosus; sepsis; viral infection; chemotherapy;  
 KW cytostatic; virucide; fungicide; antibacterial; antiparasitic;  
 KW immunosuppressive; antiinflammatory; dermatological; ss.  
 XX Synthetic.  
 OS  
 XX US2004142469-A1.  
 PN 22-JUL-2004.  
 XX 26-FEB-2004; 2004US-00789051.  
 XX 15-JUL-1994; 94US-00276358.  
 PR 07-FEB-1995; 95US-00386063.  
 PR 08-OCT-1999; 99US-00415142.  
 PR 21-OCT-2003; 2003US-00690495.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLB-) COLEY PHARM GROUP INC.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX Krieg AM, Klinman D, Steinberg AD;  
 DR WPI; 2004-552569/53.  
 XX New oligonucleotides containing unmethylated CpG dinucleotide, useful for  
 PT activating a subject's B cells or natural killer cells, as vaccine, or  
 PT for treating, preventing or ameliorating an immune system deficiency.  
 XX Claim 5; SEQ ID NO 1; 14pp; English.  
 XX The invention relates to oligonucleotides containing at least one  
 CC unmethylated CpG dinucleotide. The invention relates to an  
 CC oligonucleotide delivery complex comprising an oligonucleotide of the  
 CC invention and a targeting means, a method of activating a subject's B  
 CC cells or natural killer cells by contacting the cells with an  
 CC oligonucleotide, a method of treating, preventing or ameliorating an  
 CC immune system deficiency in a subject, vaccinating a subject by  
 CC administering the composition in conjunction with a vaccine, a method of  
 CC treating a disease associated with an immune system activation in a  
 CC subject by administering a neutral oligonucleotide alone or in  
 CC conjunction with a pharmaceutical carrier, and a method of performing  
 CC antisense therapy comprising methylating CpG containing oligonucleotides  
 CC prior to administration to a subject. The oligonucleotides are useful for  
 CC treating diseases associated with immune system activation, such as  
 CC systemic lupus erythematosus and sepsis. Compositions comprising  
 CC oligonucleotides of the invention are useful for activating a subject's B  
 CC cells or natural killer cells, for treating, preventing or ameliorating  
 CC an immune system deficiency or for vaccinating a subject. The  
 CC immunoinhibitory oligonucleotides are useful for treating or preventing a  
 CC viral infection in a subject. The oligonucleotides may also be used in  
 CC conjunction with a vaccine to boost a subject's immune system to effect a  
 CC better response from the vaccine, or for increasing the responsiveness of  
 CC malignant cells to subsequent chemotherapy. This sequence represents an  
 CC unmethylated CpG dinucleotide of the invention.  
 XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 74.7%; Score 14.2; DB 12; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGGG 19  
 ||| |||||  
 Db 2 GGGTCACGTTTCAGGGGG 20  
 ||| |||||

RESULT 28

ADR20014  
 ID ADR20014 standard; DNA; 20 BP.  
 XX  
 AC ADR20014;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE B-cell stimulating oligonucleotide ODN 1585.  
 XX cellular transcription factor; immunoinhibitory; CpG;  
 KW phosphorothioate backbone; B cell activation; immune system deficiency;  
 KW natural killer cell activation; immune system deficiency;  
 KW systemic lupus erythematosus; sepsis; antisense; methylation;  
 KW antiinflammatory; dermatological; immunosuppressive; virucide; ss;  
 KW primer.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note="phosphorothioate linkage"  
 FT modified\_base 16..20  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note="phosphorothioate linkage"  
 XX  
 PN US2004152656-A1.  
 XX  
 PD 05-AUG-2004.  
 XX  
 PF 26-FEB-2004; 2004US-00788191.  
 XX  
 PR 15-JUL-1994; 94US-00276358.  
 PR 07-FEB-1995; 95US-00386063.  
 PR 08-OCT-1999; 99US-00415142.  
 PR 21-OCT-2003; 2003US-00690495.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLB-) COLEY PHARM GROUP INC.  
 PA (USSH ) US SEC HEALTH AND HUMAN SERVICES.  
 XX Krieg AM, Klinman D, Steinberg AD;  
 DR WPI; 2004-624263/60.  
 XX New oligonucleotide comprises at least one unmethylated CpG dinucleotide,  
 PT useful for stimulating an immune response or for treating diseases  
 PT associated with immune system activation, e.g. systemic lupus  
 PT erythematosus or sepsis.  
 XX Claim 5; SEQ ID NO 1; 19pp; English.  
 XX This invention describes novel oligonucleotides capable of interfering  
 CC with the activity of viral or cellular transcription factors and  
 CC containing a consensus immunoinhibitory CpG motif having the formula:  
 CC 5'GGCnCG3', where X is a nucleotide and n is 0-50 and a  
 CC phosphorothioate backbone modification. The invention also describes an  
 CC oligonucleotide delivery complex comprising the oligonucleotide and a  
 CC targeting means e.g. a pharmaceutical carrier. The oligonucleotides are  
 CC used for activating a subject's B cells or natural killer cells;  
 CC treating, preventing or ameliorating an immune system deficiency in a  
 CC subject; vaccinating a subject; treating a disease associated with an  
 CC immune system activation in a subject (systemic lupus erythematosus or  
 CC sepsis); performing antisense therapy comprising methylating CpG  
 CC containing oligonucleotides prior to administration to a subject; an  
 CC improved method for in vivo diagnoses using oligonucleotide probes  
 CC comprising methylating CpG containing oligonucleotides prior to  
 CC administration to a subject; and treating or preventing a viral infection  
 CC in a subject. The targeting means is selected from cholesterol, virosome,  
 CC liposome, lipid, or a target cell specific binding agent. The  
 CC oligonucleotides described in the invention have antiinflammatory,

CC dermatological, immunosuppressive and virucide activity. ADR20014-  
CC ADR20040 represent the oligonucleotides describes in the disclosure of  
CC the invention.  
XX  
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
Query Match 74.7%; Score 14.2; DB 13; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTTCAGGGGG 20  
RESULT 29  
ADR28877  
ID ADR28877 standard; DNA; 20 BP.  
XX  
AC ADR28877;  
DT 21-OCT-2004 (first entry)  
DE CpG-containing immunostimulatory oligonucleotide ODN 1585.  
KW ss; immunostimulatory oligonucleotide; CpG dinucleotide;  
KW transcription factor; immunoinhibitory CpG motif; B cell;  
KW natural killer cell; immune system deficiency; antisense therapy;  
KW viral infection; immune response; systemic lupus erythematosus; sepsis;  
KW vaccine.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..3  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate linkage"  
FT misc\_feature 9..10  
FT /\*tag= b  
FT /note= "CpG dinucleotide"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate linkage"  
XX  
PN US2004152657-A1.  
XX  
XX 05-AUG-2004.  
XX  
XX 26-FEB-2004; 2004US-00789536.  
XX  
XX 15-JUL-1994; 94US-00276358.  
XX 07-FEB-1995; 95US-00386063.  
XX 08-OCT-1999; 99US-00415142.  
XX 21-OCT-2003; 2003US-00690495.  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA (COLE-) COLEY PHARM GROUP INC.  
PA (USSH ) US SEC HEALTH AND HUMAN SERVICES.  
XX  
XX Krieg AM, Klinman D, Steinberg AD;  
XX WPI; 2004-624264/60.  
XX  
XX New oligonucleotide comprises at least one unethylated CpG dinucleotide,  
PT useful for stimulating an immune response or for treating diseases  
PT associated with immune system activation, e.g. systemic lupus  
PT erythematosus or sepsis.  
XX  
XX Claim 5; SEQ ID NO 1; 19pp; English.  
PS  
XX The invention relates to an oligonucleotide comprising 2-100 nucleotides

CC and containing at least one unethylated CpG dinucleotide. The  
CC oligonucleotide is capable of interfering with the activity of viral or  
CC cellular transcription factors and containing a consensus  
CC immunoinhibitory CpG motif having the formula: 5'GGXnGGG3', where X is a  
CC nucleotide and n is 0-50. Also included are an oligonucleotide delivery  
CC complex (comprising the oligonucleotide above and a targeting means), a  
CC pharmaceutical composition (comprising the oligonucleotide above and a  
CC pharmaceutical carrier), activating a subject's B cells, activating a  
CC subject's natural killer cells, treating (preventing or ameliorating) an  
CC immune system deficiency in a subject, vaccinating a subject, treating a  
CC disease associated with an immune system activation in a subject,  
CC performing antisense therapy (comprising methylating CpG containing  
CC oligonucleotides prior to administration to a subject), in vivo diagnoses  
CC using oligonucleotide probes comprising methylating CpG containing  
CC oligonucleotides prior to administration to a subject and treating or  
CC preventing a viral infection in a subject. The oligonucleotide is useful  
CC for stimulating an immune response in a subject. They are also useful for  
CC treating diseases associated with immune system activation including  
CC systemic lupus erythematosus or sepsis, or for treating, preventing, or  
CC ameliorating an immune system deficiency in a subject. The  
CC oligonucleotide is also useful for treating or preventing viral  
CC infection. It is also useful as a vaccine. The present sequence is an  
CC immunostimulatory oligonucleotide of the invention.  
XX  
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
Query Match 74.7%; Score 14.2; DB 13; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTTCAGGGGG 20  
RESULT 30  
ADR44692  
ID ADR44692 standard; DNA; 20 BP.  
XX  
AC ADR44692;  
DT 04-NOV-2004 (first entry)  
DE Mitogenic CpG oligonucleotide ODN1585 used in B-cell activation.  
XX  
KW Immunomodulatory; CpG dinucleotide; immune system deficiency;  
KW systemic lupus erythematosus; sepsis; tumour; cancer; viral infection;  
KW bacterial infection; fungal infection; cytostatic; virucidal;  
KW antibacterial; fungicidal; antiinflammatory; dermatological;  
KW immunosuppressive; vaccine; gene therapy; phosphorothioate backbone; ss.  
XX  
OS Unidentified.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..2  
FH /\*tag= a  
FH /mod\_base= OTHER  
FH /note= "Phosphorothioate backbone"  
FT modified\_base 16..20  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
XX  
PN US2004162258-A1.  
XX  
XX 19-AUG-2004.  
XX  
XX 30-JAN-2004; 2004US-00769626.  
XX  
XX 15-JUL-1994; 94US-00276358.  
XX 07-FEB-1995; 95US-00386063.  
XX 08-OCT-1999; 99US-00415142.  
XX 21-OCT-2003; 2003US-00690495.



```

XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GROUP INC.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Krieg AM, Klinman D, Steinberg AD;
XX WPI; 2004-603582/58.
XX
XX New oligonucleotide comprises at least one unmethylated CpG dinucleotide,
PT useful for treating, preventing, or ameliorating an immune system
PT deficiency or a tumor, cancer, viral, bacterial, or fungal infection.
XX
XX Disclosure; SEQ ID NO 1; 20pp; English.
XX
XX The present invention provides oligonucleotides comprising
CC immunomodulatory unmethylated CpG dinucleotide. The invention is useful
CC for treating, preventing and ameliorating immune system deficiencies such
CC as systemic lupus erythematosus and sepsis, tumour, cancer, viral,
CC bacterial and fungal infections. The invention acts as an cytostatic,
CC virucidal, antibacterial, fungicidal, antiinflammatory, dermatological
CC and immunosuppressive agent. The invention is also useful in the
CC production of vaccines and in gene therapy. The present sequence is a
CC mitogenic CpG oligonucleotide used in B-cell activation. Note: This
CC sequence is stated to be SEQ ID NO: 1 in the sequence listing. However,
CC this sequence differs from the sequence designated as SEQ ID NO: 1 in the
CC claims.
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
SQ
Query Match 74.7%; Score 14.2; DB 13; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGG 19
Db ||| ||||| ||||| |||||
2 GGGTCAACGTTTCAGGGGG 20
RESULT 31
ADR45002
ID ADR45002 standard; DNA; 20 BP.
XX
AC ADR45002;
XX
DT 04-NOV-2004 (first entry)
XX
DE CpG oligonucleotide ODN 1585 used to stimulate B-cells.
XX
KW Immune response; immune system deficiency; tumour; cancer;
KW viral infection; systemic lupus erythematosus; sepsis; vaccine;
KW gene therapy; bacterial infection; fungal infection; phosphorothioate;
KW ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1..2
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides"
FT modified_base 16..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate nucleotides"
XX
PN US2004162262-A1.
XX
XX 19-AUG-2004.
XX
XX 26-FEB-2004; 2004US-00789353.
XX
XX 15-JUL-1994; 94US-00276358.
XX
PR 07-FEB-1995; 95US-00386063.
PR 08-OCT-1999; 99US-00415142.
PR 21-OCT-2003; 2003US-00690495.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GROUP INC.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Krieg AM, Klinman D, Steinberg AD;
XX WPI; 2004-603584/58.
XX
XX New oligonucleotide comprises at least one unmethylated CpG dinucleotide,
PT useful for treating, preventing, or ameliorating an immune system
PT deficiency or a tumor, cancer, viral, bacterial, or fungal infection.
XX
XX Claim 5; SEQ ID NO 1; 19pp; English.
XX
XX The invention provides novel oligonucleotides containing unmethylated CpG
CC dinucleotides and therapeutic utilities based on their ability to
CC stimulate an immune response in a subject. Oligonucleotides of the
CC invention are useful for treating, preventing or ameliorating an immune
CC system deficiency or a tumour, cancer, viral, bacterial or fungal
CC infection. They are useful for treating diseases associated with immune
CC system activation including systemic lupus erythematosus or sepsis. They
CC are also useful as vaccines to boost subject's immune system. The
CC invention is also useful in gene therapy. The present sequence is a CpG
CC oligonucleotide used to stimulate B-cells. Note: This sequence is stated
CC to be the same as that shown as SEQ ID NO: 1 in page 18 of the
CC specification. However these sequences differ.
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
SQ
Query Match 74.7%; Score 14.2; DB 13; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGG 19
Db ||| ||||| ||||| |||||
2 GGGTCAACGTTTCAGGGGG 20
RESULT 32
ADR88228
ID ADR88228 standard; DNA; 20 BP.
XX
AC ADR88228;
XX
DT 18-NOV-2004 (first entry)
XX
DE CpG immunomodulatory oligo, ODN 1585 used in B cell stimulation.
XX
KW CpG dinucleotide; gene therapy a; vaccine; cancer; viral infection;
KW fungal infection; bacterial infection; parasitic infection;
KW systemic lupus erythematosus; sepsis; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1..3
FT /*tag= a
FT /mod_base= Phosphorothioate backbone
FT modified_base 15..20
FT /*tag= b
FT /mod_base= Phosphorothioate backbone
XX
PN US2004171150-A1.
XX
XX 02-SEP-2004.
XX
XX 26-FEB-2004; 2004US-00787737.
XX
XX 15-JUL-1994; 94US-00276358.
XX

```

```

PR 07-FEB-1995; 95US-00386063.
PR 09-OCT-1999; 99US-00415142.
PR 21-OCT-2003; 2003US-00690495.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GROUP INC.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Krieg AM, Klinman D, Steinberg AD;
PI WPI; 2004-634548/61.
XX
DR WPI; 2004-634548/61.
XX
PT New immunomodulatory oligonucleotides for preventing, treating or
PT ameliorating diseases associated with immune system deficiency or
PT activation, e.g. cancer, viral infection, systemic lupus erythematosus or
PT sepsis.
XX
XX Claim 5; SEQ ID NO 1; 19pp; English.
XX
XX The present invention relates to an oligonucleotide containing at least
CC one unmethylated CpG dinucleotide. The invention is useful in gene therapy
CC and for preparing vaccine. The invention is also useful for preventing,
CC treating or ameliorating diseases associated with immune system
CC deficiency or activation such as cancer, viral, fungal, bacterial or
CC parasitic infection, systemic lupus erythematosus or sepsis. The present
CC sequence is a CpG immunomodulatory oligonucleotide used in B cell
CC stimulation.
XX
XX Query Match 74.7%; Score 14.2; DB 13; Length 20;
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db |||||
2 GGGTCAACGTTTCAGGGGGG 20

RESULT 33
ADS17223
ID ADS17223 standard; DNA; 20 BP.
XX
XX ADS17223;
XX
XX 02-DEC-2004 (first entry)
XX
XX ODN1, oligonucleotide used to stimulate B cells.
DE Immunomodulator; immune system; systemic lupus erythematosus; sepsis;
XX viral infection; vaccine; B cell; virucide; phosphorothioate backbone;
KW ss.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..3
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 15..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
XX US2004181045-A1.
XX
XX 16-SEP-2004.
XX
XX 26-FEB-2004; 2004US-00788199.
XX
XX 15-JUL-1994; 94US-00276358.
PR 07-FEB-1995; 95US-00386063.

PR 08-OCT-1999; 99US-00415142.
PR 21-OCT-2003; 2003US-00690495.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GROUP INC.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Krieg AM, Klinman D, Steinberg AD;
PI WPI; 2004-667684/65.
XX
DR WPI; 2004-667684/65.
XX
PT New oligonucleotide comprising 2-100 nucleotides and containing an
PT unmethylated CpG dinucleotide, useful in preparing a composition for
PT treating a disease, e.g., systemic lupus erythematosus, sepsis or viral
PT infection.
XX
XX Claim 5; SEQ ID NO 1; 19pp; English.
XX
XX The invention relates to immunomodulatory oligonucleotides containing an
CC unmethylated CpG dinucleotide. The oligonucleotide of the invention is
CC useful in preparing a composition for treating a disease associated with
CC an immune system activation, e.g., systemic lupus erythematosus, sepsis or
CC viral infection. It is also useful to prepare vaccine. The present
CC sequence is an immunomodulatory oligonucleotide used to stimulate B
CC cells.
XX
XX Query Match 74.7%; Score 14.2; DB 13; Length 20;
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db |||||
2 GGGTCAACGTTTCAGGGGGG 20

RESULT 34
ADU89540
ID ADU89540 standard; DNA; 20 BP.
XX
XX ADU89540;
XX
XX 10-FEB-2005 (first entry)
XX
XX Allergic response suppressor oligonucleotide #224.
DE
XX
XX ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;
KW antibacterial; virucide; immunoglobulin E antagonist; allergy;
KW immunostimulator; asthma; rhinitis; urticaria; dermatitis;
KW bacterial infection; viral infection.
XX
XX Synthetic.
OS
XX
XX US2004235774-A1.
XX
XX 25-NOV-2004.
XX
XX 23-APR-2004; 2004US-00831778.
XX
XX 03-FEB-2000; 2000US-0179991P.
PR 02-FEB-2001; 2001US-00776479.
XX
XX (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
XX Bratzler RL, Petersen DM, Fouron Y;
PI WPI; 2004-833006/82.
XX
XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic
PT dermatitis, in a subject, comprises administering a first and second dose

```

```

PT of an immunostimulatory nucleic acid.
PS Disclosure; SEQ ID NO 224; 235pp; English.
XX
CC The invention relates to a method of suppressing a symptom of an allergic
CC response in a subject by administering a first and second dose of an
CC immunostimulatory nucleic acid that comprises a nucleotide sequence
CC comprising 5'-cg-3', and where the second dose is administered from 1 day
CC to 8 weeks after the first dose. The methods and compositions of the
CC present invention are useful for the treatment or prevention of asthma
CC and allergy, including rhinitis, urticaria and atopic dermatitis, using
CC an immunostimulatory nucleic acid alone or in combination with other
CC medicaments. They can also be used in preventing bacterial and viral
CC infections. This sequence represents an oligonucleotide used in the
CC method of the invention.
XX
SQ Sequence 20 BP; 1 A; 1 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 74.7%; Score 14.2; DB 13; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTTCAGTTTGGGGG 20

RESULT 35
ADW28066
ID ADW28066 standard; DNA; 20 BP.
AC
XX
XX ADW28066;
DT
XX
XX 24-MAR-2005 (first entry)
DE Mitogenic CpG oligonucleotide ODN1585 used in B-cell stimulation.
XX
KW Immune modulation; immunity; immunogenicity; immune disorder; tumor;
KW cancer; cytostatic; neoplasm; systemic lupus erythematosus; SLE;
KW antiinflammatory; dermatological; immunosuppressive; sepsis; infection;
KW viral infection; viricide; fungal infection; fungicide;
KW bacterial infection; antibacterial; parasitic infection; antiparasitic;
KW autoimmune disease; rheumatoid arthritis; antiarthritic; antirheumatic;
KW multiple sclerosis; neuroprotective; antisense therapy; hybridization;
KW antiviral vaccine; phosphorothioate; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1..2
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 16..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
XX US2005004062-A1.
XX
XX 06-JAN-2005.
XX
XX 17-MAY-2004; 2004US-00847650.
XX
XX 15-JUL-1994; 94US-00276358.
XX 07-FEB-1995; 95US-00386063.
XX 09-OCT-1999; 99US-00415142.
XX 21-OCT-2003; 2003US-00690495.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX (COLE-) COLEY PHARM GROUP INC.
XX (USDC ) US DEPT COMMERCE & NAT INST STANDARDS.
XX

```

---

```

PI Krieg AM, Klinman D, Steinberg AD;
XX WPI; 2005-065257/07.
XX
XX Use of an immunostimulatory oligonucleotide for boosting an immune
XX response of a subject, or for stimulating an immune response in a
XX subject, where increases in IFN-gamma and IL-12 expression are indicators
XX of the immune response.
XX
XX Disclosure; SEQ ID NO 1; 19pp; English.
XX
XX The present invention relates to immunomodulatory oligonucleotides
XX containing unmethylated CpG dinucleotides and therapeutic utilities based
XX on their ability to stimulate an immune response in a subject. The
XX invention is useful for treating, preventing or ameliorating immune
XX system deficiencies such as tumor, cancer, systemic lupus erythematosus
XX and sepsis, infections such as viral (e.g. HIV, herpes), fungal (e.g.
XX Candida sp.) and bacterial or parasitic (e.g. Leishmania, Toxoplasma) and
XX autoimmune diseases such as rheumatoid arthritis and multiple sclerosis.
XX The invention is also useful in antisense therapy, as in vivo
XX hybridization probes and as antiviral therapeutics. The present sequence
XX is a mitogenic CpG oligonucleotide used in B-cell stimulation.
XX
SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 74.7%; Score 14.2; DB 14; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 36
ADV97282
ID ADV97282 standard; DNA; 20 BP.
AC
XX
XX ADV97282;
XX
XX 07-APR-2005 (first entry)
DE Immunostimulatory oligonucleotide ODN 1585 SEQ ID NO:1.
XX
XX ss; immune modulation; pharmaceutical; immunomodulator; cytostatic;
XX viricide; fungicide; antibacterial; antiparasitic; antiinflammatory;
XX dermatological; immunosuppressive; antiarthritic; antirheumatic;
XX neuroprotective; immunostimulant; immune disorder.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..3
FT /*tag= a
FT /mod_base= phosphorothioate backbone
FT misc_feature 9..10
FT /*tag= b
FT /note= "unmethylated CpG dinucleotide"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= phosphorothioate backbone
XX
XX US2005009774-A1.
XX
XX 13-JAN-2005.
XX
XX 09-JUL-2004; 2004US-00888885.
XX
XX 15-JUL-1994; 94US-00276358.
XX 07-FEB-1995; 95US-00386063.
XX 09-OCT-1999; 99US-00415142.
XX 21-OCT-2003; 2003US-00690495.
XX

```

```

PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GROUP INC.
PA (USSA ) US SEC OF ARMY.
XX
XX Krieg AM, Klinman D, Steinberg AD;
XX WPI; 2005-080553/09.
XX
XX Oral composition, useful e.g. to treat/prevent/ameliorate an immune
XX system deficiency or diseases associated with immune system activation,
XX PT comprises an immunostimulatory nucleic acid in a pharmaceutically
XX PT acceptable carrier.
XX
XX Disclosure; SEQ ID NO 1; 18pp; English.
XX
XX The invention relates to a novel pharmaceutical composition (A) for oral
XX administration comprising an immunostimulatory nucleic acid (1) (8-100
XX nucleotides in length) in a pharmaceutically acceptable carrier. The
XX immunostimulatory nucleic acid is of the formula 5'X 1 X 2 CGX 3 X 4 3'
XX (where C and G are unmethylated). The carrier comprises an emulsion. A
XX composition of the invention has immunomodulator, cytostatic, virucide,
XX fungicide, antibacterial, antiparasitic, antinflammatory,
XX dermatological, immunosuppressive, antiarthritic, antirheumatic,
XX neuroprotective, and immunostimulant activity. A nucleic acid of the
XX invention is useful to treat/prevent/ameliorate an immune system
XX deficiency (e.g. tumors, cancers or viral, fungal, bacterial or parasitic
XX infections) or a disease (e.g. systemic lupus erythematosus, sepsis,
XX rheumatoid arthritis and multiple sclerosis) associated with immune
XX system activation. The nucleic acids are useful as vaccine adjuvants to
XX stimulate a subject's response to a vaccine, and for antisense therapies
XX or as in vivo hybridization probes. The present sequence represents an
XX immunostimulatory oligonucleotide of the invention, ODN 1585.
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
SQ Query Match 74.7%; Score 14.2; DB 14; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGGG 20
RESULT 37
ADX87198
ID ADX87198 standard; DNA; 20 BP.
AC ADX87198;
DT 05-MAY-2005 (first entry)
DE B cell-stimulating oligonucleotide - SEQ ID 1.
XX
XX HIV infection; anti-HIV; B-lymphocyte; ss.
XX
XX Unidentified.
XX
XX US2005037985-A1.
XX
XX 17-FEB-2005.
XX
XX 25-AUG-2003; 2003US-00649584.
XX
XX 15-JUL-1994; 94US-00276358.
XX
XX 07-FEB-1995; 95US-00386063.
XX
XX 09-OCT-1999; 99US-00415142.
XX
XX 16-AUG-2001; 2001US-00931583.
XX
XX (KRIE/) KRIEG A M.
XX (KLIN/) KLINMAN D.
XX (STEI/) STEINBERG A D.
XX
PI Krieg AM, Klinman D, Steinberg AD;
XX WPI; 2005-172294/18.
XX
XX Treating a subject infected with HIV comprises administering a CpG
XX nucleic acid and an anti-HIV therapy to the subject.
XX
XX Disclosure; SEQ ID NO 1; 37pp; English.
XX
XX The invention comprises a method of treating HIV by administering a CpG
XX nucleic acid (e.g. an adjuvant-type nucleic acid or an IFN-alpha-inducing
XX CpG nucleic acid) and an anti-HIV therapy (e.g. an inhibitor of HIV
XX replication). The method of the invention is useful for the treatment and
XX prevention of HIV. The present DNA sequence represents an oligonucleotide
XX that was used to stimulate B cells.
XX
XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
SQ Query Match 74.7%; Score 14.2; DB 14; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGGG 20
RESULT 38
ADX84981
ID ADX84981 standard; DNA; 20 BP.
AC ADX84981;
DT 05-MAY-2005 (first entry)
DE CpG oligonucleotide ODN 1585 used to stimulate B cells.
XX
XX Immune modulation; immunotherapy; antisense therapy; hybridization;
XX interferon-gamma; cytokine; immune deficiency; immunostimulant;
XX immune disorder; tumor; cancer; cytostatic; neoplasm; viral infection;
XX virucide; infection; fungal infection; fungicide; bacterial infection;
XX antibacterial; parasitic infection; antiparasitic; nucleic acid vaccine;
XX leukemia; systemic lupus erythematosus; antinflammatory; dermatological;
XX immunosuppressive; sepsis; autoimmune disease; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 1..2 /*tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX
XX modified_base 16..20 /*tag= b
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX
XX US2005037403-A1.
XX
XX 17-FEB-2005.
XX
XX 09-JUL-2004; 2004US-0088089.
XX
XX 15-JUL-1994; 94US-00276358.
XX
XX 07-FEB-1995; 95US-00386063.
XX
XX 09-OCT-1999; 99US-00415142.
XX
XX 21-OCT-2003; 2003US-00690495.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX (COLE-) COLEY PHARM GROUP INC.
XX (USDC ) US DEPT COMMERCE & NAT INST STANDARDS.
XX
XX Krieg AM, Klinman D, Steinberg AD;

```

XX WPI; 2005-172254/18.  
 DR Use of immunostimulatory oligonucleotide delivery complex comprising  
 PT oligonucleotide linked to biodegradable delivery complex for increasing  
 PT interferon-gamma levels and treating diseases associated with immune  
 PT system deficiency e.g. cancer.  
 XX  
 XX Disclosure; SEQ ID NO 1; 19pp; English.  
 PS  
 CC The invention relates to a method for increasing interferon (IFN)-gamma  
 CC in a subject. The method involves administering an immunostimulatory  
 CC oligonucleotide/delivery complex to modulate immune response of the  
 CC subject. The invention is useful for treating diseases associated with  
 CC immune system deficiency e.g. tumor or cancer or viral, fungal, bacterial  
 CC or parasitic infections; as vaccine; for treating leukemia, systemic  
 CC lupus erythematosus, sepsis and autoimmune diseases. The present sequence  
 CC is the CpG oligonucleotide used to stimulate B cells.  
 XX  
 SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
 Query Match 74.7%; Score 14.2; DB 14; Length 20;  
 Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGGG 19  
 Db 2 GGGTCAACGTTTCAGGGGG 20  
 RESULT 39  
 ADC24305/c  
 ID ADC24305 standard; DNA; 39 BP.  
 XX  
 AC ADC24305;  
 XX  
 DT 18-DEC-2003 (first entry)  
 DE Primer, D75N, used to mutate the RTA (x)Asp(y) motif.  
 XX  
 KW Ricin; (x)Asp(y); primer; mutant; mutagenesis; ss;  
 KW vascular leak syndrome; VLS; cancer; immunotoxin; IT; cytokine; RTA;  
 KW aphasia; myalgia; fatigue; hypotension; rhabdomyolysis; MAb;  
 KW ribosome inactivating protein; RIP; vaccine; graft vs. host disease;  
 KW GVHD; non-Hodgkin's lymphoma; Hodgkin's lymphoma; cytostatic;  
 KW immunosuppressive; myeloma; tumour; monoclonal antibody.  
 XX  
 OS Synthetic.  
 OS Ricinus communis.  
 XX  
 PN US2003143193-A1.  
 XX  
 PD 31-JUL-2003.  
 XX  
 PF 29-OCT-2002; 2002US-00282935.  
 XX  
 PR 30-MAR-2000; 2000US-00538873.  
 PR 22-SEP-2000; 2000US-00668419.  
 XX  
 PA (VITE/) VITETTA E S.  
 PA (GHET/) GHETIE V F.  
 PA (SMAL/) SMALLSHAW J E.  
 PA (BALU/) BALUNA R G.  
 XX  
 PI Vitetta ES, Ghetie VF, Smallshaw JE, Baluna RG;  
 XX WPI; 2003-744874/70.  
 DR  
 XX New modified proteinaceous composition, useful for treating e.g., tumors.  
 PT  
 XX Example 2; SEQ ID NO 18; 52pp; English.  
 PS  
 XX The invention discloses a new modified proteinaceous composition which

CC comprises a protein having a (x)Asp(y) sequence and at least one amino  
 CC acid mutation that alters the ability of a (x)Asp(y) sequence to induce  
 CC Vascular Leak Syndrome (VLS). The present invention relates to the field  
 CC of physiology and cancer biology. The invention provides immunotoxins  
 CC (ITs) and cytokines, methods for producing them, which have been mutated  
 CC to lack amino acid sequences which induce VLS or other side effects. Also  
 CC claimed is a ricin A chain toxin (RTA) with a reduced ability to promote  
 CC toxicity in a patient, where at least one amino acid flanking the  
 CC (x)Asp(y) sequence is altered. The toxicity in a patient is further  
 CC defined as VLS, aphasia, myalgia, fatigue, hypotension or rhabdomyolysis.  
 CC ITs are hybrid molecules consisting of monoclonal antibodies (MAbs), or  
 CC other cell binding ligands, which are biochemically or genetically linked  
 CC to toxins, toxin subunits or ribosome inactivating proteins (RIPs) from  
 CC plants, fungi or bacteria. The modified proteinaceous composition is  
 CC useful for treating (e.g. vaccine) graft vs. host disease (GVHD), non-  
 CC Hodgkin's and Hodgkin's lymphoma, myeloma and some solid tumours. The  
 CC sequence presented is a primer which was used to mutate the RTA (x)Asp(y)  
 CC motif.  
 XX  
 SQ Sequence 39 BP; 10 A; 10 C; 8 G; 11 T; 0 U; 0 Other;  
 Query Match 73.7%; Score 14; DB 10; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GGTGACGTTTCAGGG 16  
 Db 26 GGTGACGTTTCAGGG 13  
 RESULT 40  
 AAC89992  
 ID AAC89992 standard; DNA; 30 BP.  
 XX  
 AC AAC89992;  
 XX  
 DT 08-MAR-2001 (first entry)  
 DE Rabbit tissue factor PCR primer #4.  
 XX  
 KW PCR primer; DNA polymerase; reverse transcriptase; rabbit; tissue factor;  
 KW ss.  
 XX  
 OS Oryctolagus cuniculus.  
 XX  
 PN WO200071739-A1.  
 XX  
 PD 30-NOV-2000.  
 XX  
 PF 19-MAY-2000; 2000WO-US013960.  
 XX  
 PR 22-MAY-1999; 99US-0135437P.  
 XX  
 PA (EPIC-) EPICENTRE TECHNOLOGIES CORP.  
 XX  
 PI Schanke JET;  
 XX  
 DR WPI; 2001-032045/04.  
 XX  
 PT Bacillus stearothermophilus template-dependent DNA polymerase for  
 PT preparing cDNA molecule from RNA template comprises reverse transcriptase  
 PT activity in the presence of magnesium ions and absence of manganese ions.  
 XX  
 PS Example 3; Page 22; 37pp; English.  
 CC The present invention relates to a purified thermostable template-  
 CC dependent DNA polymerase from Bacillus stearothermophilus comprising  
 CC reverse transcriptase (RT) activity in the presence of magnesium ions at  
 CC a concentration of 1 mM and in the substantial absence of manganese ions.  
 CC The DNA polymerase is useful for preparing cDNA molecules from RNA  
 CC templates and for amplifying a nucleic acid. The present sequence is a  
 CC PCR primer for rabbit tissue factor (RTF). This sequence was used to  
 CC demonstrate the activity of the DNA polymerase of the present invention

```

XX
SQ Sequence 30 BP; 6 A; 5 C; 12 G; 7 T; 0 U; 0 Other;
    Query Match      72.6%; Score 13.8; DB 4; Length 30;
    Best Local Similarity 88.2%; Pred. No. 5.9e+03;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 19
Db 13 GCGCATGTTTCAGGGGG 29

RESULT 41
ABZ43529/c
ID ABZ43529 standard; DNA; 41 BP.
XX AC ABZ43529;
XX
XX 26-JUN-2003 (first entry)
XX
XX Human SULTX3 gene polymorphic site, #313.
DE
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;
KW polymorphic site; drug evaluation; drug screening; genotyping;
KW genetic profiling; therapeutic customisation; adverse reaction;
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
OS
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH variation replace(21,T)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
PN
XX
XX 04-JUL-2002.
PD
XX
XX 27-DEC-2001; 2001WO-JP011592.
PF
XX
XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolising enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from ABZ43217-ABZ50887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphism data, particularly that relating to single nucleotide
XX polymorphisms (SNPs), may be used in studying the relationship between
XX DNA sequence variations and human diseases, conditions, and responses to
XX drugs. SNPs are also useful as polymorphism markers for discovering genes
XX that cause or exacerbate certain diseases. SNPs are particularly useful
XX in the above respects as they are stable in populations, occur
XX frequently, and have lower mutation rates than other genome variations
XX

Query Match      72.6%; Score 13.8; DB 6; Length 41;
Best Local Similarity 88.2%; Pred. No. 6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGG 17
Db 26 GGGGTGGGGTTCAGGGG 10

RESULT 42
ABZ49680/c
ID ABZ49680 standard; DNA; 41 BP.
XX AC ABZ49680;
XX
XX 26-JUN-2003 (first entry)
XX
XX Human SULTX3 gene polymorphic site, #642.
DE
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;
KW polymorphic site; drug evaluation; drug screening; genotyping;
KW genetic profiling; therapeutic customisation; adverse reaction;
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
OS
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH variation replace(21,T)
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
PN
XX
XX 04-JUL-2002.
PD
XX
XX 27-DEC-2001; 2001WO-JP011592.
PF
XX
XX 27-DEC-2000; 2000JP-00399443.
PR
XX 02-MAY-2001; 2001JP-00135256.
PR
XX 27-AUG-2001; 2001JP-00256862.
PR
XX
XX (RIKE ) RIKEN KK.
PA
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
PI WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
XX Claim 23; Page 69; 2785pp; English.
XX
XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolising enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from ABZ43217-ABZ50887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphism data, particularly that relating to single nucleotide
XX polymorphisms (SNPs), may be used in studying the relationship between
XX DNA sequence variations and human diseases, conditions, and responses to
XX drugs. SNPs are also useful as polymorphism markers for discovering genes
XX that cause or exacerbate certain diseases. SNPs are particularly useful
XX in the above respects as they are stable in populations, occur
XX frequently, and have lower mutation rates than other genome variations
XX

```

XX Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes  
 CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from ABZ43217-ABZ50887 using a  
 CC variety of detection assays, including hybridisation assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphism data, particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolising enzymes allows the customisation of  
 CC drug therapies based upon the genetic profile of individual patients.  
 CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy  
 XX  
 SQ Sequence 41 BP; 5 A; 23 C; 2 G; 11 T; 0 U; 0 Other;  
 Query Match 72.6%; Score 13.8; DB 6; Length 41;  
 Best Local Similarity 88.2%; Pred. No. 6e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGG 17  
 ||||| |||||  
 Db 26 GGGGTGGGGTTTCAGGGG 10  
 RESULT 43  
 AAD07150  
 ID AAD07150 standard; DNA; 22 BP.  
 XX  
 AC AAD07150;  
 XX  
 DT 06-AUG-2001 (first entry)  
 XX  
 DE PCR primer PR2-379 for improving priming site 19379 specificity.  
 XX  
 KW Priming site 19379; PCR; polymerase chain reaction; amplification;  
 KW branched modular primer; front module; FM; back module; BM; PCR primer;  
 KW proofreading; ss.  
 XX  
 OS Bacteriophage lambda.  
 XX  
 FH Key Location/Qualifiers  
 FT mutation 18  
 FT /\*tag= a  
 FT /mod\_base= i  
 FT mutation 19  
 FT /\*tag= b  
 FT /mod\_base= i  
 XX  
 FN US6235889-B1.  
 XX  
 PD 22-MAY-2001.

XX 08-MAR-1999; 99US-00264466.  
 XX  
 PR 20-DEC-1991; 91US-00810898.  
 PR 06-FEB-1995; 95US-00384699.  
 PR 06-MAY-1997; 97US-00852001.  
 XX (UYCH-) UNIV CHICAGO.  
 XX  
 PI Ulanovsky L;  
 XX  
 DR WPI; 2001-366426/38.  
 XX  
 DR New composition comprising front and back oligonucleotide modules, each  
 XX module has a stem and an arm segment with varying or constant sequences,  
 PT useful for amplifying nucleic acid segments such as in polymerase chain  
 PT reaction.  
 XX  
 XX Disclosure; Col 18; 32pp; English.  
 XX  
 XX The present invention relates to compositions for branched modular  
 CC primers used in methods for amplifying a nucleic acid segment. The  
 CC branched modular primer comprises of front and back oligonucleotide  
 CC modules. The front module (FM) and back module (BM) comprise of a stem  
 CC segment having a sequence that is the same from module to module and an  
 CC arm segment having a sequence that varies from module to module. The arm  
 CC of the back and front modules are annealed to a template which contains  
 CC the priming site. These modules are designed for priming sites in lambda  
 CC phage DNA. The composition is useful for amplifying a nucleic acid  
 CC segment, e.g. by polymerase chain reaction (PCR). The present sequence is  
 CC proofreading amplification primer PR2-379 used for improving  
 CC Bacteriophage lambda reverse priming site 19379 specificity  
 XX  
 SQ Sequence 22 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 2 Other;  
 Query Match 70.5%; Score 13.4; DB 4; Length 22;  
 Best Local Similarity 93.3%; Pred. No. 9.1e+03;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 TGACGTTTCAGGGGG 19  
 ||||| |||||  
 Db 2 TGACGTTTCAGGGGTG 16  
 RESULT 44  
 AAF74944  
 ID AAF74944 standard; DNA; 22 BP.  
 XX  
 AC AAF74944;  
 XX  
 DT 23-MAY-2001 (first entry)  
 XX  
 DE Bacteriophage lambda fragment PCR amplification primer SEQ ID NO:5.  
 XX  
 KW Bacteriophage lambda; PCR primer; amplification; genome mapping;  
 KW biomedical research; clinical diagnostic; ss.  
 XX  
 OS Bacteriophage lambda.  
 OS Synthetic.  
 XX  
 FN US6197556-B1.  
 XX  
 PD 06-MAR-2001.  
 XX  
 PF 06-MAY-1997; 97US-00852001.  
 XX  
 PR 20-DEC-1991; 91US-00810898.  
 PR 06-FEB-1995; 95US-00384699.  
 XX (UYCH-) UNIV CHICAGO.  
 XX  
 PI Ulanovsky L, Raja MC;  
 XX

DR WPI; 2001-256370/26.  
XX Amplifying a template nucleic acid segment, involves annealing a  
PT combination of several branched and/or covered oligonucleotide modules  
PT selected from a pre-synthesized library, to the template DNA.  
XX  
XX Disclosure; Col 18; 33pp; English.  
PS  
CC The present invention describes a method for amplifying a template  
CC nucleic acid segment (I), comprising annealing (i) to a branched primer  
CC having front (fow) and back oligonucleotide modules with arm segments  
CC complementary to a site in (I), extending the arm of fow to form an  
CC initial extension strand, annealing the strand to a reverse primer (RP),  
CC extending RP to form second initial extension strand, and amplifying the  
CC second strand. The method can be used for amplifying nucleic acid  
CC segments, useful in genome mapping, biomedical research and clinical  
CC diagnostics. The method eliminates the need for custom primer synthesis  
CC in methods to amplify nucleic acid segments. The modular combination of  
CC just a few oligonucleotides essentially mimics the performance of a  
CC conventional, custom-made primer by matching a sequence of a priming site  
CC in the template. AAF74940 to AAF74979 represent oligonucleotide sequences  
CC used in the exemplification of the present invention. N.B. Any Ns given  
CC in the oligonucleotide sequences represent inosine bases  
XX  
XX Sequence 22 BP; 4 A; 3 C; 8 G; 5 T; 0 U; 2 Other;  
SQ  
Query Match 70.5%; Score 13.4; DB 4; Length 22;  
Best Local Similarity 93.3%; Pred. No. 9.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 TGACGTTACAGGGGG 19  
DB 2 TGACGTTACAGGGGTG 16  
RESULT 45  
ADR99754  
ID ADR99754 standard; DNA; 30 BP.  
XX  
AC ADR99754;  
XX  
DT 02-DEC-2004 (first entry)  
DE  
DE Nucleic acid cysmr to generate evolved microorganisms.  
XX  
XX ss; microorganism evolution; metabolic pathway; metabolite;  
KW biotransformation; NADPH-dependent enzyme; nucleic acid metabolism;  
KW lipid metabolism; sugar metabolism.  
XX  
OS Unidentified.  
XX  
XX WO2004076659-A2.  
PN  
XX  
XX 10-SEP-2004.  
PD  
XX  
PF 17-FEB-2004; 2004WO-FR000354.  
PP  
XX 18-FEB-2003; 2003FR-00001924.  
PR 14-MAY-2003; 2003FR-00005768.  
PR 14-MAY-2003; 2003FR-00005769.  
PR 06-NOV-2003; 2003FR-00013054.  
XX  
XX (META-) METABOLIC EXPLORER.  
PA  
XX Chateau M, Gonzalez B, Meynial-Salles I, Soucaille PNP, Zink O;  
PI  
XX WPI; 2004-653418/63.  
DR  
XX New evolved microorganisms with altered metabolic pathways, useful e.g.  
PT for production of amino acids, are selected as mutants able to grow on  
PT defined media.  
XX  
XX Disclosure; SEQ ID NO 21; 113pp; French.  
PS

XX The invention relates to a method for preparing evolved microorganisms  
CC (A) with modified metabolic pathways comprising: (a) genetic modification  
CC of a microorganism to inhibit production or consumption of a metabolite  
CC when it is grown on a defined medium, thus affecting its ability to grow;  
CC (b) growing the modified organism in the defined medium so that evolution  
CC can occur, optionally with addition of a co-substrate to allow evolution;  
CC and (c) selecting as (A) cells able to grow on the medium, optionally in  
CC presence of co-substrate. The evolved microorganisms (A), or evolved  
CC proteins (I) expressed by them, are useful in biotransformation  
CC processes, especially those involving NADPH-dependent enzymes,  
CC particularly synthesis of amino acids (Met, Cys, Thr, Lys or Ile) but  
CC also synthesis of nucleic acids or lipids, and metabolism of sugars. (A)  
CC provide more efficient production of selected metabolites than parent  
CC strains. This sequence represents a nucleic acid molecule used in the  
CC method of the invention.  
XX  
XX Sequence 30 BP; 7 A; 8 C; 9 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 70.5%; Score 13.4; DB 13; Length 30;  
Best Local Similarity 93.3%; Pred. No. 9.2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGG 15  
DB 1 GGGGTGACGTTTCAGG 15  
RESULT 46  
ADM46519/c  
ID ADM46519 standard; RNA; 19 BP.  
XX  
AC ADM46519;  
XX  
DT 07-APR-2005 (first entry)  
DE  
DE Human survivin gene-specific siRNA sequence - SEQ ID 196.  
XX  
KW survivin; antisense therapy; gene silencing; cancer; cytostatic;  
KW breast tumor; colon tumor; prostate tumor; lung tumor; bladder tumor;  
KW ovary tumor; renal tumor; pancreas tumor; non-hodgkin lymphoma;  
KW hepatocellular carcinoma; ss; siRNA; short interfering RNA;  
KW RNA interference.  
XX  
OS Homo sapiens.  
XX  
XX WO2005002507-A2.  
PN  
XX 13-JAN-2005.  
PD  
XX  
XX 03-JUN-2004; 2004WO-US017490.  
PF  
XX 03-JUN-2003; 2003US-0475324P.  
PR 11-JUL-2003; 2003US-00618553.  
PR 13-APR-2004; 2004US-00823448.  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA (ELIL ) LILLY & CO ELI.  
XX  
XX Bhat B, Patet BK, Swayze E;  
PI  
XX WPI; 2005-081840/09.  
DR  
XX Novel double-stranded compound, modulating expression of human survivin,  
PT useful for treating condition associated with survivin expression or  
PT overexpression, such as breast cancer, colon cancer, lung cancer, bladder  
PT cancer.  
XX  
XX Example 25; SEQ ID NO 196; 159pp; English.  
PS  
XX The invention comprises dsRNA oligomeric sequences which are targeted to  
CC the human survivin gene. The dsRNA oligomeric compounds of the invention  
CC are useful for inhibiting expression of the human survivin gene, and can  
CC



CC be used in the treatment of cancer, such as: hepatocellular cancer,  
CC breast cancer, colon cancer, prostate cancer, lung cancer, bladder  
CC cancer, ovarian cancer, renal cancer, glioblastoma, pancreatic cancer and  
CC non-Hodgkin's lymphoma. The present nucleic acid represents a human  
CC survivin-specific siRNA sequence of the invention.  
XX  
SQ Sequence 19 BP; 4 A; 9 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 14; Length 19;  
Best Local Similarity 83.3%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGG 18  
|||:|:|:|:|:|:|:|:|:|  
Db 18 GGGGTGAACTTCAGGTGG 1

RESULT 47  
ADW46518  
ID ADW46518 standard; RNA; 19 BP.

XX ADW46518;

DT 07-APR-2005 (first entry)

DE Human survivin gene-specific siRNA sequence - SEQ ID 195.

XX survivin; antisense therapy; gene silencing; cancer; cytostatic;  
KW breast tumor; colon tumor; prostate tumor; lung tumor; bladder tumor;  
KW ovary tumor; renal tumor; pancreas tumor; non-hodgkin lymphoma;  
KW hepatocellular carcinoma; ss; siRNA; short interfering RNA;  
KW RNA interference.

XX Homo sapiens.

XX WO2005002507-A2.

XX 13-JAN-2005.

XX 03-JUN-2004; 2004WO-US017490.

XX 03-JUN-2003; 2003US-0475324P.

PR 11-JUL-2003; 2003US-00618553.

PR 13-APR-2004; 2004US-00823448.

XX (ISIS-) ISIS PHARM INC.

PA (ELIL) LILLY & CO ELI.

XX Bhat B, Patet BK, Swayze E;

XX WPI; 2005-081840/09.

XX Novel double-stranded compound, modulating expression of human survivin,  
PT useful for treating condition associated with survivin expression or  
PT overexpression, such as breast cancer, colon cancer, lung cancer, bladder  
PT cancer.

XX Example 25; SEQ ID NO 195; 159pp; English.

XX The invention comprises dsRNA oligomeric sequences which are targeted to  
CC the human survivin gene. The dsRNA oligomeric compounds of the invention  
CC are useful for inhibiting expression of the human survivin gene, and can  
CC be used in the treatment of cancer, such as: hepatocellular cancer,  
CC breast cancer, colon cancer, prostate cancer, lung cancer, bladder  
CC cancer, ovarian cancer, renal cancer, glioblastoma, pancreatic cancer and  
CC non-Hodgkin's lymphoma. The present nucleic acid represents a human  
CC survivin-specific siRNA sequence of the invention.

XX Sequence 19 BP; 3 A; 3 C; 9 G; 0 T; 4 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 14; Length 19;  
Best Local Similarity 66.7%; Pred. No. 1.1e+04;  
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGG 18  
|||:|:|:|:|:|:|:|:|:|  
Db 2 GGGGUGAACUCUCAGGGG 19

RESULT 48  
AAF99395

ID AAF99395 standard; DNA; 20 BP.

XX AAF99395;

DT 12-JUN-2001 (first entry)

DE Immunostimulatory nucleic acid #511.

XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
KW immunostimulatory; tumour; viral infection; bacterial infection;  
KW fungal infection; parasitic infection; cancer; asthma;  
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.

XX Synthetic.

XX WO200122972-A2.

XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-US026383.

XX 25-SEP-1999; 99US-0156113P.

PR 27-SEP-1999; 99US-0156135P.

PR 23-AUG-2000; 2000US-0227436P.

XX (IOWA) UNIV IOWA RES FOUND.

PA (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

XX WPI; 2001-273485/28.

XX Claim 101; Page 48; 338pp; English.

XX The present invention relates to a method for stimulating an immune  
CC response. The method comprises administering an immunostimulatory nucleic  
CC acid to a non-rodent subject in sufficient quantity to stimulate an  
CC immune response. The present sequence is one such immunostimulatory  
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma  
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
CC also useful for preventing cancer, asthma, infectious disease, allergy or  
CC immune deficiency. The present sequence can also be used to redirect a  
CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
CC present sequence may have a phosphorothioate backbone

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 69.5%; Score 13.2; DB 4; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.1e+04;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGG 18  
|||:|:|:|:|:|:|:|:|:|  
Db 3 GGCATGACGTTTCAGGGG 20

RESULT 49  
AAF99392

ID AAF99392 standard; DNA; 20 BP.  
 XX AAF99392;  
 AC AAF99392;  
 XX 12-JUN-2001 (first entry)  
 DT 12-JUN-2001 (first entry)  
 XX Immunostimulatory nucleic acid #508.  
 DE Immunostimulatory nucleic acid #508.  
 XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX Synthetic.  
 OS Synthetic.  
 PN WO200122972-A2.  
 XX WO200122972-A2.  
 PD 05-APR-2001.  
 XX 05-APR-2001.  
 XX 25-SEP-2000; 2000WO-US026383.  
 PF 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX Krieg AM, Schetter C, Vollmer J;  
 XX WPI; 2001-273485/28.  
 DR Vaccinating against tumors, infectious diseases, allergies and asthma  
 XX using immunostimulatory Py-rich and TG nucleic acids.  
 PS Claim 101; Page 48; 338pp; English.  
 CC The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 69.5%; Score 13.2; DB 4; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGG 18  
 |||||  
 Db 3 GGCATGACGTTTCGGGGG 20  
 RESULT 50  
 ABS78040  
 ID ABS78040 standard; DNA; 20 BP.  
 XX ABS78040;  
 AC ABS78040;  
 XX 13-DEC-2002 (first entry)  
 DT 13-DEC-2002 (first entry)  
 XX Angiogenesis inhibitory oligonucleotide #524.  
 DE Angiogenesis inhibitory oligonucleotide #524.  
 XX

KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 KW rubecsis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KW plaque neovascularisation; telangiectasia; haemophilic joint;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 XX Synthetic.  
 OS Synthetic.  
 PN WO200253141-A2.  
 XX WO200253141-A2.  
 PD 11-JUL-2002.  
 XX 11-JUL-2002.  
 PF 14-DEC-2001; 2001WO-US048458.  
 PR 14-DEC-2000; 2000US-0255534P.  
 XX (COLE-) COLEY PHARM GROUP INC.  
 PA Bratzler RL;  
 PI WPI; 2002-566690/60.  
 DR Inhibiting angiogenesis in a subject, involves administering at least one  
 XX antiangiogenic nucleic acid molecule to the subject.  
 PT Claim 2; Page 28; 276pp; English.  
 XX The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubecsis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma, and  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 69.5%; Score 13.2; DB 6; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+04;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGG 18  
 |||||  
 Db 3 GGCATGACGTTTCGGGGG 20

Search completed: February 15, 2006, 18:06:56  
 Job time : 153.207 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:07:43 ; Search time 1263.74 Seconds  
(without alignments)  
703.434 Million cell updates/sec

Title: US-09-669-187A-80

Perfect score: 19  
Sequence: 1 ggggtgacgttcaggggggg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database :

EST.\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_est3.\*
- 4: gb\_btc.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_est7.\*
- 9: gb\_gss1.\*
- 10: gb\_gss2.\*
- 11: gb\_gss3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.2	74.7	50	11	CR061079 Forward s
C 2	13.8	72.6	32	2	BF568357
C 3	13.2	69.5	46	9	A2838956
C 4	12.8	67.4	41	10	BX121477
C 5	12.6	66.3	35	7	CO411608
C 6	12.6	66.3	44	10	AG215101
C 7	12.2	64.2	28	1	AA986325
C 8	12.2	64.2	37	9	A2616333
C 9	12.2	64.2	42	9	CC027439
C 10	12.2	64.2	45	9	A2307335
C 11	11.8	62.1	19	8	A2768418
C 12	11.8	62.1	29	8	AX012159
C 13	11.8	62.1	34	3	BJ033509
C 14	11.8	62.1	41	9	A2331072
C 15	11.8	62.1	50	2	BG272395
C 16	11.6	61.1	20	9	AQ074235
C 17	11.6	61.1	25	9	AQ231293
C 18	11.6	61.1	28	1	A1497442
C 19	11.6	61.1	28	10	CL686485
C 20	11.6	61.1	29	6	CD029249
C 21	11.6	61.1	30	9	A2783946
C 22	11.6	61.1	34	2	B1259582

C 96	11	57.9	49	10	CZ906497	CZ906497 4011001A0	169	10.2	53.7	46	6	CB884957	CB884957 Mai17079 H
C 97	11	57.9	50	1	AUI03929	AUI03929 AUI03929	170	10.2	53.7	46	10	CG671946	CG671946 RRO174 Ba
C 98	11	57.9	50	1	AUI04338	AUI04338 AUI04338	C 171	10.2	53.7	47	1	AA972457	AA972457 op41c04.s
C 99	11	57.9	50	1	AUI05978	AUI05978 AUI05978	C 172	10.2	53.7	47	8	R08290	R08290 yf18e09.s1
C 100	11	57.9	50	1	AUI05979	AUI05979 AUI05979	C 173	10.2	53.7	47	9	BZ286964	BZ286964 SALK_0203
C 101	11	57.9	50	1	AUI07236	AUI07236 AUI07236	C 174	10.2	53.7	48	10	AL760394	AL760394 Arabidops
C 102	11	57.9	50	1	CZ016473	CZ016473 CH240_500	C 175	10.2	53.7	49	1	AW772664	AW772664 xn02b05.y
C 103	11	57.9	50	10	CG987794	CG987794 Reverse s	C 176	10.2	53.7	49	8	H15861	H15861 ym21e03.r1
C 104	10.8	56.8	36	3	BJ060990	BJ060990 BJO60990	C 177	10.2	53.7	49	9	BZ379376	BZ379376 SALK_1132
C 105	10.8	56.8	43	5	C00370	C00370 HUMGS000366	C 178	10.2	53.7	49	11	CR396950	CR396950 Arabidops
C 106	10.8	56.8	46	8	D26039	D26039 HUMGS03662	C 179	10.2	53.7	50	1	AUI02339	AUI02339 AUI02339
C 107	10.8	56.8	46	8	N44233	N44233 yv31c08.r1	C 180	10.2	53.7	50	1	AUI04853	AUI04853 AUI04853
C 108	10.8	56.8	47	11	TA195A08P	TA195A08P T. brucei	C 181	10.2	53.7	50	1	AUI04854	AUI04854 AUI04854
C 109	10.8	56.8	50	1	AUI04145	AUI04145 AUI04145	C 182	10	52.6	19	10	CM020460	CM020460 GC0725.TI
C 110	10.8	56.8	50	1	AUI07408	AUI07408 AUI07408	C 183	10	52.6	23	9	AZ653869	AZ653869 IM0527D14
C 111	10.8	56.8	50	1	AUI07418	AUI07418 AUI07418	C 184	10	52.6	24	9	AZ314798	AZ314798 IM0031G16
C 112	10.8	56.8	50	3	BJ077206	BJ077206 BJ077206	C 185	10	52.6	25	1	AA871952	AA871952 vq43B09.r
C 113	10.6	55.8	22	1	AI521380	AI521380 t05G01.x	C 186	10	52.6	25	1	AI363940	AI363940 qw34b12.x
C 114	10.6	55.8	25	1	AA878803	AA878803 of86e04.s	C 187	10	52.6	25	1	AI445419	AI445419 t134b12.x
C 115	10.6	55.8	25	9	AZ828517	AZ828517 2M0105J02	C 188	10	52.6	25	9	AZ462642	AZ462642 IM0269M09
C 116	10.6	55.8	25	9	AZ981731	AZ981731 2M0262G13	C 189	10	52.6	25	9	AZ603284	AZ603284 IM0422E01
C 117	10.6	55.8	25	10	CG729138	CG729138 1119108C1	C 190	10	52.6	25	9	AZ794596	AZ794596 2M0048M20
C 118	10.6	55.8	30	9	AZ777592	AZ777592 2M0012A07	C 191	10	52.6	25	9	AZ802728	AZ802728 2M0061B18
C 119	10.6	55.8	31	1	AI589323	AI589323 tr61a06.x	C 192	10	52.6	25	11	CZ909972	CZ909972 4018012F0
C 120	10.6	55.8	32	10	CZ915094	CZ915094 4013010A0	C 193	10	52.6	25	11	TA42C02Q	TA42C02Q T. brucei
C 121	10.6	55.8	32	10	AG224362	AG224362 Lotus cor	C 194	10	52.6	26	10	CL650847	CL650847 PRI0110C
C 122	10.6	55.8	33	9	AZ628058	AZ628058 1M0476122	C 195	10	52.6	26	1	AA903336	AA903336 ok45G12.s
C 123	10.6	55.8	34	9	AZ431906	AZ431906 1M0217A21	C 196	10	52.6	28	9	AZ986927	AZ986927 2M0269N13
C 124	10.6	55.8	37	1	AI626589	AI626589 ic05a12.x	C 197	10	52.6	28	10	CZ917723	CZ917723 4021006G0
C 125	10.6	55.8	37	1	AW250642	AW250642 2822070.5	C 198	10	52.6	29	9	AZ610133	AZ610133 IM0435F16
C 126	10.6	55.8	37	7	CR762735	CR762735 DKFPz469H	C 199	10	52.6	29	10	CL653182	CL653182 PRI0116d
C 127	10.6	55.8	37	9	AZ501429	AZ501429 1M0340113	C 200	10	52.6	30	2	BI223044	BI223044 602943380
C 128	10.6	55.8	40	1	AA876140	AA876140 ob93h05.s	C 201	10	52.6	30	5	BX624507	BX624507 BX624507
C 129	10.6	55.8	40	1	AA878861	AA878861 of84f09.s	C 202	10	52.6	30	9	AZ664115	AZ664115 1M0544D10
C 130	10.6	55.8	40	9	AZ806060	AZ806060 2M0067E20	C 203	10	52.6	31	1	AA909238	AA909238 0108C09.s
C 131	10.6	55.8	42	8	R97402	R97402 yq53b07.s1	C 204	10	52.6	31	1	AA910965	AA910965 ok67a10.s
C 132	10.6	55.8	43	10	BX141236	BX141236 Danio rer	C 205	10	52.6	31	1	AA933748	AA933748 ct65e02.s
C 133	10.6	55.8	45	3	BJ015280	BJ015280 GTJ015280	C 206	10	52.6	31	1	AI620715	AI620715 tu96b09.x
C 134	10.6	55.8	46	1	AI355812	AI355812 BJ94h07.x	C 207	10	52.6	31	1	AI679568	AI679568 tu64g06.x
C 135	10.6	55.8	46	1	AI677817	AI677817 wC80G04.x	C 208	10	52.6	31	1	AI690328	AI690328 t215G12.x
C 136	10.6	55.8	46	1	AI809473	AI809473 wh76C10.x	C 209	10	52.6	31	9	AZ487534	AZ487534 1M0317F14
C 137	10.6	55.8	46	1	AV954968	AV954968 AV954968	C 210	10	52.6	32	2	BG419594	BG419594 602451806
C 138	10.6	55.8	48	9	AZ816555	AZ816555 2M0085B21	C 211	10	52.6	32	10	BX947451	BX947451 Arabidops
C 139	10.6	55.8	48	10	AJ588765	AJ588765 Arabidops	C 212	10	52.6	33	9	AZ961620	AZ961620 2M0230E09
C 140	10.6	55.8	49	8	CV836113	CV836113 IDOACC2BE	C 213	10	52.6	33	11	DME545578	DME545578 Drosophil
C 141	10.6	55.8	50	1	AUI02260	AUI02260 AUI02260	C 214	10	52.6	34	1	AI355502	AI355502 qul15D02.x
C 142	10.6	55.8	50	1	AUI03955	AUI03955 AUI03955	C 215	10	52.6	34	8	N73483	N73483 za05h02.s1
C 143	10.6	55.8	50	1	AUI04957	AUI04957 AUI04957	C 216	10	52.6	34	9	AZ659789	AZ659789 1M0537P19
C 144	10.6	55.8	50	1	AUI04960	AUI04960 AUI04960	C 217	10	52.6	34	10	CZ442563	CZ442563 1BB10B03.
C 145	10.6	55.8	50	1	AUI04965	AUI04965 AUI04965	C 218	10	52.6	35	9	AZ469734	AZ469734 1M0283J19
C 146	10.6	55.8	50	1	AUI05099	AUI05099 AUI05099	C 219	10	52.6	35	9	AZ976182	AZ976182 2M0251G01
C 147	10.6	55.8	50	1	AUI06995	AUI06995 AUI06995	C 220	10	52.6	36	9	AZ867309	AZ867309 2M0178B10
C 148	10.4	54.7	45	10	CZ468531	CZ468531 c03247-5p	C 221	10	52.6	36	11	TA242812Q	TA242812Q T. brucei
C 149	10.4	54.7	46	1	AA416444	AA416444 vdl1c01.s	C 222	10	52.6	37	1	AI357425	AI357425 qu01c09.x
C 150	10.4	54.7	50	11	CR028335	CR028335 Forward s	C 223	10	52.6	37	2	AI499210	AI499210 ct08e02.x
C 151	10.2	53.7	30	9	AZ602612	AZ602612 1M0421O22	C 224	10	52.6	37	2	BI080927	BI080927 602878838
C 152	10.2	53.7	33	9	AQ026144	AQ026144 1(2).s1878	C 225	10	52.6	37	9	AZ871856	AZ871856 2M0184O24
C 153	10.2	53.7	34	1	AI590768	AI590768 tw25b08.x	C 226	10	52.6	37	10	CL658108	CL658108 PRI0130B
C 154	10.2	53.7	34	9	AZ493518	AZ493518 1M0328D15	C 227	10	52.6	37	11	DR11K9T	DR11K9T Danio rer
C 155	10.2	53.7	34	9	BZ661946	BZ661946 Pan trogl	C 228	10	52.6	38	2	BE261178	BE261178 601152951
C 156	10.2	53.7	34	10	AG201486	AG201486 Pan trogl	C 229	10	52.6	38	3	BI553849	BI553849 603190807
C 157	10.2	53.7	35	9	AZ665829	AZ665829 1M0547A03	C 230	10	52.6	39	2	BG973894	BG973894 602843523
C 158	10.2	53.7	35	2	BF134431	BF134431 601784827	C 231	10	52.6	39	9	AZ640839	AZ640839 1M0503L05
C 159	10.2	53.7	37	9	AZ455844	AZ455844 1M0258G21	C 232	10	52.6	39	9	AZ997025	AZ997025 2M0283119
C 160	10.2	53.7	37	10	CZ487169	CZ487169 f04630-3p	C 233	10	52.6	39	10	AJ593066	AJ593066 Arabidops
C 161	10.2	53.7	37	10	BX949677	BX949677 Arabidops	C 234	10	52.6	40	1	AA931142	AA931142 o070b12.s
C 162	10.2	53.7	38	10	CZ473438	CZ473438 d03575-3p	C 235	10	52.6	40	1	AI613303	AI613303 cy35h11.x
C 163	10.2	53.7	40	1	AA023582	AA023582 mh78d04.r	C 236	10	52.6	40	1	AI684941	AI684941 wa74d06.x
C 164	10.2	53.7	40	10	CZ194944	CZ194944 PST14789-	C 237	10	52.6	40	1	AI745660	AI745660 tr24e02.x
C 165	10.2	53.7	41	9	AZ588779	AZ588779 1M0397P15	C 238	10	52.6	40	1	AV833488	AV833488 AV833488
C 166	10.2	53.7	42	9	BF139151	BF139151 601784191	C 239	10	52.6	40	7	CO258621	CO258621 VRK352.Vi
C 167	10.2	53.7	44	1	AA792171	AA792171 vn71d02.r	C 240	10	52.6	40	10	BX662712	BX662712 Arabidops
C 168	10.2	53.7	45	3	BI663358	BI663358 603287416	C 241	10	52.6	41	1	AV855184	AV855184 AV855184

```

242 10 52.6 41 3 BI549061 603197039
243 10 52.6 41 3 BI598393 603246901
244 10 52.6 41 3 BI669448 603294141
245 10 52.6 41 9 A2441689 1M0233K24
246 10 52.6 42 1 AV833221 AV833221
247 10 52.6 43 1 A1445618 CJ08D03.X
248 10 52.6 43 1 A1583078 TS03G05.X
249 10 52.6 43 1 A1801617 TG91G08.X
250 10 52.6 43 9 A2473927 1M0290M03
251 10 52.6 44 9 A2323644 1M0045L12
252 10 52.6 44 10 CW989647 AN0924 Sa
253 10 52.6 44 10 CW990600 BA0473 Sa
254 10 52.6 44 10 EX895201 Arabidops
255 10 52.6 44 10 CL246506 01S0569-0
256 10 52.6 45 3 BJ034331 BJ034331
257 10 52.6 45 10 CL301892 P017F01 G
258 10 52.6 46 1 AA863391 oh42d05.s
259 10 52.6 46 1 AA604908 no85d08.s
260 10 52.6 46 2 BF164185 601773130
261 10 52.6 46 6 CA501354 WHE40332.E
262 10 52.6 46 7 CN601149 EG-M01_00
263 10 52.6 46 10 CL302043 P009E05 G
264 10 52.6 47 3 BJ060786 BJ060786
265 10 52.6 47 8 CX006690 io24b07.b
266 10 52.6 47 11 TAI95B04Q
267 10 52.6 48 8 H44578
268 10 52.6 48 10 CL528695
269 10 52.6 48 10 CL639450 Q007E04 G
270 10 52.6 49 1 AA934654 o071e06.s
271 10 52.6 49 1 A1119820 uc21b2.f
272 10 52.6 49 1 AA133422 z118b2.x
273 10 52.6 49 1 A1444171 fB43b07.Y
274 10 52.6 49 1 A1472245 tJ86G10.X
275 10 52.6 49 1 A1744224 tr07G01.X
276 10 52.6 49 1 AA232796 zK47a03.X
277 10 52.6 49 9 CC060036 EY00609-5
278 10 52.6 49 9 CC328433 XN471 Bay
279 10 52.6 49 9 CC455581 SALK_0841
280 10 52.6 50 1 AUI03170 AUI03170
281 10 52.6 50 1 AUI03171 AUI03171
282 10 52.6 50 1 AUI04852 AUI04852
283 10 52.6 50 1 AUI04855 AUI04855
284 10 52.6 50 1 AUI06631 AUI06631
285 10 52.6 50 1 AUI06632 AUI06632
286 10 52.6 50 1 AUI07363 AUI07363
287 10 52.6 50 1 AUI07364 AUI07364
288 10 52.6 50 1 AUI07565 AUI07565
289 10 52.6 50 9 AF039758 AF039758
290 10 52.6 50 9 AZ366252 1M0115H16
291 10 52.6 50 10 CW117680 104_493_1
292 9.8 51.6 19 9 AZ500053 1M0338M08
293 9.8 51.6 24 9 AZ442046 1M0234J06
294 9.8 51.6 24 9 AZ617422 1M0448M12
295 9.8 51.6 25 9 AZ793265 2M0046D21
296 9.8 51.6 25 10 CZ486145 f03568-Sp
297 9.8 51.6 27 9 AZ763057 1M0558C22
298 9.8 51.6 31 1 A1478693 tm01C06.X
299 9.8 51.6 33 1 A1046875 uh55f09.X
300 9.8 51.6 33 2 BI089017 602853566

ALIGNMENTS

RESULT 1
CR061079/c 50 bp DNA linear GSS 05-JUL-2004
LOCUS Forward strand read from insert in 3'HPRT insertion targeting and
DEFINITION chromosome engineering clone MHPp308j13, genomic survey sequence.
ACCESSION CR061079
VERSION CR061079.1 GI:49794551
KEYWORDS GSS; genome survey sequence; MICER.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Adams,D.O., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK http://www.sanger.ac.uk/MICER
FEATURES
source
location/Qualifiers
1..50
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone_lib="MHPp308j13"
/clone_lib="MHPp"

ORIGIN
Query Match 74.7%; Score 14.2; DB 11; Length 50;
Best Local Similarity 84.2%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTCCAGGGGG 19
Dd 35 GGGGTGAAGGCCAGGGGG 17

RESULT 2
BF568357/c 32 bp mRNA linear EST 12-DEC-2000
LOCUS 602184546F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300571 5',
DEFINITION mRNA sequence.
ACCESSION BF568357
VERSION BF568357.1 GI:11641737
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1159 row: 1 column: 12
High quality sequence stop: 32.
FEATURES
source
location/Qualifiers
1..32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4300571"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_42"

notes=Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit

```

(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library. | "

```

ORIGIN
Query Match      72.6%; Score 13.8; DB 2; Length 32;
Best Local Similarity 88.2%; Pred. No. 4.7e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 19
    |||||
Db 23 GGTGACGTTTCAGGGGG 7

RESULT 3
AZ838956
LOCUS      46 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION      2M0134D20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0134D20 R, genomic survey sequence.
ACCESSION      AZ838956
VERSION      AZ838956.1 GI:13008864
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 46)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0134 row: D column: 20
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 46.
FEATURES
source      1..46
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC2M0134D20"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /notes="vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWP42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to

```

## ORIGIN

```

Query Match      69.5%; Score 13.2; DB 9; Length 46;
Best Local Similarity 83.3%; Pred. No. 9.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 18
    |||||
Db 9 GGGTGACGTTTCAGGGGG 26

```

## RESULT 4

```

BX121477/c
LOCUS      41 bp      DNA      linear      GSS 13-MAR-2003
DEFINITION      Danio rerio genomic clone DKEY-62P9, genomic survey sequence.
ACCESSION      BX121477
VERSION      BX121477.1 GI:27952401
KEYWORDS      GSS.
SOURCE      Danio rerio (zebrafish)
ORGANISM      Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE      1 (bases 1 to 41)
AUTHORS      Humphray,S.J., Huckle,E. and Durham,J.L.
TITLE      Direct Submission
JOURNAL      Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 62P9. 62P9 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES
source      1..41
            /organism="Danio rerio"
            /mol_type="genomic DNA"
            /db_xref="taxon:7955"
            /clone="DKEY-62P9"
            /tissue_type="Testis"
            /note="vector pindigoBAC-536"

```

## ORIGIN

```

Query Match      67.4%; Score 12.8; DB 10; Length 41;
Best Local Similarity 82.4%; Pred. No. 1.5e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTGACGTTTCAGGGGG 18
    |||||
Db 39 GGGGNGCGTTCTCGGGG 23

```

## RESULT 5

```

CO411608/c
LOCUS      35 bp      mRNA      linear      EST 02-JUL-2004
DEFINITION      EST841993 Sequencing ESTs from loblolly pine embryos Pinus taeda
cDNA clone P1AM51 5' end, mRNA sequence.
ACCESSION      CO411608
VERSION      CO411608.1 GI:49627856
KEYWORDS      EST.
SOURCE      Pinus taeda (loblolly pine)
ORGANISM      Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE      1 (bases 1 to 35)
AUTHORS      Buell,C.R., Zheng,L., Cowles,A. and Cairney,J.
TITLE      Sequencing of ESTs from loblolly pine embryonic libraries
JOURNAL      Unpublished (2004)
COMMENT      Contact: C. Robin Buell
Plant Genomics Group

```

adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: rbuell@tigr.org  
This clone is available through TIGR. Please contact pine@tigr.org  
for further information  
Seq primer: ATT TAG GTG ACA CTA TAG.  
Location/Qualifiers

## FEATURES

source

```

1. 35
/organism="Pinus taeda"
/mol_type="mRNA"
/Cultivar="7-56 mother tree, open-pollinated tree from,
Lyons, Georgia, USA"
/db_xref="taxon:3352"
/clone="PIALM51"
/lab_host="E.coli DH10B-Tona"
/clone_lib="Sequencing ESTs from loblolly pine embryos"
/note="Organ: Zygotic Embryo and Megagametophyte, Somatic
Embryo; Vector: pCMV-SPORT 6.1; Site_1: NotI; Site_2:
EcoRV; tissue: Whole megagametophytes isolated from pine
seeds; Whole embryos excised from these megagametophytes,
whole somatic embryos and suspensor tissue from tissue
culture, isolated from cell line A12. Pooled RNA from
zygotic embryos, megagametophytes, and somatic embryos was
used for library construction. Pine cones were harvested
weekly from open-pollinated 7-56 mother trees, collections
occurred from 7/01/02 until 10/15/02. Whole
megagametophytes were first isolated from pine seeds, and
whole embryos excised from these megagametophytes each was
flash frozen. Embryo development was assessed using the
system of Pullman et al (Pullman GS, Johnson S, Peter G,
Carney J, Xu N. 2003. Loblolly Pine somatic
embryogenesis: development of a maturation medium and
resulting embryo quality. Plant Cell Reports 21:747-758
(http://link.springer.de/link/service/journals/00299/conte
nts/03/00586/). For photographs see Ciavatta et al 2001.
(Ciavatta VT, Morillon R, Pullman GS, Chrispeels M,
Carney J. 2001. An aquaglyceroporin is abundantly
expressed early in the development of the suspensor and
the embryo proper of loblolly pine (Pinus taeda L.). Plant
Physiol. 127: 1556-1567
(http://www.plantphysiol.org/cgi/content/full/127/4/1556))
"
```

## ORIGIN

```

Query Match      66.3%; Score 12.6; DB 7; Length 35;
Best Local Similarity 78.9%; Pred. No. 1.8e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```

Qy 1 GGGGTGACGTTACAGGGGG 19
||||| ||| |||||
Db 27 GGGGGGAATTTAGGGGG 9
```

## RESULT 6

AG215101

LOCUS

```

DEFINITION      44 bp DNA linear GSS 03-SEP-2002
Drosophila melanogaster DNA, clone:NP6643-5-1, flanking P[GawB]
transposon insertion, genomic survey sequence.
```

ACCESSION

AG215101

VERSION

AG215101.1 GI:22762101

KEYWORDS

GSS.

SOURCE

Drosophila melanogaster (fruit fly)

ORGANISM

```

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hemiptera; Drosophilidae; Drosophila.
1
Hayaishi, S., Ito, K., Sado, Y., Taniguchi, M., Akimoto, A., Takeuchi, H.,
Aigaki, T., Matsuzaki, F., Nakagoshi, H., Tanimura, T., Ueda, R.,
Uemura, T., Yoshihara, M. and Goto, S.
GTDDB, a database compiling expression patterns and molecular
locations of a collection of Gal4 enhancer traps
Genesis (2002) In press
```

## REFERENCE

AUTHORS

## REFERENCE

2 (bases 1 to 44)

Hayaishi, S.

Direct Submission

JOURNAL

Submitted (27-AUG-2002) Shigeo Hayaishi, RIKEN Center for  
Developmental Biology, Laboratory for Morphogenetic Signaling,  
Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan  
(E-mail: shayaishi@cdb.riken.go.jp, Tel: 81-78-301-3184,  
Fax: 81-78-301-3183)

This clone was isolated from genomic DNA flanking an insertion of  
the P element vector P[GawB] of a *Drosophila* strain.

## FEATURES

source

```

1. 44
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="NP6643"
/db_xref="taxon:7227"
/chromosome="3"
/map="64P2"
/clone="NP6643-5-1"
/note="flanking P[GawB] transposon insertion"
```

## ORIGIN

```

Query Match      66.3%; Score 12.6; DB 10; Length 44;
Best Local Similarity 78.9%; Pred. No. 1.8e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Qy 1 GGGGTGACGTTACAGGGGG 19

||||| ||| |||||

Db 2 GGGGGGCGTGCAGCGGG 20

## RESULT 7

AA986325/c

LOCUS

```

DEFINITION      28 bp mRNA linear EST 28-MAY-1998
uc79412.x1 Sugano mouse kidney mKia Mus musculus cDNA clone
IMAGE:1431863 3' similar to TR:014742 014742 NUCLEOLAR PROTEIN. ;,
mRNA sequence.
```

ACCESSION

AA986325

VERSION

AA986325.1 GI:3167649

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

```

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
```

The WashU-HMI Mouse EST Project

Unpublished (1996)

JOURNAL

COMMENT

Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School  
of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:915931

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: primer name ambiguous

High quality sequence stop: 1.

Location/Qualifiers

source

1. 28

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL"

/db\_xref="taxon:10090"

```

/clone="IMAGE:1431863"
/sex="female"
/lab_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse kidney mkia"
/notes="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGG); Site 2: DraIII (CAACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCGTCTCTAAAGCTGG and 3' end
primer CGACCTGCAGCTCAGACACA."

```

## ORIGIN

```

Query Match      64.2%; Score 12.2; DB 1; Length 28;
Best Local Similarity 82.4%; Pred. NO. 2.8e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTACAGGG 17
    |||||
Db 22 GGTGTGAGTTCAGTGG 6

```

## RESULT 8

```

AZ616333
LOCUS
DEFINITION
M0446A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0446A08 F, genomic survey sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE

```

```

ORGANISM
Mus musculus (house mouse)

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE
1 (bases 1 to 37)

```

```

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

```

```

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

```

JOURNAL
Unpublished (2000)

```

```

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center

```

```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

```

Tel: 801 585 5606

```

```

Fax: 801 585 7177

```

```

Email: ddunn@genetics.utah.edu

```

```

Insert Length: 10000 Std Error: 0.00

```

```

Plate: 0446 Row: A Column: 08

```

```

Seq primer: CGTGTAAACGACGCGCAGT

```

```

Class: plasmid ends

```

```

High quality sequence stop: 37.

```

## FEATURES

```

source

```

```

1..37
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0446A08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

```

```

/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

## ORIGIN

```

Query Match      64.2%; Score 12.2; DB 9; Length 37;
Best Local Similarity 82.4%; Pred. NO. 2.9e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTACAGGG 17
    |||||
Db 7 GGCGTACCGTTCAGGG 23

```

## RESULT 9

```

CC027439/c

```

```

LOCUS
DEFINITION
3591_1_5_1_D10.1EL_Y_1 3591 - RescueMu Grid P Zea mays genomic,
genomic survey sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE

```

```

ORGANISM
Zea mays

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

```

```

1 (bases 1 to 42)

```

```

AUTHORS
Walbot,V.

```

```

TITLE
Maize genomic sequences found using engineered RescueMu transposon

```

```

JOURNAL
Unpublished (2001)

```

```

COMMENT
Contact: Walbot V
Department of Biological Sciences

```

```

Stanford University
855 California Ave, Palo Alto, CA 94304, USA

```

```

Tel: 650 723 2227

```

```

Fax: 650 725 8221

```

```

Email: walbot@stanford.edu

```

```

Very probable ligation site of ends cut by single endonuclease.

```

```

Reverse complemented post-ligation sequence from source sequence.

```

```

Plate: 3591 1 5 1 row: 4

```

```

Class: transposon-tagged.

```

```

Location/Qualifiers

```

```

1..42

```

```

/organism="Zea mays"

```

```

/mol_type="genomic DNA"

```

```

/cultivar="mixed background W23/A188/B73/K55"

```

```

/db_xref="taxon:4577"

```

```

/tissue_type="leaf"

```

```

/dev_stage="adult"

```

```

/lab_host="DH10B"

```

```

/clone_lib="3591 - RescueMu Grid P"

```

```

/notes="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription

```



units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid p was grown at Molokai in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## ORIGIN

Query Match 64.2%; Score 12.2; DB 9; Length 42;  
Best Local Similarity 82.4%; Pred. No. 2.9e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGTGACGTTTCAGGGG 17  
||||| ||||| ||||| |||||  
Db 17 GGGTCGCGTCGACGGGG 1

## RESULT 10

AZ307335/c  
LOCUS  
DEFINITION MW008K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M008K13 R, genomic survey sequence.

ACCESSION AZ307335  
VERSION AZ307335.1 GI:10346236  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 45)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0008 row: K column: 13

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 45.

## FEATURES

## source

1. .45  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M008K13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gil4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 64.2%; Score 12.2; DB 9; Length 45;  
Best Local Similarity 82.4%; Pred. No. 2.9e+05;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGG 17  
||||| ||||| ||||| |||||  
Db 20 GGGGGAATGTTTCAGGGG 4

## RESULT 11

AZ768418  
LOCUS  
DEFINITION MW0568H23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0568H23 F, genomic survey sequence.

ACCESSION AZ768418  
VERSION AZ768418.1 GI:12887506  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0568 row: H column: 23

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

## source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0568H23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 62.1%; Score 11.8; DB 9; Length 19;  
Best Local Similarity 86.7%; Pred. No. 4.3e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGG 15  
||||| |||||  
Db 4 GGGGTGAGGTTCTCG 18

## RESULT 12

CX012159  
LOCUS  
DEFINITION i057g07.b1 Whole Heart Library (DOGE5T5) Canis familiaris cDNA,  
mRNA sequence.  
ACCESSION CX012159.1 GI:56394570  
VERSION CX012159  
KEYWORDS Canis familiaris (dog)  
SOURCE Canis familiaris  
ORGANISM Canis familiaris

1 (bases 1 to 29)  
Baliya, V.S., Nascimento, L.U. and McCombie, W.R.  
ESTs from Canis familiaris whole heart (dog)  
Unpublished (2004)  
Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mccombie@cshl.org.

## REFERENCE

1 (bases 1 to 29)  
Baliya, V.S., Nascimento, L.U. and McCombie, W.R.  
ESTs from Canis familiaris whole heart (dog)  
Unpublished (2004)  
Contact: W. Richard McCombie  
Lita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mccombie@cshl.org.

## FEATURES

source  
1..29  
Location/Qualifiers  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/sex="Unknown"  
/dev\_stage="3 month old normal canine"  
/lab\_host="XL10 Gold"  
/clone\_lib="Whole Heart Library (DOGE5T5)"  
/notes="Organ: Heart; Vector: pBluescript II SK; Site 1:  
ECORI; Site 2: XhoI; Library constructed using pBluescript  
XR kit from Stratagene. Cloned cDNA was size selected  
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and  
Medical Genetics, School of Veterinary Medicine,  
University of Pennsylvania, 3800 Spruce Street,  
Philadelphia, PA 19104-6051"

## ORIGIN

Query Match 62.1%; Score 11.8; DB 8; Length 29;  
Best Local Similarity 86.7%; Pred. No. 4.4e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTGACGTTTCAGGGG 18  
||||| |||||  
Db 6 GTGATGTGCAGGGG 20

## RESULT 13

BJ035059

LOCUS  
DEFINITION BJ035059 NTBB Mochii normalized Xenopus neurula library Xenopus  
laevis cDNA clone XL031m15 5', mRNA sequence.  
ACCESSION BJ035059  
VERSION BJ035059.1 GI:17414312  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
REFERENCE 1 (bases 1 to 34)  
AUTHORS Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and  
Kohata, Y.

TITLE Expressed genes in X. laevis embryo  
JOURNAL Unpublished (2001)  
COMMENT Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp  
The information of this clone is available through the following  
URL:  
http://xenopus.nibb.ac.jp.

## FEATURES

source  
1..34  
Location/Qualifiers  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="XL031m15"  
/tissue\_type="whole embryo"  
/dev\_stage="stage 15"  
/clone\_lib="NIBB Mochii normalized Xenopus neurula  
library"

## ORIGIN

Query Match 62.1%; Score 11.8; DB 3; Length 34;  
Best Local Similarity 86.7%; Pred. No. 4.5e+05;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGCTGACGTTTCAGG 16  
||||| |||||  
Db 17 GGCTAACGTTTCAGG 31

## RESULT 14

AZ331072/c  
LOCUS  
DEFINITION AZ331072 41 bp DNA linear GSS 29-SEP-2000  
clone UUGCLM0056A13 R, genomic survey sequence.  
ACCESSION AZ331072.1 GI:10393242  
VERSION AZ331072.1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Muridae; Mus.  
REFERENCE 1 (bases 1 to 41)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D. Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

```

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: A column: 13
Seq primer: CACACGAGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 41.

FEATURES
    source
        1..41
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUCGIM0056A13"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUCIM library"
            /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
    Query Match      62.1%; Score 11.8; DB 9; Length 41;
    Best Local Similarity 86.7%; Pred. No. 4.5e+05;
    Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TGACGTTTCAGGGGGG 19
    ||||| |||||
Db 26 TGACTTTCTGGGGG 12

RESULT 15
BG272395
LOCUS      nab29f02.x1 NCI_CGAP_HN21 Homo sapiens cDNA clone IMAGE:4232571 3',
DEFINITION mRNA sequence.
ACCESSION BG272395
VERSION   BG272395.1 GI:12981506
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
            1 (bases 1 to 50)
            NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute / National Institute of Dental Research,
            Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            cDNA Library Preparation: David B. Krizman, Ph.D.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:

FEATURES
    source
        1..20
            /organism="Oryza sativa (indica cultivar-group)"
            /mol_type="genomic DNA"
            /cultivar="IR36"
            /db_xref="RiceGenes:RG152"
            /clone="RG152"

info@image.llnl.gov
Seq primer: -40UP from Gibco.
Location/Qualifiers
    source
        1..50
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4232571"
            /tissue_type="nasopharyngeal carcinoma"
            /lab_host="DH10B"
            /clone_lib="NCI_CGAP_HN21"
            /note="Organ: head/neck; Vector: pAMP1; mRNA made from head/neck tumor, cDNA made by oligo-dT priming. Directionally cloned into UDG sites. Size-selected on agarose gel, average insert size 300 bp. Primary library. cDNA Library Preparation: David B. Krizman, Ph.D."

ORIGIN
    Query Match      62.1%; Score 11.8; DB 2; Length 50;
    Best Local Similarity 86.7%; Pred. No. 4.6e+05;
    Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TGACGTTTCAGGGGGG 19
    ||||| |||||
Db 6 TGTCTTCTGGGGGG 20

RESULT 16
AQ074235
LOCUS      21 pUC8 PstI Rice Etiolated Leaf Genomic Library Oryza sativa
DEFINITION (indica cultivar-group) genomic clone RG152, genomic survey
            sequence.
ACCESSION AQ074235
VERSION   AQ074235.1 GI:3435354
KEYWORDS GSS.
SOURCE    Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 20)
            McCouch,S.R., Kochert,G., Yu,Z.H., Wang,Z.Y., Khush,G.S.,
            Coffman,W.R., and Tankalev,S.D.
            Molecular mapping of rice chromosomes
            Theor. Appl. Genet. 76, 815-829 (1988)
            Contact: Susan R. McCouch
            Cornell University
            Dept. Plant Breeding, Ithaca, NY 14853-1901, USA
            Tel: 607 255 0420
            Fax: 607 255 6683
            Email: srm4@cornell.edu
            For mapping information, additional citations and other related
            information concerning this probe, please refer to the RiceGenes
            database at
            http://ars-genome.cornell.edu/cgi%2Dbin/WebAce/webace?db=ricegenes&
            class=Marker&object=RG152 DNA Sequencing was done by the DOE Plant
            Research Lab, Michigan State University. Informatics was done at
            the Computational Biology Centers, University of Minnesota.
            PCR Primers
            FORWARD: M13 Forward
            BACKWARD: M13 Reverse
            Insert Length: 1 Std Error: 0.00
            Seq primer: M13 -21 dye primer
            Class: RFLP probe, Location/Qualifiers
            source
                1..20
                    /organism="Oryza sativa (indica cultivar-group)"
                    /mol_type="genomic DNA"
                    /cultivar="IR36"
                    /db_xref="RiceGenes:RG152"
                    /clone="RG152"

```

/clone lib="pUC8 PstI Rice Etiolated Leaf Genomic Library"  
/note="vector: pUC8; Total leaf DNA was digested with the  
restriction enzyme PstI. DH5-alpha bacterial cells were  
then transformed with ligated plasmid. Random genomic  
clones were given consecutive numbers (RG-#) as they were  
prepared. The same numbers were then used to designate  
loci in the genome as detected by genetic mapping."

## ORIGIN

Query Match 61.1%; Score 11.6; DB 9; Length 20;  
Best Local Similarity 77.8%; Pred. No. 5.4e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 18  
|||||  
Db 1 GGGCGACCTGCAGGGAG 18

## RESULT 17

AZ312923/c 25 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION  
IM0029L01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0029L01 F, genomic survey sequence.

AZ312923  
AZ312923.1 GI:10357337

VERSION  
GSS.

KEYWORDS  
Mus musculus (house mouse)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 25)

AUTHORS

Dunn D., Aoyagi A., Barber M., Beacorn T., Duval B., Hamil C.,  
Islam H., Longacre S., Mahmoud M., Meenen E., Pedersen T.,  
Reilly M., Rose M., Rose R., Stokes R., Tingey A., von  
Niederhausern A., and Wright D., Weiss R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0029 row: L column: 01

Seq primer: CGTTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

## FEATURES

source

1. .25  
/location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0029L01"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel

## ORIGIN

Query Match 61.1%; Score 11.6; DB 9; Length 25;  
Best Local Similarity 77.8%; Pred. No. 5.5e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGTGACGTTTCAGGGGG 19  
|||||  
Db 25 GGGTGACATCCAGAGTGG 8

## RESULT 18

AI497442/c 28 bp mRNA linear EST 07-JUN-2001  
LOCUS  
DEFINITION  
fb53f02.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone  
IMAGE:3715611 3' similar to SW:COPE\_RAT P23514 COATOMER BETA  
SUBUNIT ;, mRNA sequence.

AI497442  
AI497442.1 GI:4398445

VERSION  
EST.

KEYWORDS  
Danio rerio (zebrafish)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 28)

AUTHORS

Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M.,  
Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,  
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,  
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

JOURNAL

COMMENT

Contact: Stephen L. Johnson

Washington University School

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu

cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:  
Matthew Clark. DNA Sequencing by: Washington University Genome  
Sequencing Center Clone Distribution: Genome Systems, St. Louis,  
Missouri (web address: www.genomesystems.com) (email contact:  
info@genomesystems.com) and Research Genetics, Huntsville, Alabama  
(web address: www.resgen.com) (email contact: info@resgen.com) and  
ResourcencentrumPrimaDatenbank, Berlin, Germany (web address:  
www.rzpd.de)

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Possible reversed clone: polyT not found

Seq primer: T7 ET from Amersham

High quality sequence stop: 1

POLYA=No.

## FEATURES

source

1. .28  
/location/Qualifiers

/organism="Danio rerio"

/mol\_type="mRNA"

/db\_xref="taxon:7955"

/clone="IMAGE:3715611"

/sex="mixed"

/tissue type="26 somite embryos, adult livers, shield

stage embryos"

/lab\_host="Xl1-blue MRF"

/clone\_lib="Zebrafish WashU MPIMG EST"

electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid RL. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

/note="Vector: pSPORT1; Site\_1: NotI; Site\_2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'pGACTAGTCTAGATCGAGCGCGCCCTTTTITTTTIT3]; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."

## ORIGIN

Query Match 61.1%; Score 11.6; DB 1; Length 28;  
Best Local Similarity 77.8%; Pred. No. 5.5e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTGACGTTTCAGGGG 18  
||||| |||  
Db 27 GGGTGAGTTTGAGTGG 10

## RESULT 19

CL686485  
LOCUS  
DEFINITION  
PRI0144b.D10.2 - PRI0144b.BR (28) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CL686485  
CL686485.1 GI:50194988  
GSS.

Pristionchus pacificus  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498

Email: raif.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.  
Seq primer: T7  
Class: fosmid ends.

## FEATURES

source  
1..28  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus var. California"  
/note="Vector: pBpifos-5 Fosmid vector"

## ORIGIN

Query Match 61.1%; Score 11.6; DB 10; Length 28;  
Best Local Similarity 77.8%; Pred. No. 5.5e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGG 19  
||||| |||  
Db 7 GGGTTAGTGTAGGGGG 24

## RESULT 20

CD029249/c  
LOCUS  
DEFINITION  
mgn012x001f.b Magnaporthe grisea NS Uni-Zap XR Library Magnaporthe grisea cDNA clone mgn012x001 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CD029249  
CD029249.1 GI:30410705  
EST.

Magnaporthe grisea (anamorph: Pyricularia grisea)

Magnaporthe grisea  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes; incertae sedis; Magnaportheaceae; Magnaporthe.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 29)  
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,  
Bhatterai,K. and Dean,R.A.  
Expressed sequence tags from the rice blast fungus, Magnaporthe grisea  
Unpublished (2002)

Contact: Ebbole DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483

Email: d-ebbole@tamu.edu  
Chromatogram file of this sequence is available, see contact person;  
PCR Primers  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgn012 row: 0 column: 01  
Seq primer: T3.

FEATURES  
source  
1..29  
/organism="Magnaporthe grisea"  
/mol\_type="mRNA"  
/strain="Guy11"  
/db\_xref="taxon:148305"  
/clone="mgn012x001"  
/sex="Mat1-2 hermaphrodite"  
/cell\_type="mycelium"  
/clone\_lib="Magnaporthe grisea NS Uni-Zap XR Library"  
/note="Vector: pBluescriptSK-; Site\_1: EcoRI; Site\_2: XhoI; Unidirectional cloning. EcoRI site has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Nitrogen starvation library. Cells were inoculated into minimal medium and grown for two days with shaking (150 rpm) at room temperature. Culture was harvested, blended, inoculated into minimal medium as above for 24 h. Cells were harvested, washed with water and inoculated into minimal medium base lacking nitrogen source for 6 h. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

Query Match 61.1%; Score 11.6; DB 6; Length 29;  
Best Local Similarity 77.8%; Pred. No. 5.6e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGG 19  
||||| |||  
Db 21 GGGTCAGATTTCAGTGG 4

```

RESULT 21
AZ783946/c
LOCUS          30 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION     2M0026B08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                clone UUGC2M0026B08 F, genomic survey sequence.
ACCESSION      AZ783946
VERSION        AZ783946.1  GI:12919186
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE      1 (bases 1 to 30)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0026 row: B column: 08
                Seq primer: CGTGTGTAACGACGGCCACT
                Class: Plasmid ends
                High quality sequence stop: 30.
FEATURES       source
                1..30
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0026B08"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adapted DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWP42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adapted mouse DNA was annealed to
                adapted vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
ORIGIN
Query Match      61.1%; Score 11.6; DB 9; Length 30;
Best Local Similarity 77.8%; Pred. No. 5.6e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTACGGGG 18
|||||
Db 25 GGGGTGGGTGAGGGGG 8

RESULT 22
AZ783946
LOCUS          34 bp      mRNA      linear      EST 17-JUL-2001
DEFINITION     602968347F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5108146 5',
                mRNA sequence.
ACCESSION      BI259582
VERSION        BI259582.1  GI:14817058
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 34)
AUTHORS        NIH-MGC http://mgc.nhl.nih.gov/
                National Institutes of Health, Mammalian Gene Collection (MGC)
                Unpublished (1999)
JOURNAL        Contact: Robert Strausberg, Ph.D.
                Email: cgabbs@mail.nih.gov
                Tissue Procurement: ATCC
                CDNA Library Preparation: Life Technologies, Inc.
                CDNA Library Arrayed by: Incyte Genomics, Inc.
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLAM11261 row: m column: 11
                High quality sequence stop: 28.
FEATURES       source
                1..34
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5108146"
                /tissue_type="cervical carcinoma cell line"
                /lab_host="DH10B"
                /clone_lib="NIH MGC 12"
                /notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
                Site 2: Sall; Cloned unidirectionally. Primer: Oligo dt.
                Average insert size 1.4 kb. Library prepared by Life
                Technologies."
ORIGIN
Query Match      61.1%; Score 11.6; DB 2; Length 34;
Best Local Similarity 77.8%; Pred. No. 5.6e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTACGGGG 18
|||||
Db 16 GGGCAGACGACGAGGGGG 33

RESULT 23
AU263853/c
LOCUS          35 bp      mRNA      linear      EST 26-APR-2004
DEFINITION     AU263853 VS Dictyostelium discoideum cDNA clone VSD330 3', mRNA
                sequence.
ACCESSION      AU263853
VERSION        AU263853.1  GI:20522851
KEYWORDS       EST.
SOURCE         Dictyostelium discoideum
ORGANISM       Dictyostelium discoideum
REFERENCE      1 (bases 1 to 35)
AUTHORS        Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                Urushihara,H., Morio,T., Saito,T., Kohara,Y., Koriki,E., Ochiai,H.,
                Maeda,M., Williams,J.G., Takeuchi,I. and Tanaka,Y.
                Analyses of cDNAs from growth and slug stages of Dictyostelium
                discoideum
                Nucleic Acids Res. 32 (5), 1647-1653 (2004)
                15010511
                Contact: Hideko Urushihara

```

Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.

#### FEATURES

location/Qualifiers  
1..35  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clones="VSD330"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"

#### ORIGIN

Query Match 61.1%; Score 11.6; DB 1; Length 35;  
Best Local Similarity 77.8%; Pred. No. 5.6e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGGG 19

Db 18 GGGTACTTTTGGGGGGGG 1

#### RESULT 24

AA986717/c

LOCUS

DEFINITION AA986717 37 bp mRNA linear EST 28-MAY-1998  
IMAGE:1431288 3' similar to SW:PRP2 MOUSE P05142 PROLINE-RICH  
PROTEIN NP-2 PRECURSOR. ; mRNA sequence.

ACCESSION AA986717.1 GI:3167719

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

1 (bases 1 to 37)

Marra, M., Haller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:915356

Trace considered overall poor quality

Possible reversed clone; similarity on wrong strand

Seq primer: primer name ambiguous

High quality sequence stop: 1.

#### FEATURES

location/Qualifiers  
1..37  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clones="IMAGE:1431288"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="DH10B"

#### ORIGIN

Query Match 61.1%; Score 11.6; DB 6; Length 38;  
Best Local Similarity 77.8%; Pred. No. 5.6e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGGG 19

|||||

|||||

|||||

|||||

|||||

|||||

|||||

/clone\_lib="Sugano mouse liver mlia"  
/notes="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII  
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA  
was primed with an oligo(dT) primer  
[ATGTGGCTTTTTTTTTTTTTT]; double-stranded cDNA was  
ligated to a DraIII adaptor [TGTGGCTACTGG]; digested  
and cloned into distinct draIII sites of the pME18S-FL3  
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should  
be used to isolate the cDNA insert. Size selection was  
performed to exclude fragments <1.5kb. Library  
constructed by Dr. Sumio Sugano (University of Tokyo  
Institute of Medical Science). Custom primers for  
sequencing: 5' end primer CTCTGCTCTTAAAGCTGCG and 3' end  
primer CGACCTGCAGCTCGAGCAC."

#### ORIGIN

Query Match 61.1%; Score 11.6; DB 1; Length 37;  
Best Local Similarity 77.8%; Pred. No. 5.6e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGGG 19

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

```

Db      32 GGCTGACGGCAGGGGG 15

RESULT 26
LOCUS   BI669410
DEFINITION 41 bp mRNA linear EST 12-SEP-2001
          603295295F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5314750 5',
          mRNA sequence.
ACCESSION BI669410
VERSION   BI669410.1 GI:15583643
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.
REFERENCE 1 (bases 1 to 41)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
          Email: cgabs@email.nih.gov
          Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
          cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
          Toshiyuki and Piero Carninci (RIKEN)
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1AM11797 row: m column: 23
          High quality sequence stop: 41.
          Location/Qualifiers
            1..41
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:5314750"
              /tissue_type="hypothalamus"
              /lab_host="DH10B"
              /clone_lib="NIH_MGC_96"
              /notes="Organ: Brain; Vector: pBluescriptR (modified
              pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
              (gtcgag); Oligo-dT primed using primer
              5'-TTTTTTTTTTTTTTVN-3', size-selected for average
              insert size 2.3 kb and normalized to ROT 5. This is a
              primary library enriched for full-length clones and
              constructed using the Cap-trapper method (Carninci, in
              preparation). Library constructed by M. Brownstein
              (NIH/NHGRI, National Institutes of Health). Note: this is
              a NIH_MGC Library."

ORIGIN
Query Match 61.1%; Score 11.6; DB 3; Length 41;
Best Local Similarity 77.8%; Pred. No. 5.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 18
    ||| |||| |||| |||| ||||
Db 9 GGCAGACGACGACGAGGGGG 26

RESULT 27
LOCUS   AA948503/c
DEFINITION 43 bp mRNA linear EST 23-JUN-1998
          on53c06.s1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1560394 3',
          similar to SW:2F36_HUMAN P16415 ZINC FINGER PROTEIN ZFP-36 ;, mRNA
          sequence.
ACCESSION AA948503
VERSION   AA948503.1 GI:3109756
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.
REFERENCE 1 (bases 1 to 43)
AUTHORS  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Unpublished (1997)
JOURNAL  Unpublished (1997)
COMMENT  Contact: Robert Strausberg, Ph.D.
          Email: cgabs@email.nih.gov
          Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
          Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: M. Bento Soares, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbr/image/image.html

Trace considered overall poor quality
Insert Length: 1892 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
  1..43
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:1560394"
    /tissue_type="adenocarcinoma"
    /lab_host="DH10B"
    /clone_lib="NCI_CGAP_C08"
    /notes="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
    modified polylinker; 1st strand cDNA was prepared from
    colon adenocarcinoma, and was then primed with a Not I -
    oligo(dT) primer. Double-stranded cDNA was ligated to Eco
    RI adaptors (Pharmacia), digested with Not I and cloned
    into the Not I and Eco RI sites of the modified pT7T3
    vector. Library is normalized. Library was constructed by
    Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 61.1%; Score 11.6; DB 1; Length 43;
Best Local Similarity 77.8%; Pred. No. 5.7e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGG 19
    ||| |||| |||| |||| ||||
Db 38 GGATGACGTTTCATTGTGG 21

RESULT 28
LOCUS   BX569627
DEFINITION 44 bp mRNA linear EST 14-OCT-2003
          BX569627 Glossina morsitans morsitans adult infected gut Glossina
          morsitans morsitans cDNA clone Tse9f08_q1c, mRNA sequence.
ACCESSION BX569627
VERSION   BX569627.1 GI:33437816
KEYWORDS EST.
SOURCE    Glossina morsitans morsitans
          Glossina morsitans morsitans
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
          Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 44)
AUTHORS  Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
          Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
          Adult midgut expressed sequence tags from the tsetse fly Glossina
          morsitans morsitans and expression analysis of putative immune
          response genes
          Genome Biol. 4 (10), R63 (2003)
JOURNAL   PUBLISHED
LOCUS     14519198
COMMENT   Contact: Hall N

```



Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5',  
end of the cDNA all plc reads are from  
the 3' end.

#### FEATURES

source  
1. .44  
Location/Qualifiers  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse9f08\_q1c"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T. brucei"

#### ORIGIN

Query Match 61.1%; Score 11.6; DB 5; Length 44;  
Best Local Similarity 73.7%; Pred. No. 5.7e+05;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
||||| | |||||  
Db 7 GGGGTGAGGNGAGGGGG 25

#### RESULT 29

AZ648348  
LOCUS  
DEFINITION  
1M0517013F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0517013 F, genomic survey sequence.

ACCESSION  
AZ648348  
GSS.  
GI:11780725

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS  
1 (bases 1 to 45)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
UNPUBLISHED (2000)

COMMENT  
Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0517 row: 0 column: 13

Seq primer: CGTTGTAACGAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 45.

Location/Qualifiers

1. .45

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

#### FEATURES

source

/db\_xref="taxon:10090"  
/clone="UUGC1M0517013"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (G114732114[GB|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

#### ORIGIN

Query Match 61.1%; Score 11.6; DB 9; Length 45;  
Best Local Similarity 77.8%; Pred. No. 5.7e+05;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 18  
||||| | |||||  
Db 11 GGGTTGAGGAGCAGGGGG 28

#### RESULT 30

BI544737  
LOCUS  
DEFINITION  
603242001F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5284488 5',  
mRNA sequence.

ACCESSION  
BI544737  
EST.  
KEYWORDS  
SOURCE

ORGANISM

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE

1 (bases 1 to 47)  
NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS  
TITLE  
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)

JOURNAL  
UNPUBLISHED (1999)

COMMENT  
Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L1AM11719 row: a column: 01

High quality sequence stop: 47.

Location/Qualifiers

1. .47

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5284488"

/tissue\_type="hippocampus"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_95"

```

/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
5'-TTTTTTTTTTTTTNN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

ORIGIN
  Query Match      61.1%; Score 11.6; DB 3; Length 47;
  Best Local Similarity 77.8%; Pred. No. 5.7e+05;
  Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 18
    ||| ||| ||| ||| |||
Db 15 GGGCAGACGACGAGGGGG 32

RESULT 31
CX013593/c
LOCUS
DEFINITION i06b06.b1 Whole Heart Library (DOGEST5) Canis familiaris cDNA,
mRNA sequence.
ACCESSION CX013593
VERSION CX013593.1 GI:56396004
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 47)
AUTHORS BaliJa,V.S., Nascimento,L.U. and McCombie,W.R.
TITLES ESTs from Canis familiaris whole heart (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8894
Fax: 516 367 8874
Email: mccombie@cshl.org.

FEATURES
  source
  1..47
    /organism="Canis familiaris"
    /mol_type="mRNA"
    /db_xref="taxon:9615"
    /sex="Unknown"
    /dev_stage="3 month old normal canine"
    /lab_host="XLI0 Gold"
    /clone_lib="Whole Heart Library (DOGEST5)"
    /note="Organ: Heart; Vector: pBluescript II SK; Site 1:
    EcoRI; Site 2: XhoI; Library constructed using pBluescript
    XR kit from Stratagene. Cloned cDNA was size selected
    between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
    Medical Genetics, School of Veterinary Medicine,
    University of Pennsylvania, 3800 Spruce Street,
    Philadelphia, PA 19104-6051"

ORIGIN
  Query Match      61.1%; Score 11.6; DB 8; Length 47;
  Best Local Similarity 77.8%; Pred. No. 5.7e+05;
  Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGG 19
    ||| ||| ||| ||| |||
Db 47 GGCTGACCTCGAGGGGG 30

RESULT 32

```

```

AA922976/c
LOCUS
DEFINITION ok7e06.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1520002 3',
similar to TR:Q39614 Q39614 PROLINE-RICH PROTEIN. ;, mRNA sequence.
ACCESSION AA922976
VERSION AA922976.1 GI:3070285
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 49)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
  source
  1..49
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:1520002"
    /tissue_type="pooled germ cell tumors"
    /lab_host="DH10B"
    /clone_lib="NCI CGAP GC4"
    /note="Vector: pT73D-Pac (Pharmacia) with a modified
    polylinker; 1st strand cDNA was prepared from 3 pooled
    germ cell tumors, and was then primed with a Not I -
    oligo(dT) primer. Double-stranded cDNA was ligated to Eco
    RI adaptors (Pharmacia), digested with Not I and cloned
    into the Not I and Eco RI sites of the modified pT73
    vector. Library is normalized. Library was constructed by
    Bento Soares and M. Fatima Bonaldo."

ORIGIN
  Query Match      61.1%; Score 11.6; DB 1; Length 49;
  Best Local Similarity 77.8%; Pred. No. 5.7e+05;
  Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGG 19
    ||| ||| ||| ||| |||
Db 49 GGCTGGGTTTAAAGGGGG 32

RESULT 33
BE615718/c
LOCUS
DEFINITION 601279832F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622110 5',
mRNA sequence.
ACCESSION BE615718
VERSION BE615718.1 GI:9897317
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 49)

```

**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Straubeberg, Ph.D.  
 Email: csapbs@mail.nih.gov  
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CM296 row: o column: 07.

#### FEATURES

Location/Qualifiers

1..49

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3622110"  
 /tissue\_type="adenocarcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_39"  
 /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed  
 by Ling Hong in the laboratory of Gerald M. Rubin  
 (University of California, Berkeley) using ZAP-cDNA  
 synthesis kit (Stratagene) and Superscript II RT (Life  
 Technologies)."

#### ORIGIN

Query Match 61.1%; Score 11.6; DB 2; Length 49;  
 Best Local Similarity 77.8%; Pred. No. 5.7e+05;  
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGG 19

Db 19 GGGTGACGTTTCAGGGGG 2

#### RESULT 34

AU102320  
 LOCUS  
 DEFINITION AU102320 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 ADSE01801, mRNA sequence.

ACCESSION AU102320

VERSION AU102320.1 GI:13551840

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

11375929

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: [ysuzuki@ims.u-tokyo.ac.jp](mailto:ysuzuki@ims.u-tokyo.ac.jp)

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

#### FEATURES

source

1..50

#### ORIGIN

Query Match 61.1%; Score 11.6; DB 1; Length 50;  
 Best Local Similarity 77.8%; Pred. No. 5.7e+05;  
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAGGGGG 19

Db 13 GCGGGACGGTTCAGGGGAG 30

#### RESULT 35

AG204798/c

LOCUS

DEFINITION AG204798 Pan troglodytes DNA, clone: RP43-090K13.T7, genomic survey  
 sequence.

ACCESSION AG204798

VERSION AG204798.1 GI:45236973

KEYWORDS Pan troglodytes (chimpanzee)

SOURCE

ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Pan.

#### REFERENCE

AUTHORS

1 Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J.,

Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

BAC end sequences of Library RP-43

Unpublished

REFERENCE 2 (bases 1 to 35)

Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C. J.,

Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

Direct Submission

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of

Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);

52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea

(E-mail: [redstone@mail.kribb.re.kr](mailto:redstone@mail.kribb.re.kr), URL: <http://phs.grc.kribb.re.kr/>,

Tel: 82-42-886-7181, Fax: 82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC

end was generated during the R&D process and may have higher chance

of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI.

Location/Qualifiers

1..35

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="RP43-090K13.T7"

/sex="male"

/cell\_type="lymphocytes"

/clone\_lib="RP-43 Chimpanzee Male BAC Library"

#### ORIGIN

Query Match 60.0%; Score 11.4; DB 10; Length 35;

Best Local Similarity 92.3%; Pred. No. 7e+05;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GTGACGTTTCAGGG 16

Db 35 GTGACGTTTCAGGG 23

#### RESULT 36

```

CV933742/c
LOCUS          CV933742          36 bp      mRNA      linear      EST 25-JAN-2005
DEFINITION     PMPCm_4081 mating of 88069 (A1) and 618 (A2) Phytophthora
                infestans cDNA, mRNA sequence.
ACCESSION      CV933742
VERSION        CV933742.1  GI:58123357
KEYWORDS       EST.
SOURCE         Phytophthora infestans (potato late blight agent)
ORGANISM       Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                Phytophthora.
REFERENCE      1 (bases 1 to 36)
AUTHORS       Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
                Keikar,H., Fong,A.M., Gates,K., Roberts,S., Yatskan,E., Gaffney,T.,
                Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
                Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
                Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
                Lam,S.T. and Judelson, H.S.
TITLE         Large-scale gene discovery in the oomycete Phytophthora infestans
                reveals likely components of phytopathogenicity shared with true
                fungi
JOURNAL        Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
PUBMED        15782637
COMMENT       Contact: Judelson HS
                Department of Plant Pathology
                University of California
                Webber Hall, Riverside, CA 92521, USA
                Tel: 909 787 4199
                Fax: 909 787 4294
                Email: howard.judelson@ucr.edu.
FEATURES       Location/Qualifiers
                1..36
                /organism="Phytophthora infestans"
                /mol_type="mRNA"
                /strain="88069 and 618"
                /db_xref="taxon:4787"
                /sex="A1 and A2"
                /clone_lib="mating of 88069 (A1) and 618 (A2)"
                /note="Vector: pSPORT1"
ORIGIN
Query Match      60.0%; Score 11.4; DB 8; Length 36;
Best Local Similarity 92.3%; Pred. NO. 7e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAG 14
    ||| |||||
Db 28 GGGCGACGTTTCAG 16

RESULT 37
AZ340800
LOCUS          AZ340800          22 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION     IM0072G21R Mouse 10kb plasmid UUC1M library Mus musculus genomic
                clone UUGC1M0072G21 R, genomic survey sequence.
ACCESSION      AZ340800
VERSION        AZ340800.1  GI:10416416
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 22)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,S., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D., Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
                University of Utah Genome Center
CV933742
LOCUS          CV933742          36 bp      mRNA      linear      EST 25-JAN-2005
DEFINITION     PMPCm_4081 mating of 88069 (A1) and 618 (A2) Phytophthora
                infestans cDNA, mRNA sequence.
ACCESSION      CV933742
VERSION        CV933742.1  GI:58123357
KEYWORDS       EST.
SOURCE         Phytophthora infestans (potato late blight agent)
ORGANISM       Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                Phytophthora.
REFERENCE      1 (bases 1 to 36)
AUTHORS       Randall,T., Dwyer,R.A., Huitema,E., Beyer,K., Cvitanich,C.,
                Keikar,H., Fong,A.M., Gates,K., Roberts,S., Yatskan,E., Gaffney,T.,
                Law,M., Testa,A., Torto-Alalibo,A., Zhang,M., Zheng,L., Mueller,E.,
                Windass,J., Binder,A., Birch,P.R.J., Gisi,U., Govers,F., Gow,N.A.,
                Mauch,F., van West,P., Waugh,M.E., Yu,J., Boller,T., Kamoun,S.,
                Lam,S.T. and Judelson, H.S.
TITLE         Large-scale gene discovery in the oomycete Phytophthora infestans
                reveals likely components of phytopathogenicity shared with true
                fungi
JOURNAL        Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)
PUBMED        15782637
COMMENT       Contact: Judelson HS
                Department of Plant Pathology
                University of California
                Webber Hall, Riverside, CA 92521, USA
                Tel: 909 787 4199
                Fax: 909 787 4294
                Email: howard.judelson@ucr.edu.
FEATURES       Location/Qualifiers
                1..36
                /organism="Phytophthora infestans"
                /mol_type="mRNA"
                /strain="88069 and 618"
                /db_xref="taxon:4787"
                /sex="A1 and A2"
                /clone_lib="mating of 88069 (A1) and 618 (A2)"
                /note="Vector: pSPORT1"
ORIGIN
Query Match      60.0%; Score 11.4; DB 8; Length 36;
Best Local Similarity 92.3%; Pred. NO. 7e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGTGACGTTTCAG 14
    ||| |||||
Db 28 GGGCGACGTTTCAG 16

RESULT 37
AZ340800
LOCUS          AZ340800          22 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION     IM0072G21R Mouse 10kb plasmid UUC1M library Mus musculus genomic
                clone UUGC1M0072G21 R, genomic survey sequence.
ACCESSION      AZ340800
VERSION        AZ340800.1  GI:10416416
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 22)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,S., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D., Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
                University of Utah Genome Center

```

```

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0072 row: G column: 21
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0072G21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnarses/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI:4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
Query Match      58.9%; Score 11.2; DB 9; Length 22;
Best Local Similarity 81.2%; Pred. NO. 8.6e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGG 16
    ||| |||||
Db 1 GGGCTGACITTCATGG 16

RESULT 38
TA246H09Q
LOCUS          TA246H09Q          29 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION     T. brucei sheared genomic DNA clone 246h09, reverse sequence,
                genomic survey sequence.
ACCESSION      AL488820
VERSION        AL488820.1  GI:11864016
KEYWORDS       GSS.
SOURCE         Trypanosoma brucei
ORGANISM       Trypanosoma brucei
                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                Trypanosoma.
REFERENCE      1 (bases 1 to 29)
AUTHORS       Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
                Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
                Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE         Direct Submision
JOURNAL        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
                project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
                Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                nh@sanger.ac.uk
COMMENT       Constructed at the Institute for Genomic Research (TIGR),

```

Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsaye@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

#### FEATURES

Location/Qualifiers  
1..29  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="246h09"

#### ORIGIN

Query Match 58.9%; Score 11.2; DB 11; Length 29;  
Best Local Similarity 81.2%; Pred. No. 8.7e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GTGACGTTTCAGGGGG 19  
||||| ||||| |||||  
Db 9 GTGAAC TTCAGGGG 24

#### RESULT 39

AZ483233  
LOCUS  
DEFINITION  
M0308H16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0308H16 R, genomic survey sequence.

ACCESSION  
AZ483233  
VERSION  
GSS.  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)

#### ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE

AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

#### JOURNAL

COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0308 row: H column: 16  
Seq primer: CACACGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 30.

#### FEATURES

Location/Qualifiers  
1..30  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0308H16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

Query Match 58.9%; Score 11.2; DB 10; Length 30;  
Best Local Similarity 81.2%; Pred. No. 8.7e+05;

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### ORIGIN

Query Match 58.9%; Score 11.2; DB 9; Length 30;  
Best Local Similarity 81.2%; Pred. No. 8.7e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCTGACGTTTCAGGGG 17  
||||| ||||| |||||  
Db 14 GGCTGATATTCATGGG 29

#### RESULT 40

CL684027  
LOCUS  
DEFINITION  
CL684027 H10 2 - PRI0138b.BR (30) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION  
CL684027  
VERSION  
GSS.  
KEYWORDS  
SOURCE  
PRISTIONCHUS PACIFICUS

#### ORGANISM

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

#### REFERENCE

AUTHORS  
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

AppADB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

#### JOURNAL

#### PUBMED

COMMENT  
14681447  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1..30  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus var. California"  
/notes="Vector: pEpifos-5 Fosmid vector"

#### ORIGIN

Query Match 58.9%; Score 11.2; DB 10; Length 30;  
Best Local Similarity 81.2%; Pred. No. 8.7e+05;



**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
**JOURNAL** Tumor Gene Index  
**COMMENT** Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

**FEATURES** source  
 Location/Qualifiers  
 1..37  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2240851"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DHI0B"  
 /clone\_lib="NCI-CGAP GC6"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
 from the normalized library NCI-CGAP GC4 was prepared, and  
 ss circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (cloneIDs  
 1257096-1258631, 1469064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."

**ORIGIN**  
 Query Match 58.9%; Score 11.2; DB 1; Length 37;  
 Best Local Similarity 81.2%; Pred. No. 8.8e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGG 16  
 |||||  
 Db 21 GGGCTGATGTTTCATGG 6

**RESULT 44**  
**C2294761**  
**LOCUS** C2294761 39 bp mRNA linear GSS 22-MAR-2005  
**DEFINITION** M093F02 GGTC Gene Trap Library GV14C05 Mus musculus cDNA clone  
 M093F02, mRNA sequence.  
**ACCESSION** C2294761  
**VERSION** C2294761.1 GI:61682511  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 1 (bases 1 to 39)  
**REFERENCE** Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,  
**AUTHORS** Arnold, H.H., Schmutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.  
 A large-scale, gene-driven mutagenesis approach for the functional  
 analysis of the mouse genome  
**TITLE** Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
**JOURNAL** 12904583  
**PUBMED** Contact: GGTC  
 German Genetrap Consortium (GGTC)  
 Email: info@genetrap.de  
 FlipROSAceC-2 gene trap. Sequence tag generated by 5'RACE.  
 Additional sequence information can be found at:  
 'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=M093F02' ES cell line harboring insertion mutation of  
 target gene is available at:

'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm  
 1' Inhouse Sequence Identifier: 18341  
**Class:** Gene Trap.

**FEATURES** source  
 Location/Qualifiers  
 1..39  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129 Sv"  
 /db\_xref="taxon:10090"  
 /clones="M093F02"  
 /sex="Male"  
 /cell\_type="Embryonic stem cell"  
 /cell\_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"  
 /clone\_lib="GGTC Gene Trap Library GV14C05"  
 /note="Vector: FlipROSAceC-2"

**ORIGIN**  
 Query Match 58.9%; Score 11.2; DB 10; Length 39;  
 Best Local Similarity 68.4%; Pred. No. 8.9e+05;  
 Matches 13; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGGG 19  
 |||||  
 Db 4 GGGGTGCCGTCNNNGAGGG 22

**RESULT 45**  
**R87616**  
**LOCUS** R87616 40 bp mRNA linear EST 16-AUG-1995  
**DEFINITION** YN91902.r1 Soares adult brain N2b4H855Y Homo sapiens cDNA clone  
 IMAGE:166322 5; similar to SP:S27887 S27887 NEUREXIN II-ALPHA  
 PRECURSOR -, mRNA sequence.  
**ACCESSION** R87616  
**VERSION** R87616.1 GI:946429  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 40)  
**REFERENCE** Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
**AUTHORS** Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.  
**TITLE** The Washu-Merck EST Project  
**JOURNAL** Unpublished (1995)  
**COMMENT** Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 2019  
 High quality sequence starts: 1 High quality sequence stops: 1  
 Source: IMAGE Consortium, LLNL This clone is available royalty-free  
 through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov)  
 for further information. Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand  
 Insert Length: 2019 Std Error: 0.00  
 Seq primer: M13RP1  
 High quality sequence stop: 1.

**FEATURES** source  
 Location/Qualifiers  
 1..40  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:587017"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:166322"  
 /sex="Male"  
 /dev\_stage="55-year old"  
 /lab\_host="DHI0B (ampicillin resistant)"

/clone lib="Soares adult brain N2b4HB55V"  
 /note="Organ: brain; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

## ORIGIN

Query Match 58.9%; Score 11.2; DB 8; Length 40;  
 Best Local Similarity 81.2%; Pred. No. 8.9e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGCTGAGGTCAGGGG 17  
 ||||| ||||| |||||

Db 10 GGCTGAGGTCAGGGG 25

## RESULT 46

EX128210/c 41 bp DNA linear GSS 28-JAN-2003  
 LOCUS  
 DEFINITION Danio rerio genomic clone DKEY-279M17, genomic survey sequence.  
 ACCESSION EX128210  
 VERSION EX128210.1 GI:27959164  
 KEYWORDS GSS.

SOURCE Danio rerio (zebrafish)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 41)

Humphray,S.J., Huckle,E. and Durham,J.L.

Direct Submission  
 Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished

This sequence was generated from the SP6 end of BAC 279M17. 279M17 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details: http://www.sanger.ac.uk/projects/D\_rerio/.

## FEATURES

source  
 1..41  
 Location/Qualifiers  
 /organism="Danio rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="DKEY-279M17"  
 /tissue\_type="Testis"  
 /note="vector pindigoBAC-536"

## ORIGIN

Query Match 58.9%; Score 11.2; DB 10; Length 41;  
 Best Local Similarity 81.2%; Pred. No. 8.9e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GTGACGTTTCAGGGGG 19  
 ||||| ||||| |||||

Db 19 GTGTCGGTCGGGGGG 4

## RESULT 47

W34290/c

LOCUS W34290 46 bp mRNA linear EST 12-SEP-1996  
 DEFINITION m99c07.r1 Soares mouse p3NNF19.5 Mus musculus cDNA clone IMAGE:318828 5' similar to SW:GBG3 BOVIN P29798 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-3 SUBUNIT. [1] ; mRNA sequence.

## ACCESSION

W34290

## VERSION

W34290.1 GI:1316200

## KEYWORDS

EST.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 46)  
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

## TITLE

The WashU-HHMI Mouse EST Project

## JOURNAL

Unpublished (1996)

## COMMENT

Contact: Marra M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:209444

## FEATURES

source  
 1..46  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:318828"  
 /dev\_stage="19.5 dpc total fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares mouse p3NNF19.5"  
 /note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTACCAATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

## ORIGIN

Query Match 58.9%; Score 11.2; DB 8; Length 46;  
 Best Local Similarity 81.2%; Pred. No. 8.9e+05;  
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GTGACGTTTCAGGGGG 19  
 ||||| ||||| |||||

Db 21 GTGATGTTAACGGGGG 6

## RESULT 48

BH802996/c

## LOCUS

DEFINITION

survey sequence.

ACCESSION

VERSION

BH802996 48 bp DNA linear GSS 25-APR-2002  
 1008098B12.2EL.y1 1008 - RescueMu Grid 1 Zea mays genomic, genomic survey sequence.

BH802996 48 bp DNA linear GSS 25-APR-2002  
 BH802996.1 GI:20317698



```

KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008098 row: 14
Class: transposon-tagged.
Location/Qualifiers
FEATURES
source
1..48
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1008 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmdb.iastate.edu and follow the links for
'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN
Query Match 58.9%; Score 11.2; DB 9; Length 48;
Best Local Similarity 81.2%; Pred. No. 9e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTGACGTTTCAGGGGG 18
||||| ||| |||
Db 29 GGTGACGTCGCCGGG 14

RESULT 49
CG732711
LOCUS
DEFINITION
CG732711 49 bp DNA linear GSS 20-OCT-2003
survey sequence.
CG732711.1 GI:37775203
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 49)
Walbot,V.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences

GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 48)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences

Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 119150 row: 46
Class: transposon-tagged.
Location/Qualifiers
FEATURES
source
1..49
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN
Query Match 58.9%; Score 11.2; DB 10; Length 49;
Best Local Similarity 81.2%; Pred. No. 9e+05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GGTGACGTTTCAGGGGG 18
||||| ||| |||
Db 20 GGTGACGTTGAGCTGG 35

RESULT 50
CC458057
LOCUS
DEFINITION
CC458057 50 bp DNA linear GSS 30-MAY-2003
SALK_115432.18.90.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_115432.18.90.x, genomic
survey sequence.
CC458057
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 50)
Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 3' end of
At5g05810.

```

Class: TDNA tagged.

FEATURES  
source  
1. .50  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="SALK\_115432.18.90.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

ORIGIN

Query Match 58.9%; Score 11.2; DB 9; Length 50;  
Best Local Similarity 81.2%; Pred. No. 9e+05;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTACGG 16  
||| ||| ||| |||  
Db 29 GGGGAGATGTTAAGG 44

Search completed: February 15, 2006, 21:10:07  
Job time : 1283.74 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:56:18 ; Search time 42.7107 Seconds  
(without alignments)  
790.754 Million cell updates/sec

Title: US-09-669-187A-80  
Perfect score: 19  
Sequence: 1 ggggtgacgttcaggggg 19

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/PCRUS COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	74.7	20	3	US-08-386-063-1
2	14.2	74.7	20	3	US-08-386-063-1
3	14.2	74.7	20	3	US-09-082-649B-63
4	14.2	74.7	20	3	US-09-965-101-63
5	14	73.7	39	3	US-09-358-873-18
6	14	73.7	39	3	US-10-282-935-18
7	13.4	70.5	22	3	US-08-852-001-5
8	13.2	69.5	50	3	US-10-131-827-3663
9	12.8	67.4	20	3	US-08-666-221B-29
10	12.8	67.4	25	3	US-09-396-196G-120261
11	12.8	67.4	32	2	US-07-951-715A-43
12	12.8	67.4	32	2	US-08-459-448A-43
13	12.8	67.4	32	3	US-08-459-595A-43
14	12.8	67.4	32	3	US-08-459-504B-43
15	12.8	67.4	32	3	US-08-459-444-43
16	12.8	67.4	32	3	US-09-547-422-43
17	12.8	67.4	32	3	US-09-988-462-43
18	12.8	67.4	50	3	US-10-131-827-4733
19	12.6	66.3	19	3	US-09-672-126B-27
20	12.6	66.3	20	3	US-08-738-652-12
21	12.6	66.3	20	3	US-09-030-701-63
22	12.6	66.3	20	3	US-08-960-774-90
23	12.6	66.3	20	3	US-08-082-649B-52
24	12.6	66.3	20	3	US-09-082-649B-59

98	11.6	61.1	26	2	US-08-153-051B-33	Sequence 33, Appl	171	11.2	58.9	25	3	US-09-396-196G-104710	Sequence 104710,
99	11.6	61.1	26	2	US-08-060-952C-23	Sequence 23, Appl	C 172	11.2	58.9	25	3	US-09-396-196G-112559	Sequence 112559,
100	11.6	61.1	26	2	US-08-151-477A-33	Sequence 33, Appl	C 173	11.2	58.9	25	3	US-09-396-196G-112560	Sequence 112560,
101	11.6	61.1	26	3	US-08-819-867-11	Sequence 11, Appl	C 174	11.2	58.9	25	3	US-09-396-196G-117698	Sequence 117698,
102	11.6	61.1	26	3	US-08-464-011B-23	Sequence 23, Appl	C 175	11.2	58.9	25	3	US-09-396-196G-123560	Sequence 123560,
103	11.6	61.1	26	3	US-09-378-535-11	Sequence 11, Appl	C 176	11.2	58.9	25	3	US-09-396-196G-123561	Sequence 123561,
104	11.6	61.1	27	3	US-09-311-784A-94	Sequence 94, Appl	C 177	11.2	58.9	26	3	US-09-023-082A-108	Sequence 108, Appl
105	11.6	61.1	28	3	US-09-631-863A-37	Sequence 37, Appl	C 178	11.2	58.9	26	3	US-09-393-554-15	Sequence 15, Appl
106	11.6	61.1	30	3	US-09-346-277A-6	Sequence 6, Appl	C 179	11.2	58.9	26	3	US-09-218-444-29	Sequence 29, Appl
107	11.6	61.1	31	3	US-08-641-294-5	Sequence 5, Appl	C 180	11.2	58.9	26	3	US-09-248-998-108	Sequence 108, Appl
108	11.6	61.1	33	3	US-09-180-109A-51	Sequence 51, Appl	C 181	11.2	58.9	26	3	US-09-853-666-29	Sequence 29, Appl
109	11.6	61.1	33	3	US-09-170-496D-135	Sequence 135, Appl	C 182	11.2	58.9	26	3	US-09-610-651-108	Sequence 108, Appl
110	11.6	61.1	36	2	US-08-600-783-29	Sequence 29, Appl	C 183	11.2	58.9	26	3	US-09-345-373-108	Sequence 108, Appl
111	11.6	61.1	36	2	US-08-600-783-31	Sequence 31, Appl	C 184	11.2	58.9	26	3	US-10-075-446-108	Sequence 108, Appl
112	11.6	61.1	36	2	US-08-600-783-33	Sequence 33, Appl	C 185	11.2	58.9	27	3	US-09-688-017-342	Sequence 342, Appl
113	11.6	61.1	37	2	US-09-641-638-1260	Sequence 1260, Ap	C 186	11.2	58.9	30	3	US-08-567-200A-35	Sequence 35, Appl
114	11.6	61.1	47	3	US-09-422-978-103	Sequence 103, App	C 187	11.2	58.9	30	3	US-08-691-794-38	Sequence 38, Appl
115	11.6	61.1	47	3	US-09-422-978-2213	Sequence 2213, Ap	C 188	11.2	58.9	31	6	PCT-US92-10792-29	Sequence 29, Appl
116	11.6	61.1	47	3	US-10-170-097-1260	Sequence 1260, Ap	C 189	11.2	58.9	33	2	US-08-332-562A-62	Sequence 62, Appl
117	11.6	61.1	50	3	US-10-131-827-3951	Sequence 3951, Ap	C 190	11.2	58.9	44	3	US-09-546-934-18	Sequence 18, Appl
118	11.4	60.0	20	3	US-09-422-978-7152	Sequence 7152, Ap	C 191	11.2	58.9	45	3	US-09-139-802-212	Sequence 212, Appl
119	11.4	60.0	22	2	US-08-410-779B-64	Sequence 64, Appl	C 192	11.2	58.9	45	3	US-09-425-638A-8	Sequence 8, Appl
120	11.4	60.0	22	2	US-08-410-779B-74	Sequence 74, Appl	C 193	11.2	58.9	45	3	US-09-543-004-8	Sequence 8, Appl
121	11.4	60.0	22	2	US-08-749-852-6	Sequence 6, Appl	C 194	11.2	58.9	45	3	US-09-659-786-212	Sequence 212, Appl
122	11.4	60.0	22	2	US-08-749-852-19	Sequence 19, Appl	C 195	11.2	58.9	50	3	US-08-956-171E-3530	Sequence 3530, Ap
123	11.4	60.0	22	6	PCT-US95-04477-64	Sequence 64, Appl	C 196	11.2	58.9	50	3	US-08-781-986A-3530	Sequence 3530, Ap
124	11.4	60.0	22	6	PCT-US95-04477-74	Sequence 74, Appl	C 197	11.2	58.9	50	3	US-10-131-827-1276	Sequence 1276, Ap
125	11.4	60.0	25	3	US-09-396-196G-88230	Sequence 88230, A	C 198	11.2	58.9	20	3	US-09-629-645A-24	Sequence 24, Appl
126	11.4	60.0	25	3	US-09-396-196G-102778	Sequence 102778,	C 199	11.2	58.9	20	3	US-09-198-452A-5783	Sequence 5783, Ap
127	11.4	60.0	30	3	US-09-619-758-13	Sequence 13, Appl	C 200	11.2	58.9	20	3	US-09-474-140-12	Sequence 12, Appl
128	11.4	60.0	30	3	US-09-886-607-13	Sequence 13, Appl	C 201	11.2	58.9	20	3	US-09-672-126B-3	Sequence 3, Appl
129	11.4	60.0	35	2	US-08-765-081-11	Sequence 11, Appl	C 202	11.2	58.9	21	3	US-09-672-126B-149	Sequence 149, Appl
130	11.4	60.0	35	3	US-09-098-082-11	Sequence 11, Appl	C 203	11.2	58.9	21	3	US-08-913-547-13	Sequence 13, Appl
131	11.4	60.0	35	6	PCT-US95-06994-13	Sequence 13, Appl	C 204	11.2	58.9	21	3	US-09-672-126B-35	Sequence 35, Appl
132	11.4	60.0	47	3	US-09-641-638-1046	Sequence 1046, Ap	C 205	11.2	58.9	23	2	US-08-519-777-72	Sequence 72, Appl
133	11.4	60.0	47	3	US-09-671-317-535	Sequence 535, App	C 206	11.2	58.9	23	2	US-08-742-035-72	Sequence 72, Appl
134	11.4	60.0	47	3	US-10-170-097-1046	Sequence 1046, Ap	C 207	11.2	58.9	23	2	US-08-777-019-72	Sequence 72, Appl
135	11.4	60.0	50	3	US-10-131-827-3166	Sequence 3166, Ap	C 208	11.2	58.9	23	2	US-08-777-143-72	Sequence 72, Appl
136	11.2	58.9	17	3	US-09-474-432B-518	Sequence 518, App	C 209	11.2	58.9	23	3	US-08-775-414-72	Sequence 72, Appl
137	11.2	58.9	17	3	US-09-476-387-517	Sequence 517, App	C 210	11.2	58.9	23	3	US-08-209-668-23	Sequence 23, Appl
138	11.2	58.9	19	3	US-08-594-452-59	Sequence 59, Appl	C 211	11.2	58.9	23	3	US-08-931-858E-72	Sequence 72, Appl
139	11.2	58.9	19	3	US-09-258-408-59	Sequence 59, Appl	C 212	11.2	58.9	23	3	US-08-981-739-72	Sequence 72, Appl
140	11.2	58.9	20	3	US-08-765-340-35	Sequence 35, Appl	C 213	11.2	58.9	23	3	US-09-128-026-72	Sequence 72, Appl
141	11.2	58.9	20	3	US-09-112-580-145	Sequence 145, App	C 214	11.2	58.9	23	3	US-09-220-616-72	Sequence 72, Appl
142	11.2	58.9	21	2	US-08-410-779B-63	Sequence 63, Appl	C 215	11.2	58.9	23	3	US-09-220-527-72	Sequence 72, Appl
143	11.2	58.9	21	2	US-08-410-779B-73	Sequence 73, Appl	C 216	11.2	58.9	23	3	US-09-220-407-72	Sequence 72, Appl
144	11.2	58.9	21	2	US-08-410-779B-89	Sequence 89, Appl	C 217	11.2	58.9	23	3	US-09-219-952-72	Sequence 72, Appl
145	11.2	58.9	21	3	US-09-422-978-8127	Sequence 8127, Ap	C 218	11.2	58.9	24	2	US-08-859-998-31	Sequence 31, Appl
146	11.2	58.9	21	3	US-09-422-978-11411	Sequence 11411, A	C 219	11.2	58.9	24	3	US-09-225-928-31	Sequence 31, Appl
147	11.2	58.9	21	6	PCT-US95-04477-63	Sequence 63, Appl	C 220	11.2	58.9	24	3	US-09-225-201B-31	Sequence 31, Appl
148	11.2	58.9	21	6	PCT-US95-04477-73	Sequence 73, Appl	C 221	11.2	58.9	24	3	US-09-907-794A-404	Sequence 404, Appl
149	11.2	58.9	21	6	PCT-US95-04477-89	Sequence 89, Appl	C 222	11.2	58.9	24	3	US-09-583-447A-19	Sequence 19, Appl
150	11.2	58.9	22	3	US-09-332-785-96	Sequence 96, Appl	C 223	11.2	58.9	24	3	US-09-905-125A-404	Sequence 404, Appl
151	11.2	58.9	23	2	US-08-743-637B-57	Sequence 57, Appl	C 224	11.2	58.9	24	3	US-09-902-775A-404	Sequence 404, Appl
152	11.2	58.9	23	3	US-08-526-840B-57	Sequence 57, Appl	C 225	11.2	58.9	24	3	US-09-906-700-404	Sequence 404, Appl
153	11.2	58.9	23	3	US-08-594-452-60	Sequence 60, Appl	C 226	11.2	58.9	24	3	US-09-903-603A-404	Sequence 404, Appl
154	11.2	58.9	23	3	US-09-358-408-60	Sequence 60, Appl	C 227	11.2	58.9	24	3	US-09-904-920A-404	Sequence 404, Appl
155	11.2	58.9	24	2	US-08-335-583C-38	Sequence 38, Appl	C 228	11.2	58.9	24	3	US-09-909-064-404	Sequence 404, Appl
156	11.2	58.9	24	3	US-09-172-045-21	Sequence 21, Appl	C 229	11.2	58.9	24	3	US-09-905-381A-404	Sequence 404, Appl
157	11.2	58.9	24	3	US-09-342-325C-21	Sequence 21, Appl	C 230	11.2	58.9	24	3	US-09-906-618-404	Sequence 404, Appl
158	11.2	58.9	24	3	US-10-244-367-21	Sequence 21, Appl	C 231	11.2	58.9	24	3	US-09-906-646-404	Sequence 404, Appl
159	11.2	58.9	25	2	US-08-412-376-3	Sequence 3, Appl	C 232	11.2	58.9	24	3	US-09-904-462-404	Sequence 404, Appl
160	11.2	58.9	25	3	US-09-396-196G-578	Sequence 578, App	C 233	11.2	58.9	24	3	US-09-902-736A-404	Sequence 404, Appl
161	11.2	58.9	25	3	US-08-396-196G-10055	Sequence 10055, A	C 234	11.2	58.9	24	3	US-09-906-722A-404	Sequence 404, Appl
162	11.2	58.9	25	3	US-09-396-196G-36507	Sequence 36507, A	C 235	11.2	58.9	24	3	PCT-US93-05085-27	Sequence 27, Appl
163	11.2	58.9	25	3	US-09-396-196G-36508	Sequence 36508, A	C 236	11.2	58.9	25	3	US-08-930-500-33	Sequence 33, Appl
164	11.2	58.9	25	3	US-09-396-196G-36509	Sequence 36509, A	C 237	11.2	58.9	25	3	US-08-853-774-19	Sequence 19, Appl
165	11.2	58.9	25	3	US-09-396-196G-36511	Sequence 36511, A	C 238	11.2	58.9	25	3	US-08-985-492-28	Sequence 28, Appl
166	11.2	58.9	25	3	US-09-396-196G-38689	Sequence 38689, A	C 239	11.2	58.9	25	3	US-09-396-196G-41590	Sequence 41590, A
167	11.2	58.9	25	3	US-09-396-196G-63408	Sequence 63408, A	C 240	11.2	58.9	25	3	US-09-396-196G-52109	Sequence 52109, A
168	11.2	58.9	25	3	US-09-396-196G-78260	Sequence 78260, A	C 241	11.2	58.9	25	3	US-09-396-196G-111375	Sequence 111375,
169	11.2	58.9	25	3	US-09-396-196G-82486	Sequence 82486, A	C 242	11.2	58.9	25	3	US-09-254-032B-2	Sequence 2, Appl
170	11.2	58.9	25	3	US-09-396-196G-104668	Sequence 104668,	C 243	11.2	58.9	25	3		

244 11 57.9 27 2 US-08-375-116A-126 Sequence 126, App  
c 245 11 57.9 27 3 US-09-050-739-162 Sequence 162, App  
246 11 57.9 28 3 US-09-622-745B-16 Sequence 16, App  
247 11 57.9 28 3 US-09-622-745B-17 Sequence 17, App  
248 11 57.9 29 2 US-07-931-473B-32 Sequence 32, App  
249 11 57.9 29 2 US-07-714-131C-32 Sequence 32, App  
250 11 57.9 29 2 US-08-412-110-32 Sequence 32, App  
251 11 57.9 29 2 US-08-409-442A-32 Sequence 32, App  
252 11 57.9 29 3 US-08-469-609A-32 Sequence 32, App  
253 11 57.9 29 3 US-09-143-190-32 Sequence 32, App  
254 11 57.9 29 3 US-09-502-344-32 Sequence 32, App  
c 255 11 57.9 29 3 US-09-304-232-10 Sequence 10, App  
256 11 57.9 29 3 US-10-037-986-32 Sequence 32, App  
257 11 57.9 30 3 US-08-979-608A-39 Sequence 39, App  
c 258 11 57.9 30 3 US-09-517-849-39 Sequence 39, App  
c 259 11 57.9 30 3 US-09-616-289-39 Sequence 39, App  
c 260 11 57.9 30 3 US-09-976-740-39 Sequence 39, App  
261 11 57.9 32 3 US-09-214-453A-70 Sequence 70, App  
c 262 11 57.9 33 2 US-08-138-608-11 Sequence 11, App  
c 263 11 57.9 33 3 US-09-050-739-99 Sequence 99, App  
c 264 11 57.9 33 3 US-08-030-175-36 Sequence 36, App  
c 265 11 57.9 33 3 US-10-111-552A-5 Sequence 5, App  
266 11 57.9 34 3 US-09-308-759A-39 Sequence 39, App  
267 11 57.9 37 3 US-09-143-270-8 Sequence 8, App  
268 11 57.9 37 3 US-09-450-083-8 Sequence 8, App  
269 11 57.9 37 3 US-09-417-418-2 Sequence 2, App  
270 11 57.9 37 3 US-09-887-854-8 Sequence 8, App  
271 11 57.9 39 2 US-08-222-124-5 Sequence 5, App  
272 11 57.9 39 2 US-08-842-657A-5 Sequence 5, App  
273 11 57.9 39 3 US-10-030-203-2 Sequence 2, App  
c 274 11 57.9 42 2 US-08-087-387-2 Sequence 2, App  
c 275 11 57.9 42 2 US-08-455-627-2 Sequence 2, App  
c 276 11 57.9 42 2 US-08-461-271-2 Sequence 2, App  
c 277 11 57.9 42 2 US-08-713-685A-2 Sequence 2, App  
c 278 11 57.9 42 2 US-08-689-856-2 Sequence 2, App  
c 279 11 57.9 42 3 US-09-070-477-2 Sequence 15, App  
c 280 11 57.9 42 3 US-08-872-056-15 Sequence 86, App  
c 281 11 57.9 42 3 US-09-475-947A-86 Sequence 46, App  
282 11 57.9 46 2 US-08-596-387B-46 Sequence 46, App  
283 11 57.9 46 3 US-09-067-615-46 Sequence 46, App  
c 284 11 57.9 46 6 PCT-US95-09816A-46 Sequence 584, App  
c 285 11 57.9 47 3 US-09-422-978-584 Sequence 3391, App  
286 11 57.9 47 3 US-09-422-978-3391 Sequence 345, App  
287 11 57.9 50 3 US-09-025-769B-345 Sequence 346, App  
c 288 11 57.9 50 3 US-09-025-769B-346 Sequence 347, App  
c 289 11 57.9 50 3 US-09-025-769B-347 Sequence 6, App  
290 11 57.9 50 3 US-09-293-505-6 Sequence 345, App  
291 11 57.9 50 3 US-09-490-070A-345 Sequence 346, App  
c 292 11 57.9 50 3 US-09-490-070A-346 Sequence 347, App  
293 11 57.9 50 3 US-09-490-070A-347 Sequence 345, App  
294 11 57.9 50 3 US-09-490-153-345 Sequence 346, App  
c 295 11 57.9 50 3 US-09-490-153-346 Sequence 347, App  
296 11 57.9 50 3 US-09-490-153-347 Sequence 6, App  
297 11 57.9 50 3 US-09-060-939A-6 Sequence 345, App  
c 298 11 57.9 50 3 US-09-490-324-345 Sequence 346, App  
c 299 11 57.9 50 3 US-09-490-324-346 Sequence 347, App  
300 11 57.9 50 3 US-09-490-324-347

## ALIGNMENTS

RESULT 1  
US-08-386-063-1  
; Sequence 1, Application US/08386063  
; Patent No. 608200  
; GENERAL INFORMATION:  
; APPLICANT: Arthur M. Krieg, M.D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/386,063  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ARNOLD, BETH E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: UIZ-013CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-386-063-1  
Query Match 74.7%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 7.1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGGTGACGTTGAGGGGG 19  
||| ||||| |||||  
Db 2 GGGTCAACGTTGAGGGGG 20  
||| ||||| |||||  
RESULT 2  
US-08-386-063-1  
; Sequence 1, Application US/08386063  
; Patent No. 6194388  
; GENERAL INFORMATION:  
; APPLICANT: Arthur M. Krieg, M.D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 STATE STREET, SUITE 510  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/386,063  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ARNOLD, BETH E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: UIZ-013CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-386-063-1

Query Match          74.7%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
    ||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 3
US-09-082-649B-63
; Sequence 63, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Kries, Arthur M.
; APPLICANT: Schorr, Joachim
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-63

Query Match          74.7%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
    ||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 4
US-09-965-101-63
; Sequence 63, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Kries, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCl/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-63

Query Match          74.7%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
    ||| ||||| |||||
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 5
US-09-538-873-18/c
; Sequence 18, Application US/09538873
; Patent No. 6566500
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
; TITLE OF INVENTION: SYNDROME (VLS)
; FILE REFERENCE: UTSD:603
; CURRENT APPLICATION NUMBER: US/09/538,873
; CURRENT FILING DATE: 2000-03-30
; EARLIER APPLICATION NUMBER: 60/126,826
; EARLIER FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-538-873-18

Query Match          73.7%; Score 14; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGG 16
    ||| ||||| |||||
Db 26 GGTGACGTTTCAGGG 13

RESULT 6
US-10-282-935-18/c
; Sequence 18, Application US/10282935
; Patent No. 6960652
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
; TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
; FILE REFERENCE: UTSD:884US
; CURRENT APPLICATION NUMBER: US/10/282,935
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
```

; SEQ ID NO 18  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
US-10-282-935-18

Query Match 73.7%; Score 14; DB 3; Length 39;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGTGACGTCAGG 16  
|||||  
Db 26 GGTGACGTCAGG 13

RESULT 7  
US-08-852-001-5  
; Sequence 5, Application US/08852001  
; Patent No. 6197556  
; GENERAL INFORMATION:  
; APPLICANT: Ulanovsky, Levy  
; APPLICANT: Mugasimangalam, Raja C.  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION USING MODULAR  
; TITLE OF INVENTION: BRANCHED PRIMERS  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BRINKS, HOFER, GILSON & LIONE  
; STREET: NBC Tower - Suite 3600, 455 N. Cityfront  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60611-5599

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/852,001  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Martin, Alice O.  
; REGISTRATION NUMBER: 35,601  
; REFERENCE/DOCKET NUMBER: 6837/7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-321-4200  
; TELEFAX: 312-321-4299  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "primer"  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 18..19  
; OTHER INFORMATION: /product= "N = inosine"  
US-08-852-001-5

Query Match 70.5%; Score 13.4; DB 3; Length 22;  
Best Local Similarity 93.3%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TGACGTCAGGGGG 19  
|||||  
Db 2 TGACGTCAGGGGTG 16

RESULT 8

US-10-131-827-3663  
; Sequence 3663, Application US/10131827  
; Patent No. 6905827  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Lv, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131,827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290  
; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3663  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-3663

Query Match 69.5%; Score 13.2; DB 3; Length 50;  
Best Local Similarity 83.3%; Pred. No. 2.4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTCAGGGG 18  
|||||  
Db 1 GCGTGCCGTTGAGGGG 18

RESULT 9

US-08-666-221B-29/c  
; Sequence 29, Application US/08666221B  
; Patent No. 6136544  
; GENERAL INFORMATION:  
; APPLICANT: Kamboj, Rajender  
; APPLICANT: Nutt, Stephen  
; TITLE OF INVENTION: GLUTAMATE RECEPTOR (OR EAA RECEPTOR)  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/666,221B  
; FILING DATE: 20-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 016777/0308  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399

; TELEX: 904136					
; INFORMATION FOR SEQ ID NO: 29:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 20 base pairs					
; TYPE: nucleic acid					
; STRANDEDNESS: single					
; TOPOLOGY: linear					
; MOLECULE TYPE: other nucleic acid					
; DESCRIPTION: /desc = "primer"					
US-08-666-221B-29					
Query Match 67.4%; Score 12.8; DB 3; Length 20;					
Best Local Similarity 87.5%; Pred. No. 3.5e+03;					
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
Qy	2	GGGTGACGTTTCAGGGG	17		
Db	16	GGGTGATGGTTCAGGGG	1		
RESULT 10					
US-09-396-196G-120261/c					
; Sequence 120261, Application US/09396196G					
; Patent No. 6821724					
; GENERAL INFORMATION:					
; APPLICANT: Michael Mittmann					
; APPLICANT: David Mack					
; APPLICANT: David Lockhart					
; APPLICANT: Affimetrix, Inc.					
; TITLE OF INVENTION: Methods of Genetic Analysis					
; FILE REFERENCE: 3101.1					
; CURRENT APPLICATION NUMBER: US/09/396,196G					
; CURRENT FILING DATE: 1999-09-15					
; PRIOR APPLICATION NUMBER: 60/100,678					
; PRIOR FILING DATE: 1998-09-17					
; NUMBER OF SEQ ID NOS: 127806					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 120261					
; LENGTH: 25					
; TYPE: DNA					
; ORGANISM: mus musculus					
US-09-396-196G-120261					
Query Match 67.4%; Score 12.8; DB 3; Length 25;					
Best Local Similarity 87.5%; Pred. No. 3.6e+03;					
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
Qy	2	GGGTGACGTTTCAGGGG	17		
Db	18	GGGTGAAGTTTCATGGG	3		
RESULT 11					
US-07-951-715A-43/c					
; Sequence 43, Application US/07951715A					
; Patent No. 5625136					
; GENERAL INFORMATION:					
; APPLICANT: Koziel, Michael G.					
; APPLICANT: Desai, Nalini M.					
; APPLICANT: Lewis, Kelly S.					
; APPLICANT: Kramer, Vance C.					
; APPLICANT: Warren, Gregory W.					
; APPLICANT: Evola, Stephen V.					
; APPLICANT: Croesland, Lyle D.					
; APPLICANT: Wright, Martha S.					
; APPLICANT: Merlin, Ellis J.					
; APPLICANT: Launis, Karen L.					
; APPLICANT: Rothstein, Steven J.					
; APPLICANT: Bowman, Cindy G.					
; APPLICANT: Dawson, John L.					
; APPLICANT: Dunder, Erik M.					
; APPLICANT: Pace, Gary M.					
; APPLICANT: Suttie, Janet L.					
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED					
; INSECTICIDAL ACTIVITY IN MAIZE					
; NUMBER OF SEQUENCES: 94					



APPLICANT: Suttle, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 607518artis Corporation

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/459,504B

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/459,595

; FILING DATE: 02-JUN-1995

; APPLICATION NUMBER: US 07/951,715

; FILING DATE: 25-SEP-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8587

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 32 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "primer P5(a) "

; HYPOTHETICAL: NO

; US-08-459-504B-43

Query Match

Best Local Similarity 67.4%; Score 12.8; DB 3; Length 32;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 18

||||| ||||| |||||

Db 18 GGTGCCGTACAGGGGG 3

RESULT 15

US-08-459-444-43/c

; Sequence 43, Application US/08459444A

; Patent No. 6121014

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; Desai, Nalini M.

; Lewis, Kelly S.

; Kramer, Vance C.

; Warren, Gregory W.

; Evola, Stephen V.

; Crossland, Lyle D.

; Wright, Martha S.

; Merlin, Ellis J.

; Launis, Karen L.

; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED

; NUCLEIC ACID CODING SEQUENCE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/459,444A

; FILING DATE: 02-Jun-1995

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/951,715

; FILING DATE: 25-SEP-1992

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8587

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 32 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "primer P5(a) "

; HYPOTHETICAL: NO

; SEQUENCE DESCRIPTION: SEQ ID NO: 43:

; US-08-459-444-43

Query Match

Best Local Similarity 67.4%; Score 12.8; DB 3; Length 32;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 18

||||| ||||| |||||

Db 18 GGTGCCGTACAGGGGG 3

RESULT 16

US-09-547-422-43/c

; Sequence 43, Application US/09547422

; Patent No. 6320100

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; Desai, Nalini M.

; Lewis, Kelly S.

; Kramer, Vance C.

; Warren, Gregory W.

; Evola, Stephen V.

; Crossland, Lyle D.

; Wright, Martha S.

; Merlin, Ellis J.

; Launis, Karen L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: NC

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

```
/
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/547,422
/ FILING DATE: 11-Apr-2000
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/459,595
/ FILING DATE: 02-JUN-1995
/ APPLICATION NUMBER: US 07/951,715
/ FILING DATE: 25-SEP-1992
/ APPLICATION NUMBER: US 07/772,027
/ FILING DATE: 04-OCT-1991
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meigs, J. Timothy
/ REGISTRATION NUMBER: 38,241
/ REFERENCE/DOCKET NUMBER: S-18805H
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (919)541-8587
/ TELEFAX: (919)541-8689
/
/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 32 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "primer P5(a)"
/ HYPOTHETICAL: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-547-422-43

Query Match 57.4%; Score 12.8; DB 3; Length 32;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 18
Db 18 GGTGCGGTACAGGGGG 3

RESULT 17
US-09-988-462-43/c
; Sequence 43, Application US/09988462
; Patent No. 6720488
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
;
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
;
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Syngenta Biotechnology, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
;
; COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/988,462
/ FILING DATE: 20-No. 6720488-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 09/547,422
/ FILING DATE: 11-Apr-2000
/ APPLICATION NUMBER: US 08/459,504
/ FILING DATE: 02-JUN-1995
/ APPLICATION NUMBER: US 07/951,715
/ FILING DATE: 25-SEP-1992
/ APPLICATION NUMBER: US 07/772,027
/ FILING DATE: 04-OCT-1991
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meigs, J. Timothy
/ REGISTRATION NUMBER: 38,241
/ REFERENCE/DOCKET NUMBER: S-18805I
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (919)541-8587
/ TELEFAX: (919)541-8689
/
/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 32 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "primer P5(a)"
/ HYPOTHETICAL: NO
/ SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-988-462-43

Query Match 67.4%; Score 12.8; DB 3; Length 32;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGGG 18
Db 18 GGTGCGGTACAGGGGG 3

RESULT 18
US-10-131-827-4733/c
; Sequence 4733, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4733
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; US-10-131-827-4733

Query Match 67.4%; Score 12.8; DB 3; Length 50;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTGACGTTTCAGGGGG 19
Db 19 GTGACGTTTCAGGGGG 19
```

```
Db      21 GTGACGTTCTGGGAGG 6

RESULT 19
US-09-672-126B-27
; Sequence 27, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic Oligonucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)...(13)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)...(18)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)...(19)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
US-09-672-126B-27

Query Match      66.3%; Score 12.6; DB 3; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGGG 19
Db      1 GGGTCGACGTCGAGGGGGG 19

RESULT 20
US-08-738-652-12
; Sequence 12, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-12

Query Match      66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGGG 19
Db      2 GGGTCAACGTTGAGGGGGG 20

RESULT 21
US-09-030-701-63
; Sequence 63, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-63

Query Match      66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGGG 19
Db      2 GGGTCAACGTTGAGGGGGG 20

RESULT 22
US-08-960-774-90
; Sequence 90, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieg et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
```

```
/ FILING DATE: October 30, 1996
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Haile, Lisa A.
/ REGISTRATION NUMBER: 38,347
/ REFERENCE/DOCKET NUMBER: 08918/012001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619/678-5070
/ TELEFAX: 619/678-5099
/ INFORMATION FOR SEQ ID NO: 90:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-08-960-774-90

Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 23
US-09-082-649B-52
/ Sequence 52, Application US/09082649B
/ Patent No. 6339068
/ GENERAL INFORMATION:
/ APPLICANT: Davis, Heather L.
/ APPLICANT: Krieg, Arthur M.
/ APPLICANT: Schorzi, Joachim
/ APPLICANT: Wu, Tong
/ TITLE OF INVENTION: Vectors and Methods for Immunization or
/ TITLE OF INVENTION: Therapeutic Protocols
/ FILE REFERENCE: C1039/7009
/ CURRENT APPLICATION NUMBER: US/09/082,649B
/ PRIOR FILING DATE: 1997-05-20
/ PRIOR FILING DATE: 1997-05-20
/ PRIOR FILING DATE: 1997-05-20
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 52
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic oligonucleotide
/ NAME/KEY: misc_Feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Has a phosphorothioate backbone.
US-09-082-649B-52

Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 24
US-09-082-649B-59
/ Sequence 59, Application US/09082649B
/ Patent No. 6339068
/ GENERAL INFORMATION:
/ APPLICANT: Davis, Heather L.
```

```
/ APPLICANT: Krieg, Arthur M.
/ APPLICANT: Schorzi, Joachim
/ APPLICANT: Wu, Tong
/ TITLE OF INVENTION: Vectors and Methods for Immunization or
/ TITLE OF INVENTION: Therapeutic Protocols
/ FILE REFERENCE: C1039/7009
/ CURRENT APPLICATION NUMBER: US/09/082,649B
/ PRIOR FILING DATE: 1998-05-20
/ PRIOR FILING DATE: 1997-05-20
/ PRIOR FILING DATE: 1997-05-20
/ PRIOR FILING DATE: 1997-05-20
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 59
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic oligonucleotide
/ NAME/KEY: misc_Feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Has SOS-ODN backbone with two S-linkages at the 5'
/ OTHER INFORMATION: end, five S-linkages at the 3' end, and O-linkages
/ OTHER INFORMATION: in between.
US-09-082-649B-59
```

```
Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTGAGGGGG 20
```

```
RESULT 25
US-09-191-170-47
/ Sequence 47, Application US/09191170
/ Patent No. 6429199
/ GENERAL INFORMATION:
/ APPLICANT: Krieg, Arthur M.
/ APPLICANT: Hartmann, Gunther
/ TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
/ TITLE OF INVENTION: for Activating Dendritic Cells
/ FILE REFERENCE: C1039/7017
/ CURRENT APPLICATION NUMBER: US/09/191,170
/ PRIOR FILING DATE: 1998-11-13
/ EARLIER FILING DATE: 1997-10-30
/ EARLIER FILING DATE: 1997-10-30
/ EARLIER FILING DATE: 1996-10-30
/ EARLIER FILING DATE: 1995-02-07
/ EARLIER FILING DATE: 1994-07-15
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 47
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic oligonucleotide
US-09-191-170-47
```

```
Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTGAGGGGG 20
```

RESULT 26  
US-09-337-619-12  
; Sequence 12, Application US/09337619  
; Patent No. 6653292  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; TITLE OF INVENTION: Methods of Treating Cancer Using  
; FILE REFERENCE: C1039/7021/HCL  
; CURRENT APPLICATION NUMBER: US/09/337,619  
; CURRENT FILING DATE: 1999-06-21  
; EARLIER APPLICATION NUMBER: US 08/960,774  
; EARLIER FILING DATE: 1997-10-30  
; EARLIER APPLICATION NUMBER: US 08/738,652  
; EARLIER FILING DATE: 1996-10-30  
; EARLIER APPLICATION NUMBER: US 08/386,063  
; EARLIER FILING DATE: 1995-02-07  
; EARLIER APPLICATION NUMBER: US 08/276,358  
; EARLIER FILING DATE: 1994-07-15  
; NUMBER OF SEQ ID NOS: 123  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-09-337-619-12

Query Match 66.3%; Score 12.6; DB 3; Length 20;  
Best Local Similarity 78.9%; Pred. No. 4.4e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19  
||| ||||| ||||| |||||  
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 27  
US-09-965-101-52  
; Sequence 52, Application US/09965101  
; Patent No. 6821957  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Heather L.  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Wu, Tong  
; TITLE OF INVENTION: Vectors and Methods for Immunization or  
; FILE REFERENCE: C1039/7057 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/965,101  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 09/082,649  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,233  
; PRIOR FILING DATE: 1997-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,209  
; PRIOR FILING DATE: 1997-05-20  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 52  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
; NAME/KEY: misc feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Has a phosphorothioate backbone.  
US-09-965-101-52

Query Match 66.3%; Score 12.6; DB 3; Length 20;

Best Local Similarity 78.9%; Pred. No. 4.4e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19  
||| ||||| ||||| |||||  
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 28  
US-09-965-101-59  
; Sequence 59, Application US/09965101  
; Patent No. 6821957  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Heather L.  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Wu, Tong  
; TITLE OF INVENTION: Vectors and Methods for Immunization or  
; FILE REFERENCE: C1039/7057 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/965,101  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 09/082,649  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,233  
; PRIOR FILING DATE: 1997-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,209  
; PRIOR FILING DATE: 1997-05-20  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 59  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
; NAME/KEY: misc feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Has SOS-ODN backbone with two S-linkages at the 5',  
; OTHER INFORMATION: end, five S-linkages at the 3' end, and O-linkages  
; OTHER INFORMATION: in between.  
US-09-965-101-59

Query Match 66.3%; Score 12.6; DB 3; Length 20;  
Best Local Similarity 78.9%; Pred. No. 4.4e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19  
||| ||||| ||||| |||||  
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 29  
US-09-672-126B-1  
; Sequence 1, Application US/09672126B  
; Patent No. 6949520  
; GENERAL INFORMATION:  
; APPLICANT: Hartmann, Gunther  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Krieg, Arthur  
; TITLE OF INVENTION: Methods Related to Immunostimulatory  
; FILE REFERENCE: C1039/7044  
; CURRENT APPLICATION NUMBER: US/09/672,126B  
; CURRENT FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/156,147  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA

Query Match 66.3%; Score 12.6; DB 3; Length 20;  
Best Local Similarity 78.9%; Pred. No. 4.4e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19  
||| ||||| ||||| |||||  
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 28  
US-09-965-101-59  
; Sequence 59, Application US/09965101  
; Patent No. 6821957  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Heather L.  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Wu, Tong  
; TITLE OF INVENTION: Vectors and Methods for Immunization or  
; FILE REFERENCE: C1039/7057 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/965,101  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 09/082,649  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,233  
; PRIOR FILING DATE: 1997-05-20  
; PRIOR APPLICATION NUMBER: US 60/047,209  
; PRIOR FILING DATE: 1997-05-20  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 59  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
; NAME/KEY: misc feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: Has SOS-ODN backbone with two S-linkages at the 5',  
; OTHER INFORMATION: end, five S-linkages at the 3' end, and O-linkages  
; OTHER INFORMATION: in between.  
US-09-965-101-59

Query Match 66.3%; Score 12.6; DB 3; Length 20;  
Best Local Similarity 78.9%; Pred. No. 4.4e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19  
||| ||||| ||||| |||||  
Db 2 GGGTCAACGTTGAGGGGG 20

RESULT 29  
US-09-672-126B-1  
; Sequence 1, Application US/09672126B  
; Patent No. 6949520  
; GENERAL INFORMATION:  
; APPLICANT: Hartmann, Gunther  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Krieg, Arthur  
; TITLE OF INVENTION: Methods Related to Immunostimulatory  
; FILE REFERENCE: C1039/7044  
; CURRENT APPLICATION NUMBER: US/09/672,126B  
; CURRENT FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/156,147  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(2)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)...(14)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)...(19)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (20)...(20)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
;
US-09-672-126B-1
```

```
Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GGGGTGACGTTTCAGGGGGG 19
   ||| ||||| |||||
Db 2 GGGTCAACGTTGAGGGGGG 20
```

```
RESULT 30
US-09-672-126B-5
; Sequence 5, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(20)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
;
US-09-672-126B-5
```

```
Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GGGGTGACGTTTCAGGGGGG 19
   ||| ||||| |||||
Db 2 GGGTCAACGTTGAGGGGGG 20
```

```
RESULT 31
US-09-672-126B-135
; Sequence 135, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
```

```
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 135
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
;
US-09-672-126B-135
```

```
Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GGGGTGACGTTTCAGGGGGG 19
   ||| ||||| |||||
Db 2 GGGTCAACGTTGAGGGGGG 20
```

```
RESULT 32
US-09-672-126B-136
; Sequence 136, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 136
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
;
US-09-672-126B-136
```

```
Query Match 66.3%; Score 12.6; DB 3; Length 20;
Best Local Similarity 78.9%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 GGGGTGACGTTTCAGGGGGG 19
   ||| ||||| |||||
Db 2 GGGTCAACGTTGAGGGGGG 20
```

```
RESULT 33
US-09-672-126B-156
; Sequence 156, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon
```

```

; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 156
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)...(15)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)...(20)
; OTHER INFORMATION: Backbone has phosphorothioate linkages.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)...(21)
; OTHER INFORMATION: Backbone has phosphodiester linkages.
US-09-672-126B-156
```

```

Query Match          66.3%; Score 12.6; DB 3; Length 21;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 GGGGTGACGTTTCAGGGGGG 19
      ||| ||||| ||||| |||||
Db       3 GGGTCACGTTGAGGGGGG 21
```

```

RESULT 34
US-09-396-196G-78259/c
; Sequence 78259, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78259
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-78259
```

```

Query Match          66.3%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 GGGGTGACGTTTCAGGGGGG 19
      ||| ||||| ||||| |||||
Db      19 GGTGTCAGATCAGGGGAG 1
```

RESULT 35

```

US-09-672-126B-165
; Sequence 165, Application US/09672126B
; Patent No. 6949520
; GENERAL INFORMATION:
; APPLICANT: Hartmann, Gunther
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Krieg, Arthur
; TITLE OF INVENTION: Methods Related to Immunostimulatory
; FILE REFERENCE: C1039/7044
; CURRENT APPLICATION NUMBER: US/09/672,126B
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/156,147
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 165
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-672-126B-165
```

```

Query Match          66.3%; Score 12.6; DB 3; Length 30;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 GGGGTGACGTTTCAGGGGGG 19
      ||| ||||| ||||| |||||
Db       8 GGGGGAACGTTGGGGGGG 26
```

```

RESULT 36
US-09-907-794A-225/c
; Sequence 225, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
```





APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Faoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/902,775A  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 225  
LENGTH: 44  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: oligonucleotide probe

US-09-902-775A-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;  
Best Local Similarity 78.9%; Pred. No. 4.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 39  
US-09-906-700-225/c  
Sequence 225, Application US/09906700  
Patent No. 6723535  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Faoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/906,700  
CURRENT FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 225  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide probe  
US-09-906-700-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;  
Best Local Similarity 78.9%; Pred. No. 4.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19  
Db 19 GGAGCGTCGCTCAGGGGGG 1

## RESULT 40

US-09-903-603A-225/c

; Sequence 225, Application US/09903603A

; Patent No. 6767995

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: GNE.1618P2C12

; CURRENT APPLICATION NUMBER: US/09/903,603A

; CURRENT FILING DATE: 2001-07-11

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR FILING DATE: 1999-07-07

; PRIOR FILING DATE: 1999-07-07

; PRIOR FILING DATE: 1999-07-26

; PRIOR FILING DATE: 1999-07-28

; PRIOR FILING DATE: 1999-09-08

; PRIOR FILING DATE: 1999-09-13

; PRIOR FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1999-09-15

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 225  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide probe  
US-09-903-603A-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;

Best Local Similarity 78.9%; Pred. No. 4.8e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19

Db 19 GGAGCGTCGCTCAGGGGGG 1

## RESULT 41

US-09-904-920A-225/c

; Sequence 225, Application US/09904920A

; Patent No. 6806352

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/904,920A

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

;  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 225  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide probe  
US-09-904-920A-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;  
Best Local Similarity 78.9%; Pred. No. 4.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19  
Db 19 GGAGCGTCGCTCAGGGGG 1

RESULT 42  
US-09-909-064-225/c  
; Sequence 225, Application US/09909064  
; Patent No. 6818449  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, A.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth, J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Mather, Jennie P.

;  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William, I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: 10466-14  
; CURRENT APPLICATION NUMBER: US/09/909,064  
; CURRENT FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: US 60/143,048  
; PRIOR FILING DATE: 1999-07-07  
; PRIOR APPLICATION NUMBER: US 60/145,698  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: US 60/146,222  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: PCT/US99/20594  
; PRIOR FILING DATE: 1999-09-08  
; PRIOR APPLICATION NUMBER: PCT/US99/20944  
; PRIOR FILING DATE: 1999-09-13  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/21547  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: PCT/US99/23089  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: PCT/US99/28214  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: PCT/US99/28564  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/28565  
; PRIOR FILING DATE: 1999-12-02  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: PCT/US99/30911  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US99/30999  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 423  
; SEQ ID NO 225  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: oligonucleotide probe  
US-09-909-064-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;  
Best Local Similarity 78.9%; Pred. No. 4.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19  
Db 19 GGAGCGTCGCTCAGGGGG 1

RESULT 43  
US-09-905-381A-225/c  
; Sequence 225, Application US/09905381A  
; Patent No. 6818746  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, A.  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth, J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Mather, Jennie P.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William, I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: 10466-14  
 ; CURRENT APPLICATION NUMBER: US/09/905,381A  
 ; CURRENT FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: 2000-02-22  
 ; PRIOR APPLICATION NUMBER: US 60/143,048  
 ; PRIOR FILING DATE: 1999-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/145,698  
 ; PRIOR FILING DATE: 1999-07-26  
 ; PRIOR APPLICATION NUMBER: US 60/146,222  
 ; PRIOR FILING DATE: 1999-07-28  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594  
 ; PRIOR FILING DATE: 1999-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944  
 ; PRIOR FILING DATE: 1999-09-13  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089  
 ; PRIOR FILING DATE: 1999-10-05  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214  
 ; PRIOR FILING DATE: 1999-11-29  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: 1999-11-30  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219  
 ; PRIOR FILING DATE: 2000-01-05  
 ; NUMBER OF SEQ ID NOS: 423  
 ; SEQ ID NO 225  
 ; LENGTH: 44  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: oligonucleotide probe  
 ; US-09-905-381A-225  
 Query Match 66.3%; Score 12.6; DB 3; Length 44;  
 Best Local Similarity 78.9%; Pred. No. 4.8e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 GGGGTGACGTTTCAGGGGG 19  
 |||||  
 Db 19 GGAGCGTCGCTCAGGGGG 1  
 |||||  
 RESULT 44  
 ; US-09-906-618-225/c  
 ; Sequence 225, Application US/09906618  
 ; Patent No. 6828146  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genentech, Inc.  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, A.  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth, J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Mather, Jennie P.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William, I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: 10466-14  
 ; CURRENT APPLICATION NUMBER: US/09/906,618  
 ; CURRENT FILING DATE: 2001-07-16  
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414  
 ; PRIOR FILING DATE: 2000-02-22  
 ; PRIOR APPLICATION NUMBER: US 60/143,048  
 ; PRIOR FILING DATE: 1999-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/145,698  
 ; PRIOR FILING DATE: 1999-07-26  
 ; PRIOR APPLICATION NUMBER: US 60/146,222  
 ; PRIOR FILING DATE: 1999-07-28  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20594  
 ; PRIOR FILING DATE: 1999-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US99/20944  
 ; PRIOR FILING DATE: 1999-09-13  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/21547  
 ; PRIOR FILING DATE: 1999-09-15  
 ; PRIOR APPLICATION NUMBER: PCT/US99/23089  
 ; PRIOR FILING DATE: 1999-10-05  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28214  
 ; PRIOR FILING DATE: 1999-11-29  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313  
 ; PRIOR FILING DATE: 1999-11-30  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28564  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28565  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30911  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30999  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US00/00219  
 ; PRIOR FILING DATE: 2000-01-05  
 ; NUMBER OF SEQ ID NOS: 423  
 ; SEQ ID NO 225  
 ; LENGTH: 44  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: oligonucleotide probe  
 ; US-09-905-381A-225

PRIOR FILING DATE: 1999-09-15

;  
PRIOR APPLICATION NUMBER: 03

;  
PRIOR APPLICATION NUMBER: 03

; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 225
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe
US-09-904-462-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;
Best Local Similarity 78.9%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
||| ||| ||| ||| ||| |||
Db 19 GGAGCGTCGCTCAGGGGG 1

RESULT 47
US-09-902-736A-225/c
; Sequence 225, Application US/09902736A
; Patent No. 6894148
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,736A
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 225
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe
US-09-902-736A-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;
Best Local Similarity 78.9%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
||| ||| ||| ||| ||| |||
Db 19 GGAGCGTCGCTCAGGGGG 1

RESULT 48
US-09-906-722A-225/c
; Sequence 225, Application US/09906722A
; Patent No. 6946262
; GENERAL INFORMATION:

APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: GNE.1618P2C61  
CURRENT APPLICATION NUMBER: US/09/906,722A  
CURRENT FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 225  
LENGTH: 44  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: oligonucleotide probe  
US-09-906-722A-225

Query Match 66.3%; Score 12.6; DB 3; Length 44;  
Best Local Similarity 78.9%; Pred. No. 4.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGG 19  
DB 19 GGAGCGTCGCTCAGGGGG 1  
RESULT 49  
US-09-641-638-1255/c  
Sequence 1255, Application US/09641638  
Patent No. 6432648  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
FILE REFERENCE: GENSET.051CPI  
CURRENT APPLICATION NUMBER: US/09/641,638  
CURRENT FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent.pm  
SEQ ID NO 1255  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 10-387-371 : polymorphic base C or T  
US-09-641-638-1255  
Query Match 66.3%; Score 12.6; DB 3; Length 47;  
Best Local Similarity 78.9%; Pred. No. 4.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1 GGGGTGACGTTTCAGGGGG 19  
DB 44 GGGGTGCTGTCAGGGGTGG 26  
RESULT 50  
US-10-170-097-1255/c  
Sequence 1255, Application US/10170097  
Patent No. 6794143  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
FILE REFERENCE: GEN-T114XC2D1  
CURRENT APPLICATION NUMBER: US/10/170,097  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: US 09/641,638  
PRIOR FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07



```
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 1255
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-387-371 : polymorphic base C or T
US-10-170-097-1255
```

```
Query Match      66.3%; Score 12.6; DB 3; Length 47;
Best Local Similarity 78.9%; Pred. No. 4.8e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTCCAGGGGG 19
        ||||| ||||| ||
Db      44 GGGGTGCTGTCAGGGTGG 26
```

Search completed: February 15, 2006, 21:14:14  
Job time : 47.7107 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 01:43:22 ; Search time 275.736 Seconds  
(without alignments) 569.815 Million cell updates/sec

**Title:** US-09-669-187A-80

Perfect score:

Sequence: 1 qqqqtqacqttcagggggg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs. 4134689005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0

Maximum DB seq length:	0
Maximum DB seq length:	50

Post-processing: Minimum Match 0%

POST-PROCESSING: Minimum Match 0%  
Maximum Match 100%

Maximum Match 100%  
Listing first 300 summaries

Database :

Database : Published Applications NA Main:\*

Database : Eukaryotic Applications - In Public  
1: /cqn2\_6/ptodata/1/pubpna/US07 PUBCOMB.seq.\*

2: /cqn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:★

3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:

4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:

5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:

6: /cgn2\_6/ptodata/1/pubpna/us10b\_PUBCOMB.seq:

```
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
```

```
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
```

9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:

10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C	1	19	100.0	19	3	US-09-888-326-447 Sequence 447, App
	2	19	100.0	19	3	US-09-776-479-80 Sequence 80, Appl
	3	19	100.0	19	3	US-09-776-479-80 Sequence 80, Appl
	4	19	100.0	19	5	US-10-112-653-74 Sequence 74, Appl
	5	19	100.0	19	5	US-10-017-995-80 Sequence 80, Appl
	6	19	100.0	19	6	US-10-314-578-80 Sequence 80, Appl
	7	19	100.0	19	8	US-10-831-778-80 Sequence 80, Appl
	8	17.4	91.6	19	3	US-09-888-326-448 Sequence 448, App
	9	17.4	91.6	19	3	US-09-776-479-82 Sequence 82, Appl
	10	17.4	91.6	19	3	US-09-776-479-82 Sequence 82, Appl
	11	17.4	91.6	19	5	US-10-112-653-76 Sequence 76, Appl
	12	17.4	91.6	19	5	US-10-017-995-82 Sequence 82, Appl
	13	17.4	91.6	19	6	US-10-314-578-82 Sequence 82, Appl
	14	17.4	91.6	19	8	US-10-831-778-82 Sequence 82, Appl
	15	15.4	81.1	25	10	US-11-036-317-815104 Sequence 815104, App
	16	14.2	74.7	20	3	US-09-415-142-1 Sequence 1, Appli
	17	14.2	74.7	20	3	US-09-888-326-449 Sequence 449, App
	18	14.2	74.7	20	3	US-09-931-583-1 Sequence 1, Appli
	19	14.2	74.7	20	3	US-09-776-479-224 Sequence 224, App
	20	14.2	74.7	20	3	US-09-776-479-224 Sequence 224, App
	21	14.2	74.7	20	3	US-09-965-101-63 Sequence 63, Appl
	22	14.2	74.7	20	5	US-10-112-653-216 Sequence 216, App
	23	14.2	74.7	20	5	US-10-017-995-224 Sequence 224, App

C 97	12.8	67.4	25	9	US-10-809-189-120261	Sequence 120261,	170	12.6	66.3	20	8	US-10-877-407-30	Sequence 30, Appl
C 98	12.8	67.4	25	9	US-10-956-157-186456	Sequence 186456,	171	12.6	66.3	20	8	US-10-831-778-519	Sequence 519, App
C 99	12.8	67.4	25	9	US-10-956-157-265641	Sequence 265641,	172	12.6	66.3	20	8	US-10-831-778-767	Sequence 767, App
100	12.8	67.4	25	9	US-10-956-157-278238	Sequence 278238,	173	12.6	66.3	20	8	US-10-831-778-909	Sequence 909, App
101	12.8	67.4	25	9	US-10-956-157-280869	Sequence 280869,	174	12.6	66.3	20	8	US-10-831-778-968	Sequence 968, App
102	12.8	67.4	25	9	US-10-956-157-280870	Sequence 280870,	175	12.6	66.3	20	8	US-10-831-778-969	Sequence 969, App
C 103	12.8	67.4	25	10	US-11-036-317-42252	Sequence 42252, A	176	12.6	66.3	20	8	US-10-486-755-14	Sequence 14, Appl
C 104	12.8	67.4	25	10	US-11-036-317-503752	Sequence 503752,	177	12.6	66.3	20	8	US-10-789-758-4	Sequence 4, Appl
C 105	12.8	67.4	25	10	US-11-036-317-703160	Sequence 703160,	178	12.6	66.3	20	8	US-10-847-642-12	Sequence 12, Appl
C 106	12.8	67.4	25	10	US-11-036-317-703160	Sequence 703160,	179	12.6	66.3	20	8	US-10-838-659-52	Sequence 52, Appl
C 107	12.8	67.4	25	10	US-11-036-317-894738	Sequence 894738,	180	12.6	66.3	20	8	US-10-838-659-59	Sequence 59, Appl
C 108	12.8	67.4	25	10	US-11-036-317-954962	Sequence 954962,	181	12.6	66.3	20	8	US-10-888-785-12	Sequence 12, Appl
C 109	12.8	67.4	25	10	US-11-060-756-219170	Sequence 219170,	182	12.6	66.3	20	9	US-10-888-449-12	Sequence 12, Appl
C 110	12.8	67.4	31	3	US-09-801-274-1698	Sequence 13, Appl	183	12.6	66.3	20	9	US-10-894-862-30	Sequence 30, Appl
C 111	12.8	67.4	32	3	US-09-988-462-43	Sequence 1698, Ap	184	12.6	66.3	20	9	US-10-894-862-30	Sequence 30, Appl
C 112	12.8	67.4	41	7	US-10-035-833A-822	Sequence 43, Appl	185	12.6	66.3	20	9	US-10-884-852-12	Sequence 12, Appl
C 113	12.8	67.4	50	6	US-10-131-827-4733	Sequence 822, App	186	12.6	66.3	20	9	US-10-613-916-12	Sequence 12, Appl
C 114	12.6	66.3	19	3	US-09-776-479-976	Sequence 4733, Ap	187	12.6	66.3	20	9	US-10-627-413-12	Sequence 12, Appl
C 115	12.6	66.3	19	3	US-09-776-479-1046	Sequence 976, App	188	12.6	66.3	20	9	US-10-921-086-12	Sequence 12, Appl
C 116	12.6	66.3	19	3	US-09-776-479-976	Sequence 1046, Ap	189	12.6	66.3	20	9	US-10-928-762-12	Sequence 12, Appl
C 117	12.6	66.3	19	3	US-09-776-479-1046	Sequence 976, App	190	12.6	66.3	20	9	US-10-987-146-12	Sequence 12, Appl
C 118	12.6	66.3	19	5	US-10-112-653-930	Sequence 1046, Ap	191	12.6	66.3	20	9	US-10-484-991-60	Sequence 60, Appl
C 119	12.6	66.3	19	5	US-10-017-995-976	Sequence 930, App	192	12.6	66.3	20	9	US-10-972-301-30	Sequence 30, Appl
C 120	12.6	66.3	19	5	US-10-017-995-1046	Sequence 976, App	193	12.6	66.3	20	9	US-10-831-647-12	Sequence 12, Appl
C 121	12.6	66.3	19	6	US-10-314-578-976	Sequence 1046, Ap	194	12.6	66.3	20	9	US-10-956-494-12	Sequence 12, Appl
C 122	12.6	66.3	19	6	US-10-831-778-976	Sequence 1046, Ap	195	12.6	66.3	20	10	US-10-956-494-12	Sequence 12, Appl
C 123	12.6	66.3	19	8	US-10-831-778-976	Sequence 976, App	196	12.6	66.3	20	10	US-11-056-463-12	Sequence 12, Appl
C 124	12.6	66.3	19	10	US-11-056-463-27	Sequence 1046, Ap	197	12.6	66.3	20	10	US-11-056-463-5	Sequence 5, Appl
C 125	12.6	66.3	19	10	US-09-888-326-436	Sequence 27, Appl	198	12.6	66.3	20	10	US-11-056-463-135	Sequence 135, App
C 126	12.6	66.3	20	3	US-09-888-326-437	Sequence 436, App	199	12.6	66.3	20	10	US-11-056-463-136	Sequence 136, App
C 127	12.6	66.3	20	3	US-09-888-326-437	Sequence 437, App	200	12.6	66.3	20	10	US-11-036-527-12	Sequence 12, Appl
C 128	12.6	66.3	20	3	US-09-888-326-443	Sequence 443, App	201	12.6	66.3	20	10	US-11-071-836-12	Sequence 12, Appl
C 129	12.6	66.3	20	3	US-09-818-918-12	Sequence 12, Appl	202	12.6	66.3	21	3	US-09-776-479-1004	Sequence 1004, Ap
C 130	12.6	66.3	20	3	US-09-776-479-519	Sequence 519, App	203	12.6	66.3	21	3	US-09-776-479-1004	Sequence 1004, Ap
C 131	12.6	66.3	20	3	US-09-776-479-767	Sequence 767, App	204	12.6	66.3	21	5	US-10-112-653-957	Sequence 957, App
C 132	12.6	66.3	20	3	US-09-776-479-909	Sequence 909, App	205	12.6	66.3	21	5	US-10-017-995-1004	Sequence 1004, Ap
C 133	12.6	66.3	20	3	US-09-776-479-968	Sequence 968, App	206	12.6	66.3	21	6	US-10-224-523-57	Sequence 57, Appl
C 134	12.6	66.3	20	3	US-09-776-479-969	Sequence 969, App	207	12.6	66.3	21	8	US-10-314-578-1004	Sequence 1004, Ap
C 135	12.6	66.3	20	3	US-09-367-464-3	Sequence 3, Appl	208	12.6	66.3	21	8	US-10-831-778-1004	Sequence 1004, Ap
C 136	12.6	66.3	20	3	US-09-776-479-519	Sequence 519, App	209	12.6	66.3	21	10	US-11-056-463-156	Sequence 156, App
C 137	12.6	66.3	20	3	US-09-776-479-767	Sequence 767, App	210	12.6	66.3	24	3	US-09-776-479-518	Sequence 518, App
C 138	12.6	66.3	20	3	US-09-776-479-909	Sequence 909, App	211	12.6	66.3	24	3	US-09-776-479-518	Sequence 518, App
C 139	12.6	66.3	20	3	US-09-776-479-968	Sequence 968, App	212	12.6	66.3	24	5	US-10-112-653-495	Sequence 495, App
C 140	12.6	66.3	20	3	US-09-776-479-969	Sequence 969, App	213	12.6	66.3	24	5	US-10-017-995-518	Sequence 518, App
C 141	12.6	66.3	20	3	US-09-865-101-52	Sequence 52, Appl	214	12.6	66.3	24	6	US-10-314-578-518	Sequence 518, App
C 142	12.6	66.3	20	3	US-09-865-101-59	Sequence 59, Appl	215	12.6	66.3	24	6	US-10-831-778-518	Sequence 518, App
C 143	12.6	66.3	20	5	US-10-112-653-496	Sequence 496, App	216	12.6	66.3	25	5	US-10-098-2638-9004	Sequence 9004, Ap
C 144	12.6	66.3	20	5	US-10-112-653-740	Sequence 740, App	217	12.6	66.3	25	7	US-10-451-323-8	Sequence 8, Appl
C 145	12.6	66.3	20	5	US-10-112-653-878	Sequence 878, App	218	12.6	66.3	25	9	US-10-809-189-78259	Sequence 78259, A
C 146	12.6	66.3	20	5	US-10-112-653-923	Sequence 923, App	219	12.6	66.3	25	10	US-11-036-317-175123	Sequence 175123,
C 147	12.6	66.3	20	5	US-10-112-653-1040	Sequence 1040, Ap	220	12.6	66.3	25	10	US-11-036-317-208273	Sequence 208273,
C 148	12.6	66.3	20	5	US-10-017-995-519	Sequence 519, App	221	12.6	66.3	25	10	US-11-036-317-233148	Sequence 233148,
C 149	12.6	66.3	20	5	US-10-017-995-767	Sequence 767, App	222	12.6	66.3	25	10	US-11-036-317-244155	Sequence 244155,
C 150	12.6	66.3	20	5	US-10-017-995-909	Sequence 909, App	223	12.6	66.3	25	10	US-11-036-317-244353	Sequence 244353,
C 151	12.6	66.3	20	5	US-10-017-995-968	Sequence 968, App	224	12.6	66.3	25	10	US-11-036-317-360572	Sequence 360572,
C 152	12.6	66.3	20	5	US-10-017-995-969	Sequence 969, App	225	12.6	66.3	25	10	US-11-060-756-265364	Sequence 265364,
C 153	12.6	66.3	20	6	US-10-161-229-47	Sequence 47, Appl	226	12.6	66.3	25	10	US-11-060-756-301924	Sequence 301924,
C 154	12.6	66.3	20	6	US-10-194-035-89	Sequence 89, Appl	227	12.6	66.3	26	5	US-10-010-476-58	Sequence 58, Appl
C 155	12.6	66.3	20	6	US-10-224-523-35	Sequence 35, Appl	228	12.6	66.3	26	5	US-10-010-476-109	Sequence 109, App
C 156	12.6	66.3	20	6	US-10-187-264A-12	Sequence 12, Appl	229	12.6	66.3	30	3	US-09-874-991C-5	Sequence 5, Appl
C 157	12.6	66.3	20	6	US-10-306-522-12	Sequence 12, Appl	230	12.6	66.3	30	3	US-09-874-991C-8	Sequence 8, Appl
C 158	12.6	66.3	20	6	US-10-314-578-519	Sequence 519, App	231	12.6	66.3	30	3	US-09-874-991C-10	Sequence 10, Appl
C 159	12.6	66.3	20	6	US-10-314-578-767	Sequence 767, App	232	12.6	66.3	30	10	US-11-056-463-165	Sequence 165, App
C 160	12.6	66.3	20	6	US-10-314-578-909	Sequence 909, App	233	12.6	66.3	33	9	US-10-498-333-55	Sequence 55, Appl
C 161	12.6	66.3	20	6	US-10-314-578-968	Sequence 968, App	234	12.6	66.3	33	3	US-09-909-320-225	Sequence 225, App
C 162	12.6	66.3	20	6	US-10-455-247-3	Sequence 3, Appl	235	12.6	66.3	44	3	US-09-909-088B-225	Sequence 225, App
C 163	12.6	66.3	20	6	US-10-719-493-12	Sequence 12, Appl	236	12.6	66.3	44	3	US-09-902-853-225	Sequence 225, App
C 164	12.6	66.3	20	7	US-10-627-331-12	Sequence 12, Appl	237	12.6	66.3	44	3	US-09-907-824-225	Sequence 225, App
C 165	12.6	66.3	20	7	US-10-743-625-12	Sequence 12, Appl	238	12.6	66.3	44	3	US-09-907-841-225	Sequence 225, App
C 166	12.6	66.3	20	7	US-10-679-710-12	Sequence 12, Appl	239	12.6	66.3	44	3	US-09-904-011-225	Sequence 225, App
C 167	12.6	66.3	20	7	US-10-769-282-12	Sequence 12, Appl	240	12.6	66.3	44	3	US-09-903-640-225	Sequence 225, App
C 168	12.6	66.3	20	8	US-10-817-165-12	Sequence 12, Appl	241	12.6	66.3	44	3	US-09-908-093-225	Sequence 225, App
C 169	12.6	66.3	20	8			242	12.6	66.3	44	3		

C 243 12.6 66.3 44 3 US-09-906-742-225 Sequence 225, App  
C 244 12.6 66.3 44 3 US-09-906-838-225 Sequence 225, App  
C 245 12.6 66.3 44 3 US-09-907-613-225 Sequence 225, App  
C 246 12.6 66.3 44 3 US-09-907-942-225 Sequence 225, App  
C 247 12.6 66.3 44 3 US-09-904-859-225 Sequence 225, App  
C 248 12.6 66.3 44 3 US-09-909-204-225 Sequence 225, App  
C 249 12.6 66.3 44 3 US-09-904-820-225 Sequence 225, App  
C 250 12.6 66.3 44 3 US-09-904-786-225 Sequence 225, App  
C 251 12.6 66.3 44 3 US-09-906-646-225 Sequence 225, App  
C 252 12.6 66.3 44 3 US-09-906-700-225 Sequence 225, App  
C 253 12.6 66.3 44 3 US-09-903-786-225 Sequence 225, App  
C 254 12.6 66.3 44 3 US-09-902-903-225 Sequence 225, App  
C 255 12.6 66.3 44 3 US-09-903-749A-225 Sequence 225, App  
C 256 12.6 66.3 44 3 US-09-904-119-225 Sequence 225, App  
C 257 12.6 66.3 44 3 US-09-904-956-225 Sequence 225, App  
C 258 12.6 66.3 44 3 US-09-902-736-225 Sequence 225, App  
C 259 12.6 66.3 44 3 US-09-907-794-225 Sequence 225, App  
C 260 12.6 66.3 44 3 US-09-903-943-225 Sequence 225, App  
C 261 12.6 66.3 44 3 US-09-904-462-225 Sequence 225, App  
C 262 12.6 66.3 44 3 US-09-907-525-225 Sequence 225, App  
C 263 12.6 66.3 44 3 US-09-902-692-225 Sequence 225, App  
C 264 12.6 66.3 44 3 US-09-903-520-225 Sequence 225, App  
C 265 12.6 66.3 44 3 US-09-905-056-225 Sequence 225, App  
C 266 12.6 66.3 44 3 US-09-909-064-225 Sequence 225, App  
C 267 12.6 66.3 44 3 US-09-904-553-225 Sequence 225, App  
C 268 12.6 66.3 44 3 US-09-905-381-225 Sequence 225, App  
C 269 12.6 66.3 44 3 US-09-904-485-225 Sequence 225, App  
C 270 12.6 66.3 44 3 US-09-905-348-225 Sequence 225, App  
C 271 12.6 66.3 44 3 US-09-905-088-225 Sequence 225, App  
C 272 12.6 66.3 44 3 US-09-907-575-225 Sequence 225, App  
C 273 12.6 66.3 44 3 US-09-905-075-225 Sequence 225, App  
C 274 12.6 66.3 44 3 US-09-902-759-225 Sequence 225, App  
C 275 12.6 66.3 44 3 US-09-902-634-225 Sequence 225, App  
C 276 12.6 66.3 44 3 US-09-902-713-225 Sequence 225, App  
C 277 12.6 66.3 44 3 US-09-907-979-225 Sequence 225, App  
C 278 12.6 66.3 44 3 US-09-902-615-225 Sequence 225, App  
C 279 12.6 66.3 44 3 US-09-903-525-225 Sequence 225, App  
C 280 12.6 66.3 44 3 US-09-906-760A-225 Sequence 225, App  
C 281 12.6 66.3 44 3 US-09-903-823-225 Sequence 225, App  
C 282 12.6 66.3 44 3 US-09-907-652-225 Sequence 225, App  
C 283 12.6 66.3 44 3 US-09-902-572A-225 Sequence 225, App  
C 284 12.6 66.3 44 3 US-09-902-979-225 Sequence 225, App  
C 285 12.6 66.3 44 3 US-09-905-125-225 Sequence 225, App  
C 286 12.6 66.3 44 3 US-09-906-815A-225 Sequence 225, App  
C 287 12.6 66.3 44 3 US-09-905-449-225 Sequence 225, App  
C 288 12.6 66.3 44 3 US-09-903-806-225 Sequence 225, App  
C 289 12.6 66.3 44 3 US-09-904-992-225 Sequence 225, App  
C 290 12.6 66.3 44 3 US-09-904-838-225 Sequence 225, App  
C 291 12.6 66.3 44 3 US-09-906-777-225 Sequence 225, App  
C 292 12.6 66.3 44 3 US-09-903-603A-225 Sequence 225, App  
C 293 12.6 66.3 44 3 US-09-904-532-225 Sequence 225, App  
C 294 12.6 66.3 44 3 US-09-904-766-225 Sequence 225, App  
C 295 12.6 66.3 44 3 US-09-904-920A-225 Sequence 225, App  
C 296 12.6 66.3 44 3 US-09-904-877A-225 Sequence 225, App  
C 297 12.6 66.3 44 3 US-09-903-562-225 Sequence 225, App  
C 298 12.6 66.3 44 3 US-09-906-618-225 Sequence 225, App  
C 299 12.6 66.3 44 3 US-09-907-728-225 Sequence 225, App  
C 300 12.6 66.3 44 3 US-09-904-805-225 Sequence 225, App

ALIGNMENTS

RESULT 1  
US-09-888-326-447  
; Sequence 447, Application US/09888326  
; Publication No. US20030026801A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Hartmann, Gunther  
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
; TITLE OF INVENTION: Cell Lysis and Treating Cancer  
; FILE REFERENCE: C1039/7052 (AWS)

; CURRENT APPLICATION NUMBER: US/09/888,326  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/213,346  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 848  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 447  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone  
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends  
US-09-888-326-447

Query Match 100.0%; Score 19; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGGG 19  
|||||  
Db 1 GGGGTGACGTTTCAGGGGGG 19

RESULT 2  
US-09-776-479-80  
; Sequence 80, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/NAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 80  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-80

Query Match 100.0%; Score 19; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGGG 19  
|||||  
Db 1 GGGGTGACGTTTCAGGGGGG 19

RESULT 3  
US-09-776-479-80  
; Sequence 80, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/NAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479

```

; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-80

```

```

Query Match      100.0%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTTCAGGGGGG 19
    |||||
Db 1 GGGGTGACGTTTCAGGGGGG 19
    |||||

```

```

RESULT 4
US-10-112-653-74
; Sequence 74, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-74

```

```

Query Match      100.0%; Score 19; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTTCAGGGGGG 19
    |||||
Db 1 GGGGTGACGTTTCAGGGGGG 19
    |||||

```

```

RESULT 5
US-10-017-995-80
; Sequence 80, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence

```

```

; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-80
Query Match      100.0%; Score 19; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTTCAGGGGGG 19
    |||||
Db 1 GGGGTGACGTTTCAGGGGGG 19
    |||||

```

```

RESULT 6
US-10-314-578-80
; Sequence 80, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Vollmer, Jorg
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-80

```

```

Query Match      100.0%; Score 19; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGGGTGACGTTTCAGGGGGG 19
    |||||
Db 1 GGGGTGACGTTTCAGGGGGG 19
    |||||

```

```

RESULT 7
US-10-831-778-80
; Sequence 80, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fourton, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence

```

## US-10-831-778-80

Query Match 100.0%; Score 19; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
| | | | | | | | | | | | | | | | | |  
Db 1 GGGGTGACGTTTCAGGGGG 19

## RESULT 8

US-09-888-326-448  
; Sequence 448, Application US/09888326  
; Publication No. US20030026801A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Hartmann, Gunther  
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
; TITLE OF INVENTION: Cell Lysis and Treating Cancer  
; FILE REFERENCE: C1039/7052 (AWS)  
; CURRENT APPLICATION NUMBER: US/09/888,326  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/213,346  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 848  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 448  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
; NAME/KEY: misc feature  
; LOCATION: (0)\_ (0)  
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone  
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends  
US-09-888-326-448

Query Match 91.6%; Score 17.4; DB 3; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
| | | | | | | | | | | | | | | | | |  
Db 1 GGGGTGCGTTTCAGGGGG 19

## RESULT 9

US-09-776-479-82  
; Sequence 82, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 82  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-82

Query Match 91.6%; Score 17.4; DB 3; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
| | | | | | | | | | | | | | | | | |  
Db 1 GGGGTGCGTTTCAGGGGG 19

## RESULT 10

US-09-776-479-82  
; Sequence 82, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 82  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-82

Query Match 91.6%; Score 17.4; DB 3; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
| | | | | | | | | | | | | | | | | |  
Db 1 GGGGTGCGTTTCAGGGGG 19

## RESULT 11

US-10-112-653-76  
; Sequence 76, Application US/10112653  
; Publication No. US20030050268A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR  
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES  
; FILE REFERENCE: C01039/70060(AWS)  
; CURRENT APPLICATION NUMBER: US/10/112,653  
; CURRENT FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 76  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-112-653-76

Query Match 91.6%; Score 17.4; DB 5; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19  
| | | | | | | | | | | | | | | | | |

```
Db      1 GGGGTGTCGTTTCAGGGGG 19

RESULT 12
US-10-017-995-82
; Sequence 82, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/NAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-82
Query Match      91.6%; Score 17.4; DB 5; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 19
      ||||| ||||| ||||| |||||
Db      1 GGGGTGTCGTTTCAGGGGG 19

RESULT 13
US-10-314-578-82
; Sequence 82, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/NAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-82
Query Match      91.6%; Score 17.4; DB 6; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 19
      ||||| ||||| ||||| |||||
Db      1 GGGGTGTCGTTTCAGGGGG 19

RESULT 14
US-10-831-778-82
; Sequence 82, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/NAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-82
Query Match      91.6%; Score 17.4; DB 8; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGGG 19
      ||||| ||||| ||||| |||||
Db      1 GGGGTGTCGTTTCAGGGGG 19

RESULT 15
US-11-036-317-815104/c
; Sequence 815104, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 815104
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-815104
Query Match      81.1%; Score 15.4; DB 10; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGGG 17
      ||||| ||||| ||||| |||||
Db      21 GGGGTACGTTTCAGGGG 5

RESULT 16
US-09-415-142-1
; Sequence 1, Application US/09415142
; Publication No. US20030026782A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/09/415,142
```



; CURRENT FILING DATE: 1999-10-09  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Synthetic oligonucleotide  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-09-415-142-1

Query Match 74.7%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGTGACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGGTCAACGTTTCAGGGGG 20

## RESULT 17

US-09-888-326-449  
; Sequence 449, Application US/09888326  
; Publication No. US20030026801A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Hartmann, Gunther  
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
; TITLE OF INVENTION: Cell Lysis and Treating Cancer  
; FILE REFERENCE: C1039/7052 (AWS)  
; CURRENT APPLICATION NUMBER: US/09/888,326  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 60/213,346  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 848  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 449  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
; NAME/KEY: misc feature  
; LOCATION: (0)-(0)  
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone  
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends  
US-09-888-326-449

Query Match 74.7%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGTGACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGGTCAACGTTTCAGGGGG 20

## RESULT 18

US-09-931-583-1  
; Sequence 1, Application US/09931583  
; Publication No. US20030050263A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred  
; TITLE OF INVENTION: Methods and Products for Treating HIV Infection  
; FILE REFERENCE: C1039/7053 (HCL)  
; CURRENT APPLICATION NUMBER: US/09/931,583  
; CURRENT FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: US 08/276,358  
; PRIOR FILING DATE: 1994-07-15

; PRIOR APPLICATION NUMBER: US 09/415,142  
; PRIOR FILING DATE: 1999-10-09  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-931-583-1

Query Match 74.7%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGTGACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGGTCAACGTTTCAGGGGG 20

## RESULT 19

US-09-776-479-224  
; Sequence 224, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 224  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-224

Query Match 74.7%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGTGACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGGTCAACGTTTCAGGGGG 20

## RESULT 20

US-09-776-479-224  
; Sequence 224, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0

```
; SEQ ID NO 224
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-224

Query Match          74.7%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||||| |||||
Db  2 GGGTTCACGTTTGGGGG 20

RESULT 21
US-09-965-101-63
; Sequence 63, Application US/09965101
; Publication No. US20040186067A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-63

Query Match          74.7%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||||| |||||
Db  2 GGGTTCACGTTTGGGGG 20

RESULT 22
US-10-112-653-216
; Sequence 216, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 216
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-216

Query Match          74.7%; Score 14.2; DB 5; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||||| |||||
Db  2 GGGTTCACGTTTGGGGG 20

RESULT 23
US-10-017-995-224
; Sequence 224, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 224
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-224

Query Match          74.7%; Score 14.2; DB 5; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGG 19
   ||| ||||| |||||
Db  2 GGGTTCACGTTTGGGGG 20

RESULT 24
US-10-314-578-224
; Sequence 224, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 224
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
```

## US-10-314-578-224

Query Match 74.7%; Score 14.2; DB 6; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGTGACGTTTCAGGGGG 19  
Db 2 GGGTGACGTTTTCAGGGGG 20

## RESULT 25

US-10-631-676-1  
; Sequence 1, Application US/10631676  
; Publication No. US20040087534A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/10/631,676  
; CURRENT FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-631-676-1

Query Match 74.7%; Score 14.2; DB 7; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGTGACGTTTCAGGGGG 19  
Db 2 GGGTGACGTTTCAGGGGG 20

## RESULT 26

US-10-789-051-1  
; Sequence 1, Application US/10789051  
; Publication No. US20040142469A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/10/789,051  
; CURRENT FILING DATE: 2004-02-26  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-789-051-1

Query Match 74.7%; Score 14.2; DB 7; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGTGACGTTTCAGGGGG 19

Db 2 GGGTGACGTTTCAGGGGG 20

## RESULT 27

US-10-690-495-1  
; Sequence 1, Application US/10690495  
; Publication No. US20040143112A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/10/690,495  
; CURRENT FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-690-495-1

Query Match 74.7%; Score 14.2; DB 7; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGTGACGTTTCAGGGGG 19  
Db 2 GGGTGACGTTTCAGGGGG 20

## RESULT 28

US-10-788-191-1  
; Sequence 1, Application US/10788191  
; Publication No. US20040152656A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/10/788,191  
; CURRENT FILING DATE: 2004-02-26  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-788-191-1

Query Match 74.7%; Score 14.2; DB 7; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGTGACGTTTCAGGGGG 19  
Db 2 GGGTGACGTTTCAGGGGG 20

## RESULT 29

US-10-789-536-1  
; Sequence 1, Application US/10789536

```
; Publication No. US20040152657A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/10/789,536
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; US-10-789-536-1

Query Match          74.7%; Score 14.2; DB 7; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGGG 20

RESULT 30
US-10-769-626-1
; Sequence 1, Application US/10769626
; Publication No. US20040162258A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/10/769,626
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; US-10-769-626-1

Query Match          74.7%; Score 14.2; DB 7; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGGG 20

RESULT 31
US-10-789-353-1
; Sequence 1, Application US/10789353
; Publication No. US20040162262A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
```

```
; CURRENT APPLICATION NUMBER: US/10/789,353
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; US-10-789-353-1

Query Match          74.7%; Score 14.2; DB 7; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGGG 20

RESULT 32
US-10-787-737-1
; Sequence 1, Application US/10787737
; Publication No. US20040171150A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/10/787,737
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; US-10-787-737-1

Query Match          74.7%; Score 14.2; DB 7; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGGG 20

RESULT 33
US-10-788-199-1
; Sequence 1, Application US/10788199
; Publication No. US20040181045A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/10/788,199
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
```

```
;
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-788-199-1

Query Match      74.7%; Score 14.2; DB 8; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 34
US-10-831-778-224
; Sequence 224, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 224
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-224

Query Match      74.7%; Score 14.2; DB 8; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTTCAGCTTTTCGGGGG 20

RESULT 35
US-10-847-650-1
; Sequence 1, Application US/10847650
; Publication No. US20050004062A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/10/847,650
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-847-650-1
```

```
Query Match      74.7%; Score 14.2; DB 8; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 36
US-10-888-885-1
; Sequence 1, Application US/10888885
; Publication No. US20050009774A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: C1039/7029
; CURRENT APPLICATION NUMBER: US/10/888,885
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-888-885-1

Query Match      74.7%; Score 14.2; DB 8; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGG 19
Db 2 GGGTCAACGTTTCAGGGGG 20

RESULT 37
US-10-838-659-63
; Sequence 63, Application US/10838659
; Publication No. US20050032734A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; FILE REFERENCE: C1039.70057US01
; CURRENT APPLICATION NUMBER: US/10/838,659
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 09/965,101
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-838-659-63
```

US-10-838-659-63

Query Match 74.7%; Score 14.2; DB 8; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGGTTACGTTTTCAGGGGG 20

RESULT 38

US-10-888-089-1  
; Sequence 1, Application US/10888089  
; Publication No. US20050037403A1  
; GENERAL INFORMATION:  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/10/888,089  
; CURRENT FILING DATE: 2004-07-09  
; PRIOR APPLICATION NUMBER: US/10/690,495  
; PRIOR FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-10-888-089-1

Query Match 74.7%; Score 14.2; DB 8; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGGTCACGTTTCAGGGGG 20

RESULT 39

US-10-649-584-1  
; Sequence 1, Application US/10649584  
; Publication No. US20050037985A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred  
; TITLE OF INVENTION: Methods and Products for Treating HIV Infection  
; FILE REFERENCE: C1039, 70084US00  
; CURRENT APPLICATION NUMBER: US/10/649,584  
; CURRENT FILING DATE: 2003-08-25  
; PRIOR APPLICATION NUMBER: US 09/931,583  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: US 08/276,358  
; PRIOR FILING DATE: 1994-07-15  
; PRIOR APPLICATION NUMBER: US 09/415,142  
; PRIOR FILING DATE: 1999-10-09  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Synthetic oligonucleotide

US-10-649-584-1

Query Match 74.7%; Score 14.2; DB 8; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGGTCACGTTTCAGGGGG 20

RESULT 40

US-11-067-516-1  
; Sequence 1, Application US/11067516  
; Publication No. US20050239736A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/11/067,516  
; CURRENT FILING DATE: 2005-02-25  
; PRIOR APPLICATION NUMBER: US/10/690,495  
; PRIOR FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-067-516-1

Query Match 74.7%; Score 14.2; DB 10; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTACGTTTCAGGGGG 19  
||| ||||| |||||  
Db 2 GGGTCACGTTTCAGGGGG 20

RESULT 41

US-11-036-317-185300  
; Sequence 185300, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 185300  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-185300

Query Match 74.7%; Score 14.2; DB 10; Length 25;  
Best Local Similarity 84.2%; Pred. No. 4.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTACGTTTCAGGGGG 19  
||| ||||| |||||

```
Db      7 GGGGAGACGTTTCATGGCG 25

RESULT 42
US-11-036-317-282532
; Sequence 282532, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 282532
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-282532

Query Match      74.7%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGTGACGTTTCAGGGGG 19
      ||||| ||||| ||||| |||||
Db      6 GGGGAGACGTTTCATGGCG 24

RESULT 43
US-11-036-317-382608
; Sequence 382608, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 382608
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-382608

Query Match      74.7%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGTGACGTTTCAGGGGG 19
      ||||| ||||| ||||| |||||
Db      6 GGGGAGACGTTTCATGGCG 24

RESULT 44
US-11-036-317-395403
; Sequence 395403, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317

Db      3 GGGGAGACGTTTCATGGCG 21

RESULT 45
US-11-036-317-398410
; Sequence 398410, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 398410
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-398410

Query Match      74.7%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GGGTGACGTTTCAGGGGG 19
      ||||| ||||| ||||| |||||
Db      4 GGGGAGACGTTTCATGGCG 22

RESULT 46
US-10-282-935-18/c
; Sequence 18, Application US/10282935
; Publication No. US20030143193A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETTIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
; FILE REFERENCE: UTSD:884US
; CURRENT APPLICATION NUMBER: US/10/282,935
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 39
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-282-935-18

Query Match          73.7%; Score 14; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGTGACGTTTCAGGG 16
Db      26 GGTGACGTTTCAGGG 13

RESULT 47
US-10-440-796-18/c
; Sequence 18, Application US/10440796
; Publication No. US20040009148A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SWALISHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
; TITLE OF INVENTION: SYNDROME (VLS)
; FILE REFERENCE: US20040009148A1
; CURRENT APPLICATION NUMBER: US/10/440,796
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 18
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-440-796-18

Query Match          73.7%; Score 14; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGTGACGTTTCAGGG 16
Db      26 GGTGACGTTTCAGGG 13

RESULT 48
US-11-036-317-292133
; Sequence 292133, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 292133
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-292133
```

```
Query Match          72.6%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGG 17
Db      8 GGGGAGACGTTTCATGG 24

RESULT 49
US-11-036-317-815105/c
; Sequence 815105, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 815105
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-815105

Query Match          72.6%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGG 17
Db      21 GGGGTACCTTCAGGG 5

RESULT 50
US-11-036-317-822290
; Sequence 822290, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 822290
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-822290

Query Match          72.6%; Score 13.8; DB 10; Length 25;
Best Local Similarity 88.2%; Pred. No. 7e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGGGTGACGTTTCAGGG 18
Db      2 GGGTGATGTTTCAGGAG 18

Search completed: February 16, 2006, 02:34:04
Job time : 279.736 secs
```



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 02:03:53 ; Search time 177.124 Seconds  
(without alignments)  
98.157 Million cell updates/sec

Title: US-09-669-187A-80

Perfect score: 19

Sequence: 1 ggggtgacgttcagg99ggg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6247088 seqs, 457523669 residues

Total number of hits satisfying chosen parameters: 11812030

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications NA.New.\*

1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*

2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*

3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*

4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*

5: /cgn2\_6/ptodata/2/pubpna/US05\_NEW\_PUB.seq.\*

6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*

7: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

12: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	11	US-11-127-654-74
2	17.4	91.6	19	11	US-11-127-654-76
3	14.2	74.7	19	7	US-10-310-914A-1228446
4	14.2	74.7	20	9	US-11-127-797-1
5	14.2	74.7	20	9	US-11-127-803-1
6	14.2	74.7	20	9	US-11-128-127-1
7	14.2	74.7	20	11	US-11-127-654-216
c 8	14	73.7	28	7	US-10-310-914A-1202061
9	13.8	72.6	20	7	US-10-310-914A-524757
c 10	13.8	72.6	20	7	US-10-310-914A-895375
11	13.8	72.6	20	7	US-10-310-914A-1185102
c 12	13.8	72.6	21	7	US-10-310-914A-895439
13	13.8	72.6	22	7	US-10-310-914A-1185206
c 14	13.8	72.6	23	7	US-10-310-914A-530908
c 15	13.4	70.5	19	9	US-11-101-244-1188547
c 16	13.4	70.5	19	10	US-11-083-784-1188547
c 17	13.4	70.5	22	7	US-10-310-914A-673587
c 18	13.2	69.5	18	7	US-10-310-914A-308426
19	13.2	69.5	20	11	US-11-127-654-498
20	13.2	69.5	20	11	US-11-127-654-501
21	13.2	69.5	21	7	US-10-310-914A-872061

22	7	US-10-310-914A-114797	Sequence 114797,
23	7	US-10-310-914A-456901	Sequence 456901,
24	7	US-10-310-914A-518042	Sequence 518042,
25	23	US-10-310-914A-836953	Sequence 836953,
26	23	US-10-310-914A-896494	Sequence 896494,
27	23	US-10-310-914A-837004	Sequence 837004,
28	23	US-10-310-914A-509542	Sequence 509542,
29	23	US-11-121-849-15126	Sequence 15126, A
30	11	US-11-012-353-97	Sequence 97, Appl
31	11	US-10-310-914A-1145336	Sequence 1145336,
32	11	US-10-310-914A-966814	Sequence 966814,
33	19	US-10-522-362-49	Sequence 49, Appl
34	20	US-10-310-914A-746353	Sequence 746353,
35	22	US-10-310-914A-966777	Sequence 966777,
36	23	US-10-310-914A-240915	Sequence 240915,
37	23	US-10-310-914A-411534	Sequence 411534,
38	24	US-10-310-914A-1145337	Sequence 1145337,
39	25	US-11-121-849-15921	Sequence 15921, A
40	25	US-11-121-849-22103	Sequence 22103, A
41	25	US-11-121-849-24138	Sequence 24138, A
42	25	US-11-121-849-107577	Sequence 107577,
43	25	US-11-121-849-115643	Sequence 115643,
44	25	US-11-121-849-476398	Sequence 476398,
45	25	US-11-121-849-568167	Sequence 568167,
46	25	US-11-121-849-570964	Sequence 570964,
47	32	US-10-755-092-43	Sequence 43, Appl
48	32	US-10-939-294A-19843	Sequence 19843, A
49	50	US-11-175-853-51905	Sequence 51905, A
50	19	US-10-310-914A-896490	Sequence 896490,
51	19	US-10-310-914A-1098668	Sequence 1098668,
52	19	US-11-127-654-930	Sequence 930, App
53	20	US-10-619-279-12	Sequence 12, Appl
54	20	US-10-435-656-12	Sequence 12, Appl
55	20	US-10-310-914A-142257	Sequence 142257,
56	20	US-10-310-914A-369058	Sequence 369058,
57	20	US-11-127-654-496	Sequence 496, App
58	20	US-11-127-654-740	Sequence 740, App
59	20	US-11-127-654-878	Sequence 878, App
60	20	US-11-127-654-923	Sequence 923, App
61	20	US-11-127-654-1040	Sequence 1040, App
62	20	US-11-134-918-12	Sequence 12, Appl
63	20	US-11-031-460-12	Sequence 12, Appl
64	20	US-11-067-587-12	Sequence 12, Appl
c 65	21	US-10-310-914A-65931	Sequence 65931, A
66	21	US-10-310-914A-137628	Sequence 137628,
67	21	US-10-310-914A-416718	Sequence 416718,
68	21	US-10-310-914A-1211505	Sequence 1211505,
69	21	US-11-127-654-957	Sequence 957, App
70	21	US-11-061-140-335	Sequence 335, App
71	22	US-10-310-914A-31255	Sequence 31255, A
72	22	US-10-310-914A-137654	Sequence 137654,
73	22	US-10-310-914A-369091	Sequence 369091,
74	22	US-10-310-914A-579551	Sequence 579551,
75	22	US-10-310-914A-788367	Sequence 788367,
76	22	US-10-310-914A-1037094	Sequence 1037094,
77	22	US-10-310-914A-1159829	Sequence 1159829,
78	23	US-10-310-914A-321292	Sequence 321292,
79	23	US-10-310-914A-321322	Sequence 321322,
c 80	24	US-10-310-914A-437868	Sequence 437868,
81	24	US-10-310-914A-1395431	Sequence 1395431,
82	24	US-10-310-914A-1319423	Sequence 1319423,
83	24	US-10-310-914A-1326268	Sequence 1326268,
84	24	US-11-127-654-495	Sequence 495, App
85	25	US-10-750-623-22043	Sequence 22043, A
c 86	25	US-10-750-623-22043	Sequence 22043, A
87	25	US-10-310-914A-181131	Sequence 181131,
88	25	US-10-310-914A-1198901	Sequence 1198901,
89	25	US-11-121-849-246100	Sequence 246100,
90	26	US-10-524-643-59	Sequence 59, Appl
91	26	US-10-524-643-62	Sequence 62, Appl
92	26	US-10-310-914A-1037101	Sequence 1037101,
93	26	US-10-310-914A-982860	Sequence 982860,
c 94	32	US-10-939-294A-17580	Sequence 17580, A

C 95	12.6	66.3	32	7	US-10-939-294A-19419	Sequence 19419, A	C 168	12.2	64.2	25	11	US-11-136-537-338521	Sequence 338521,
C 96	12.6	66.3	50	11	US-11-175-859-18833	Sequence 18833, A	C 169	12.2	64.2	26	7	US-10-310-914A-477171	Sequence 477171,
C 97	12.4	65.3	19	9	US-11-101-244-665663	Sequence 665663,	C 170	12.2	64.2	28	7	US-10-310-914A-860573	Sequence 860573,
C 98	12.4	65.3	19	9	US-11-101-244-1238420	Sequence 1238420,	C 171	12.2	64.2	30	7	US-10-310-914A-550477	Sequence 550477,
C 99	12.4	65.3	19	10	US-11-083-784-665663	Sequence 665663,	C 172	12.2	64.2	33	7	US-10-209-208-33	Sequence 33, Appl
C 100	12.4	65.3	19	10	US-11-083-784-1238420	Sequence 1238420,	C 173	12.2	64.2	33	7	US-10-209-208-33	Sequence 34, Appl
C 101	12.4	65.3	20	11	US-11-127-654-503	Sequence 503, App	C 174	12.2	64.2	33	11	US-11-218-880-33	Sequence 33, Appl
C 102	12.4	65.3	20	11	US-11-127-654-827	Sequence 827, App	C 175	12.2	64.2	33	11	US-11-218-880-34	Sequence 34, Appl
C 103	12.4	65.3	21	7	US-10-310-914A-746294	Sequence 746294, A	C 176	12.2	64.2	50	11	US-11-175-859-86359	Sequence 86359, A
C 104	12.4	65.3	23	7	US-10-310-914A-1278218	Sequence 1278218, A	C 177	12	63.2	19	9	US-11-101-244-5629	Sequence 208337, A
C 105	12.4	65.3	25	11	US-11-121-849-22422	Sequence 22422, A	C 178	12	63.2	19	9	US-11-101-244-208337	Sequence 5629, Ap
C 106	12.4	65.3	25	11	US-11-121-849-24698	Sequence 24698, A	C 179	12	63.2	19	10	US-11-083-784-5629	Sequence 208337
C 107	12.4	65.3	25	11	US-11-121-849-58148	Sequence 58148, A	C 180	12	63.2	19	10	US-11-083-784-208337	Sequence 12889, A
C 108	12.4	65.3	25	11	US-11-121-849-58149	Sequence 58149, A	C 181	12	63.2	20	7	US-10-750-185-12889	Sequence 12889, A
C 109	12.4	65.3	25	11	US-11-121-849-58149	Sequence 58149, A	C 182	12	63.2	20	7	US-10-750-623-12889	Sequence 112737,
C 110	12.4	65.3	25	11	US-11-121-849-278536	Sequence 278536,	C 183	12	63.2	25	11	US-11-121-849-112737	Sequence 551178,
C 111	12.4	65.3	25	11	US-11-121-849-533050	Sequence 533050,	C 184	12	63.2	25	11	US-11-121-849-583226	Sequence 583226,
C 112	12.4	65.3	25	11	US-11-121-849-533051	Sequence 533051,	C 185	12	63.2	25	11	US-11-175-859-2042	Sequence 2042, Ap
C 113	12.4	65.3	25	11	US-11-121-849-533052	Sequence 533052,	C 186	12	63.2	50	11	US-10-310-914A-399938	Sequence 399938,
C 114	12.4	65.3	25	11	US-11-121-849-533053	Sequence 533053,	C 187	11.8	62.1	18	7	US-10-310-914A-818768	Sequence 818768,
C 115	12.4	65.3	25	11	US-11-121-849-533054	Sequence 533054,	C 188	11.8	62.1	18	7	US-10-310-914A-818768	Sequence 240911,
C 116	12.4	65.3	25	11	US-11-121-849-533882	Sequence 533882,	C 189	11.8	62.1	19	7	US-10-310-914A-240911	Sequence 399939,
C 117	12.4	65.3	25	11	US-11-121-849-533883	Sequence 533883,	C 190	11.8	62.1	19	7	US-10-310-914A-399939	Sequence 818916,
C 118	12.4	65.3	25	11	US-11-121-849-533884	Sequence 533884,	C 191	11.8	62.1	19	7	US-10-310-914A-818916	Sequence 1328172,
C 119	12.4	65.3	25	11	US-11-121-849-533885	Sequence 533885,	C 192	11.8	62.1	19	7	US-10-310-914A-1328172	Sequence 174986,
C 120	12.4	65.3	25	11	US-11-121-849-533886	Sequence 533886,	C 193	11.8	62.1	19	9	US-11-101-244-174986	Sequence 631981,
C 121	12.4	65.3	25	11	US-11-121-849-534408	Sequence 534408,	C 194	11.8	62.1	19	9	US-11-101-244-1329178	Sequence 1229178,
C 122	12.4	65.3	25	11	US-11-121-849-538595	Sequence 538595,	C 195	11.8	62.1	19	9	US-11-101-244-1326203	Sequence 1326203,
C 123	12.4	65.3	28	7	US-10-310-914A-1201695	Sequence 1201695,	C 196	11.8	62.1	19	9	US-11-101-244-1522803	Sequence 1522803,
C 124	12.4	65.3	50	11	US-11-175-859-6749	Sequence 6749, Ap	C 197	11.8	62.1	19	9	US-11-101-244-1326203	Sequence 174986,
C 125	12.2	64.2	18	7	US-10-310-914A-1242715	Sequence 1242715,	C 198	11.8	62.1	19	10	US-11-083-784-431981	Sequence 631981,
C 126	12.2	64.2	18	7	US-10-310-914A-1286505	Sequence 1286505,	C 199	11.8	62.1	19	10	US-11-083-784-631981	Sequence 1229178,
C 127	12.2	64.2	19	7	US-10-310-914A-181167	Sequence 181167,	C 200	11.8	62.1	19	10	US-11-083-784-1229178	Sequence 1316203,
C 128	12.2	64.2	19	7	US-10-310-914A-394906	Sequence 394906,	C 201	11.8	62.1	19	10	US-11-083-784-174986	Sequence 174986,
C 129	12.2	64.2	19	7	US-10-310-914A-1038534	Sequence 1038534,	C 202	11.8	62.1	19	10	US-11-083-784-431981	Sequence 631981,
C 130	12.2	64.2	19	7	US-10-310-914A-1209728	Sequence 1209728,	C 203	11.8	62.1	20	7	US-10-310-914A-724380	Sequence 724380,
C 131	12.2	64.2	19	7	US-10-310-914A-1242629	Sequence 1242629,	C 204	11.8	62.1	20	7	US-10-310-914A-1145320	Sequence 1145320,
C 132	12.2	64.2	20	7	US-10-310-914A-586723	Sequence 586723,	C 205	11.8	62.1	20	7	US-10-310-914A-1228471	Sequence 1228471,
C 133	12.2	64.2	20	7	US-10-310-914A-1347887	Sequence 1347887,	C 206	11.8	62.1	20	11	US-11-043-752-3791	Sequence 3791, Ap
C 134	12.2	64.2	20	7	US-10-310-914A-1387916	Sequence 1387916,	C 207	11.8	62.1	21	7	US-10-310-914A-371102	Sequence 371102,
C 135	12.2	64.2	21	7	US-10-310-914A-404009	Sequence 404009,	C 208	11.8	62.1	21	7	US-10-310-914A-905240	Sequence 905240,
C 136	12.2	64.2	21	7	US-10-310-914A-477224	Sequence 477224, A	C 209	11.8	62.1	21	7	US-10-310-914A-1042652	Sequence 1042652,
C 137	12.2	64.2	21	7	US-10-310-914A-509581	Sequence 509581,	C 210	11.8	62.1	21	7	US-10-310-914A-1042652	Sequence 1168356,
C 138	12.2	64.2	21	7	US-10-310-914A-529206	Sequence 529206,	C 211	11.8	62.1	21	7	US-10-310-914A-1168356	Sequence 1368477,
C 139	12.2	64.2	21	7	US-10-310-914A-624047	Sequence 624047,	C 212	11.8	62.1	22	7	US-10-310-914A-1368477	Sequence 595017,
C 140	12.2	64.2	21	7	US-10-310-914A-1059674	Sequence 1059674,	C 213	11.8	62.1	22	7	US-10-310-914A-595017	Sequence 673113,
C 141	12.2	64.2	21	7	US-10-310-914A-1213768	Sequence 1213768,	C 214	11.8	62.1	22	7	US-10-310-914A-840175	Sequence 840175,
C 142	12.2	64.2	21	7	US-10-310-914A-1233960	Sequence 1233960,	C 215	11.8	62.1	22	7	US-10-310-914A-905232	Sequence 905232,
C 143	12.2	64.2	21	7	US-10-310-914A-1258075	Sequence 1258075,	C 216	11.8	62.1	22	7	US-10-310-914A-929782	Sequence 929782,
C 144	12.2	64.2	21	7	US-10-310-914A-1286506	Sequence 1286506,	C 217	11.8	62.1	22	7	US-10-310-914A-929782	Sequence 1168359,
C 145	12.2	64.2	21	7	US-10-310-914A-1314397	Sequence 1314397,	C 218	11.8	62.1	22	7	US-10-310-914A-240891	Sequence 240891,
C 146	12.2	64.2	21	7	US-10-310-914A-1387894	Sequence 1387894,	C 219	11.8	62.1	23	7	US-10-310-914A-433713	Sequence 433713,
C 147	12.2	64.2	21	11	US-11-061-140-336	Sequence 336, App	C 220	11.8	62.1	23	7	US-10-310-914A-719279	Sequence 719279,
C 148	12.2	64.2	22	7	US-10-310-914A-195030	Sequence 195030,	C 221	11.8	62.1	23	7	US-10-310-914A-929783	Sequence 929783,
C 149	12.2	64.2	22	7	US-10-310-914A-377036	Sequence 377036,	C 222	11.8	62.1	23	7	US-10-310-914A-1241476	Sequence 1241476,
C 150	12.2	64.2	22	7	US-10-310-914A-793125	Sequence 793125,	C 223	11.8	62.1	23	7	US-10-310-914A-389442	Sequence 389442,
C 151	12.2	64.2	23	7	US-10-310-914A-57224	Sequence 57224, A	C 224	11.8	62.1	24	7	US-10-310-914A-389442	Sequence 433626,
C 152	12.2	64.2	23	7	US-10-310-914A-57225	Sequence 57225, A	C 225	11.8	62.1	24	7	US-10-310-914A-433626	Sequence 433626,
C 153	12.2	64.2	23	7	US-10-310-914A-477182	Sequence 477182,	C 226	11.8	62.1	25	7	US-10-750-185-23854	Sequence 23854, A
C 154	12.2	64.2	23	7	US-10-310-914A-624007	Sequence 624007,	C 227	11.8	62.1	25	7	US-10-750-623-23854	Sequence 23854, A
C 155	12.2	64.2	23	7	US-10-310-914A-843681	Sequence 843681,	C 228	11.8	62.1	25	7	US-10-310-914A-1042586	Sequence 1042586,
C 156	12.2	64.2	23	7	US-10-310-914A-1135774	Sequence 1135774,	C 229	11.8	62.1	25	7	US-10-310-914A-1345558	Sequence 1345558,
C 157	12.2	64.2	23	7	US-10-310-914A-1319191	Sequence 1319191,	C 230	11.8	62.1	25	11	US-11-121-849-1940	Sequence 1940, Ap
C 158	12.2	64.2	23	7	US-10-310-914A-1371695	Sequence 1371695,	C 231	11.8	62.1	25	11	US-11-121-849-111128	Sequence 111128,
C 159	12.2	64.2	25	7	US-10-310-914A-308428	Sequence 308428,	C 232	11.8	62.1	25	11	US-11-121-849-263134	Sequence 263134,
C 160	12.2	64.2	25	7	US-10-310-914A-543214	Sequence 543214,	C 233	11.8	62.1	25	11	US-11-121-849-371541	Sequence 371541,
C 161	12.2	64.2	25	7	US-10-310-914A-860553	Sequence 860553,	C 234	11.8	62.1	25	11	US-11-121-849-371542	Sequence 371542,
C 162	12.2	64.2	25	11	US-11-121-849-20799	Sequence 20799, A	C 235	11.8	62.1	25	11	US-11-121-849-384139	Sequence 384139,
C 163	12.2	64.2	25	11	US-11-121-849-120766	Sequence 120766,	C 236	11.8	62.1	25	11	US-11-121-849-384140	Sequence 384140,
C 164	12.2	64.2	25	11	US-11-121-849-560750	Sequence 560750,	C 237	11.8	62.1	25	11	US-11-121-849-499269	Sequence 499269,
C 165	12.2	64.2	25	11	US-11-136-527-306106	Sequence 306106,	C 238	11.8	62.1	25	11	US-11-121-849-663289	Sequence 663289,
C 166	12.2	64.2	25	11	US-11-136-527-306350	Sequence 306350,	C 239	11.8	62.1	25	11	US-11-121-849-663290	Sequence 663290,
C 167	12.2	64.2	25	11	US-11-136-527-338502	Sequence 338502,	C 240	11.8	62.1	25	11	US-11-121-849-663291	Sequence 663291,

241 11.8 62.1 25 11 US-11-121-849-667907  
242 11.8 62.1 25 11 US-11-121-849-667908  
243 11.8 62.1 25 11 US-11-136-527-13923  
244 11.8 62.1 25 11 US-11-136-527-13924  
245 11.8 62.1 25 11 US-11-136-527-13925  
246 11.8 62.1 25 11 US-11-136-527-13933  
247 11.8 62.1 25 11 US-11-136-527-13934  
248 11.8 62.1 25 11 US-11-136-527-13935  
249 11.8 62.1 25 11 US-11-136-527-13936  
250 11.8 62.1 25 11 US-11-136-527-13938  
251 11.8 62.1 25 11 US-11-136-527-13942  
252 11.8 62.1 25 11 US-11-136-527-13946  
253 11.8 62.1 25 11 US-11-136-527-94745  
254 11.8 62.1 25 11 US-11-136-527-94751  
255 11.8 62.1 25 11 US-11-136-527-94770  
256 11.8 62.1 25 11 US-11-136-527-265957  
257 11.8 62.1 25 11 US-11-136-527-265965  
258 11.8 62.1 25 11 US-11-136-527-265981  
259 11.8 62.1 25 11 US-11-136-527-296001  
260 11.8 62.1 25 11 US-11-136-527-296022  
261 11.8 62.1 25 11 US-11-136-527-296024  
262 11.8 62.1 25 11 US-11-136-527-296028  
263 11.8 62.1 25 11 US-11-136-527-296043  
264 11.8 62.1 25 11 US-11-136-527-351683  
265 11.8 62.1 25 11 US-11-136-527-351684  
266 11.8 62.1 25 11 US-11-136-527-351693  
267 11.6 61.1 18 7 US-10-310-914A-65930  
268 11.6 61.1 18 7 US-10-310-914A-1358363  
269 11.6 61.1 19 7 US-10-310-914A-63104  
270 11.6 61.1 19 7 US-10-310-914A-147289  
271 11.6 61.1 19 7 US-10-310-914A-369060  
272 11.6 61.1 19 7 US-10-310-914A-795738  
273 11.6 61.1 19 7 US-10-310-914A-873292  
274 11.6 61.1 19 7 US-10-310-914A-920358  
275 11.6 61.1 19 7 US-10-310-914A-1049795  
276 11.6 61.1 19 11 US-11-127-654-931  
277 11.6 61.1 20 7 US-10-310-914A-53127  
278 11.6 61.1 20 7 US-10-310-914A-63105  
279 11.6 61.1 20 7 US-10-310-914A-142175  
280 11.6 61.1 20 7 US-10-310-914A-154172  
281 11.6 61.1 20 7 US-10-310-914A-200792  
282 11.6 61.1 20 7 US-10-310-914A-368126  
283 11.6 61.1 20 7 US-10-310-914A-369887  
284 11.6 61.1 20 7 US-10-310-914A-458307  
285 11.6 61.1 20 7 US-10-310-914A-543421  
286 11.6 61.1 20 7 US-10-310-914A-673169  
287 11.6 61.1 20 7 US-10-310-914A-874575  
288 11.6 61.1 20 7 US-10-310-914A-961314  
289 11.6 61.1 20 7 US-10-310-914A-1021596  
290 11.6 61.1 20 7 US-10-310-914A-1024378  
291 11.6 61.1 20 7 US-10-310-914A-1349901  
292 11.6 61.1 20 7 US-10-310-914A-1352469  
293 11.6 61.1 21 7 US-10-770-726-39373  
294 11.6 61.1 21 7 US-10-310-914A-25298  
295 11.6 61.1 21 7 US-10-310-914A-70487  
296 11.6 61.1 21 7 US-10-310-914A-954555  
297 11.6 61.1 21 7 US-10-310-914A-1062633  
298 11.6 61.1 21 7 US-10-310-914A-1122826  
299 11.6 61.1 21 7 US-10-310-914A-1181622  
300 11.6 61.1 21 7 US-10-310-914A-1211520

ALIGNMENTS

RESULT 1  
US-11-127-654-74  
; Sequence 74, Application US/11127654  
; Publication No. US20050250726A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

Sequence 667907,  
Sequence 667908,  
Sequence 13923, A  
Sequence 13924, A  
Sequence 13925, A  
Sequence 13933, A  
Sequence 13934, A  
Sequence 13935, A  
Sequence 13936, A  
Sequence 13938, A  
Sequence 13942, A  
Sequence 13946, A  
Sequence 94745, A  
Sequence 94751, A  
Sequence 94770, A  
Sequence 265957,  
Sequence 265965,  
Sequence 265981,  
Sequence 296001,  
Sequence 296022,  
Sequence 296024,  
Sequence 296028,  
Sequence 296043,  
Sequence 351683,  
Sequence 351684,  
Sequence 351693,  
Sequence 65930, A  
Sequence 1358363,  
Sequence 63104, A  
Sequence 147289,  
Sequence 369060,  
Sequence 795738,  
Sequence 873292,  
Sequence 920358,  
Sequence 1049795,  
Sequence 931, App  
Sequence 53127, A  
Sequence 63105, A  
Sequence 142175,  
Sequence 154172,  
Sequence 200792,  
Sequence 368126,  
Sequence 369887,  
Sequence 458307,  
Sequence 543421,  
Sequence 673169,  
Sequence 874575,  
Sequence 961314,  
Sequence 1021596,  
Sequence 1024378,  
Sequence 1349901,  
Sequence 1352469,  
Sequence 39373, A  
Sequence 25298, A  
Sequence 70487, A  
Sequence 954555,  
Sequence 1062633,  
Sequence 1122826,  
Sequence 1181622,  
Sequence 1211520,

; TITLE OF INVENTION: INFLAMMATORY DISEASES  
; FILE REFERENCE: C1039.70060US01  
; CURRENT APPLICATION NUMBER: US/11/127,654  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 74  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-74

Query Match 100.0%; Score 19; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGGG 19  
|||||  
Db 1 GGGGTGACGTTTCAGGGGGG 19

RESULT 2  
US-11-127-654-76  
; Sequence 76, Application US/11127654  
; Publication No. US20050250726A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

; TITLE OF INVENTION: INFLAMMATORY DISEASES  
; FILE REFERENCE: C1039.70060US01  
; CURRENT APPLICATION NUMBER: US/11/127,654  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 76  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-76

Query Match 91.6%; Score 17.4; DB 11; Length 19;  
Best Local Similarity 94.7%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGGGGG 19  
|||||  
Db 1 GGGGTGCGTTTCAGGGGGG 19

RESULT 3  
US-10-310-914A-1228446  
; Sequence 1228446, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuvzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A

;  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1228446  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1228446

Query Match 74.7%; Score 14.2; DB 7; Length 19;  
Best Local Similarity 68.4%; Pred. No. 8.1e+02;  
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19  
Db 1 GGAUGACCGUAGGGGGG 19

## RESULT 4

US-11-127-797-1  
; Sequence 1, Application US/11127797  
; Publication No. US20050245477A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/11/127,797  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US/10/690,495  
; PRIOR FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-797-1

Query Match 74.7%; Score 14.2; DB 9; Length 20;  
Best Local Similarity 84.2%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTTCAGGGGG 20

## RESULT 5

US-11-127-803-1  
; Sequence 1, Application US/11127803  
; Publication No. US20050244379A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/11/127,803  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US/10/690,495  
; PRIOR FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20

;  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-803-1

Query Match 74.7%; Score 14.2; DB 9; Length 20;  
Best Local Similarity 84.2%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTTCAGGGGG 20

## RESULT 6

US-11-128-127-1  
; Sequence 1, Application US/11128127  
; Publication No. US20050244380A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES  
; FILE REFERENCE: C1039/7029  
; CURRENT APPLICATION NUMBER: US/11/128,127  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US/10/690,495  
; PRIOR FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-128-127-1

Query Match 74.7%; Score 14.2; DB 9; Length 20;  
Best Local Similarity 84.2%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 19  
Db 2 GGGTCAACGTTTCAGGGGG 20

## RESULT 7

US-11-127-654-216  
; Sequence 216, Application US/11127654  
; Publication No. US20050250726A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC  
; FILE REFERENCE: C1039.70060US01  
; CURRENT APPLICATION NUMBER: US/11/127,654  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 216  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-216

Query Match 74.7%; Score 14.2; DB 11; Length 20;  
Best Local Similarity 84.2%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTACGGGGG 19  
||| ||||| |||||  
Db 2 GGGTTGACGTTTGGGGG 20

## RESULT 8

US-10-310-914A-1202061/c  
; Sequence 1202061, Application US/10310914A  
; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1202061

; LENGTH: 28

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1202061

Query Match 73.7%; Score 14; DB 7; Length 28;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGACGTTACGGG 16

||||| |||||

Db 28 GGTGACGTTACGGG 15

## RESULT 9

US-10-310-914A-524757

; Sequence 524757, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 524757

; LENGTH: 20

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-524757

Query Match 72.6%; Score 13.8; DB 7; Length 20;

Best Local Similarity 70.6%; Pred. No. 1.3e+03;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGTGACGTTACGGGG 19

||: ||: |||||

Db 4 GGUCAGGUUCAGGGGG 20

## RESULT 10

US-10-310-914A-895375/c

; Sequence 895375, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 895375

; LENGTH: 20

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-895375

Query Match 72.6%; Score 13.8; DB 7; Length 20;

Best Local Similarity 88.2%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTACGGGG 17

||||| |||||

Db 19 GGGTTACGTTCCAGGG 3

## RESULT 11

US-10-310-914A-1185102

; Sequence 1185102, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1185102

; LENGTH: 20

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-1185102

Query Match 72.6%; Score 13.8; DB 7; Length 20;

Best Local Similarity 70.6%; Pred. No. 1.3e+03;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTACGGGG 17

||||| |||||

Db 2 GGGGUGCCGUCUGGGG 18

## RESULT 12

US-10-310-914A-895439/c

; Sequence 895439, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 895439

; LENGTH: 21

; TYPE: RNA

; ORGANISM: Human

```
US-10-310-914A-895439
Query Match          72.6%; Score 13.8; DB 7; Length 21;
Best Local Similarity 88.2%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 17
   ||||| ||||| |||||
Db 20 GGGGTTACGTCACGGGG 4

RESULT 13
US-10-310-914A-1185206
; Sequence 1185206, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1185206
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1185206
Query Match          72.6%; Score 13.8; DB 7; Length 22;
Best Local Similarity 70.8%; Pred. No. 1.3e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 17
   ||||| ||||| |||||
Db 5 GGGGCGCCGUCUGGG 21

RESULT 14
US-10-310-914A-530908/c
; Sequence 530908, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 530908
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-530908
Query Match          72.6%; Score 13.8; DB 7; Length 23;
Best Local Similarity 88.2%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 17
   ||||| ||||| |||||
Db 19 GGGGTTACTTTCAGGG 3

RESULT 15
US-11-101-244-1188547/c
; Sequence 1188547, Application US/11101244
; Publication No. US20050246794A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1188547
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1188547
Query Match          70.5%; Score 13.4; DB 9; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGTGACGTTTCAGGG 16
   ||||| ||||| |||||
Db 15 GGGTGACGTTTCATGG 1

RESULT 16
US-11-083-784-1188547/c
; Sequence 1188547, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1188547
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1188547
Query Match          70.5%; Score 13.4; DB 10; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGTGACGTTTCAGGG 16
   ||||| ||||| |||||
Db 15 GGGTGACGTTTCATGG 1

RESULT 17
US-10-310-914A-673587/c
; Sequence 673587, Application US/10310914A
```

```
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 673587
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-673587

Query Match          70.5%; Score 13.4; DB 7; Length 22;
Best Local Similarity 93.3%; Pred. No. 1.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGTGACGTTTCAGGGG 17
Db 20 GGTGACGTTTCAGGGG 6

RESULT 18
US-10-310-914A-308426/c
; Sequence 308426, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 308426
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-308426

Query Match          69.5%; Score 13.2; DB 7; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGG 18
Db 18 GGGGTGACCTTCTTGGG 1

RESULT 19
US-11-127-654-498
; Sequence 498, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2002-03-29
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 673587
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-673587
```

```
; SEQ ID NO 498
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-498

Query Match          69.5%; Score 13.2; DB 11; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGG 18
Db 3 GGCATGACGTTTCGGGGG 20

RESULT 20
US-11-127-654-501
; Sequence 501, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR FILING DATE: 2002-03-29
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 501
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-501

Query Match          69.5%; Score 13.2; DB 11; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGG 18
Db 3 GGCATGACGTTTCGGGGG 20

RESULT 21
US-10-310-914A-872061
; Sequence 872061, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 872061
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-872061

Query Match          69.5%; Score 13.2; DB 7; Length 21;
```

```
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 518042
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-518042

Query Match          69.5%; Score 13.2; DB 7; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTACGGGGG 18
    ||||| |||||
Db 20 GGGGTGACATTCATGGTG 3

RESULT 25
US-10-310-914A-836953
; Sequence 836953, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 836953
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-836953

Query Match          69.5%; Score 13.2; DB 7; Length 22;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTGACGTTACGGGGG 19
    ||||| ||||| |||||
Db 19 GGGTGACGTCAGGAGAG 2

RESULT 23
US-10-310-914A-456901/c
; Sequence 456901, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 456901
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-456901

Query Match          69.5%; Score 13.2; DB 7; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTACGGGGG 18
    ||||| ||||| |||||
Db 23 GGGGTGACTTCAGGTGG 6

RESULT 24
US-10-310-914A-518042/c
; Sequence 518042, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
```

```
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 518042
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-518042

Query Match          69.5%; Score 13.2; DB 7; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTACGGGGG 18
    ||||| ||||| |||||
Db 20 GGGGTGACATTCATGGTG 3

RESULT 25
US-10-310-914A-836953
; Sequence 836953, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 836953
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-836953

Query Match          69.5%; Score 13.2; DB 7; Length 23;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTGACGTTACGGGGG 19
    |||: |||:: |||||
Db 3 GGGUCACGUGCGGGGGG 20

RESULT 26
US-10-310-914A-896494/c
; Sequence 896494, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 896494
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-896494

Query Match          69.5%; Score 13.2; DB 7; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.4e+03;
```



Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTGACGTTTCAGGGGG 19  
|||||  
Db 23 GGGTGACGTTTCAGGGGG 6

## RESULT 27

US-10-310-914A-837004  
; Sequence 837004, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvazat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087, 0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 837004

; LENGTH: 24

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-837004

Query Match 69.5%; Score 13.2; DB 7; Length 24;

Best Local Similarity 66.7%; Pred. No. 2.4e+03;

Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTGACGTTTCAGGGGG 19  
|||||  
Db 7 GGGTGACGTTTCAGGGGG 24

## RESULT 28

US-10-310-914A-509542/c

; Sequence 509542, Application US/10310914A

; Publication No. US20060003322A1

; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvazat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087, 0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 509542

; LENGTH: 25

; TYPE: RNA

; ORGANISM: Human

US-10-310-914A-509542

Query Match 69.5%; Score 13.2; DB 7; Length 25;

Best Local Similarity 83.3%; Pred. No. 2.4e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 18  
|||||  
Db 21 GGGTGACGTTTCAGGGGG 4

## RESULT 29

US-11-121-849-16126

; Sequence 16126, Application US/11121849

; Publication No. US2005027080A1

; GENERAL INFORMATION:

; APPLICANT: John Palma

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S

; FILE REFERENCE: Microarrays

; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 16126  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-16126

Query Match 69.5%; Score 13.2; DB 11; Length 25;

Best Local Similarity 83.3%; Pred. No. 2.4e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 18  
|||||  
Db 3 GGGTGACGTTTCAGGGGG 20

## RESULT 30

US-11-012-353-97

; Sequence 97, Application US/11012353

; Publication No. US20050249730A1

; GENERAL INFORMATION:

; APPLICANT: GOETSCH, LILIANE

; APPLICANT: CORVAIA, NATHALIE

; APPLICANT: DUFLOS, ALAIN

; APPLICANT: HAEUW, JEAN-FRANCOIS

; APPLICANT: LEGER, OLIVIER

; APPLICANT: BECK, ALAIN

; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID

; FILE REFERENCE: 017753-198

; CURRENT APPLICATION NUMBER: US/11/012,353

; CURRENT FILING DATE: 2004-12-16

; PRIOR APPLICATION NUMBER: 10/735,916

; PRIOR FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: FR 0308538

; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: PCT/FR03/00178

; PRIOR FILING DATE: 2003-01-20

; PRIOR APPLICATION NUMBER: FR 0205753

; PRIOR FILING DATE: 2002-05-07

; PRIOR APPLICATION NUMBER: FR 0200653

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: FR 0200654

; PRIOR FILING DATE: 2002-01-18

; NUMBER OF SEQ ID NOS: 162

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 97

; LENGTH: 32

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: oligonucleotide

US-11-012-353-97

Query Match 69.5%; Score 13.2; DB 11; Length 32;

Best Local Similarity 83.3%; Pred. No. 2.4e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGTGACGTTTCAGGGGG 18  
|||||  
Db 7 GGGTGACGTTTCAGGGGG 24

## RESULT 31

US-10-310-914A-1145336

; Sequence 1145336, Application US/10310914A

```
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1145336
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1145336

Query Match          67.4%; Score 12.8; DB 7; Length 18;
Best Local Similarity 75.0%; Pred. No. 3.7e+03;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 16
Db 2 GGGUUGACGUACAGGG 17

RESULT 32
US-10-310-914A-966814/c
; Sequence 966814, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 966814
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-966814

Query Match          67.4%; Score 12.8; DB 7; Length 19;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 16
Db 18 GGGGAGACGCTCAGGG 3

RESULT 33
US-10-522-362-49
; Sequence 49, Application US/10522362
; Publication No. US2005028178A1
; GENERAL INFORMATION:
; APPLICANT: De Bari, Cosimo
; APPLICANT: Dell'Accio, Francesco
; APPLICANT: Luyten, Frank
; TITLE OF INVENTION: Compositions Comprising Muscle
; FILE REFERENCE: 50304/030001
; CURRENT APPLICATION NUMBER: US/10/522,362
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: PCT/EP03/009008
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/399,745
; PRIOR FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 49
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(23)
; OTHER INFORMATION: CD90 antisense primer
US-10-522-362-49

Query Match          67.4%; Score 12.8; DB 7; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTGACGTTTCAGGGGG 19
Db 3 GTGACGTTCTGGGAGG 18

RESULT 34
US-10-310-914A-746353/c
; Sequence 746353, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 746353
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-746353

Query Match          67.4%; Score 12.8; DB 7; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 16
Db 18 GTGGGACGCTTCAGGG 3

RESULT 35
US-10-310-914A-966777/c
; Sequence 966777, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 966777
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-966777

Query Match          67.4%; Score 12.8; DB 7; Length 22;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 GGGGTGACGTTTCAGGG 16  
|||||  
Db 17 GGGGAGCGCTCAGGG 2

## RESULT 36

US-10-310-914A-240915/c  
; Sequence 240915, Application US/10310914A  
; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuizat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 240915  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-240915

Query Match 67.4%; Score 12.8; DB 7; Length 23;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTGACGTTTCAGGGGG 19  
|||||  
Db 21 GTGAAGTTTCAGGGTGG 6

## RESULT 37

US-10-310-914A-411534  
; Sequence 411534, Application US/10310914A  
; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuizat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 411534  
; LENGTH: 24  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-411534

Query Match 67.4%; Score 12.8; DB 7; Length 24;  
Best Local Similarity 81.2%; Pred. No. 3.7e+03;  
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGTGACGTTTCAGGG 17  
|||||  
Db 6 GGGGAGCGGUCAGGGG 21

## RESULT 38

US-10-310-914A-1145337  
; Sequence 1145337, Application US/10310914A  
; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuizat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1145337  
; LENGTH: 25  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1145337

Query Match 67.4%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 75.0%; Pred. No. 3.7e+03;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTTCAGGG 16  
|||||  
Db 9 GGGGAGCGGUCAGGG 24

## RESULT 39

US-11-121-849-15921/c  
; Sequence 15921, Application US/11121849  
; Publication No. US20050272080A1

## GENERAL INFORMATION:

; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 15921  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-15921

Query Match 67.4%; Score 12.8; DB 11; Length 25;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTGACGTTTCAGGGGG 18  
|||||  
Db 18 GGTGATGTTCTGGGGG 3

## RESULT 40

US-11-121-849-22103/c  
; Sequence 22103, Application US/11121849  
; Publication No. US20050272080A1

## GENERAL INFORMATION:

; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 22103  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-22103

Query Match 67.4%; Score 12.8; DB 11; Length 25;  
Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY      3 GGTGACGTTTCAGGGG 18
Db      18 GGTGATGTTCTGGGG 3

RESULT 41
US-11-121-849-24138/c
; Sequence 24138, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24138
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-24138

Query Match      67.4%; Score 12.8; DB 11; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GGTGACGTTTCAGGGG 18
Db      18 GGTGATGTTCTGGGG 3

RESULT 42
US-11-121-849-107577
; Sequence 107577, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 107577
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-107577

Query Match      67.4%; Score 12.8; DB 11; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGGTGACGTTTCAGGG 16
Db      7 GGGAGACCTTCAGG 22

RESULT 43
US-11-121-849-115643/c
; Sequence 115643, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
```

```
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 115643
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-115643

Query Match      67.4%; Score 12.8; DB 11; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GGTGACGTTTCAGGGG 18
Db      17 GATGACGTTTCAGGTG 2

RESULT 44
US-11-121-849-476398/c
; Sequence 476398, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 476398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-476398

Query Match      67.4%; Score 12.8; DB 11; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GGTGACGTTTCAGGGG 17
Db      21 GGCTGACCTTCAGGGG 6

RESULT 45
US-11-121-849-568167/c
; Sequence 568167, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 568167
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-568167
```

```
Query Match      67.4%; Score 12.8; DB 11; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTACGGG 16
Db 18 GGTGTGACGTTAAGGG 3

RESULT 46
US-11-121-849-570964
; Sequence 570964, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121.849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 570964
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-570964

Query Match      67.4%; Score 12.8; DB 11; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTACGGG 16
Db 2 GGGCTGATGTTACGGG 17

RESULT 47
US-10-755-092-43/c
; Sequence 43, Application US/10755092
; Publication No. US20060021095A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launils, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Syngenta Biotechnology, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/755,092
; FILING DATE: 08-Jan-2004

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/09/988,462
; FILING DATE: 20-Nov-2001
; APPLICATION NUMBER: US 09/547,422
; FILING DATE: 11-APR-2000
; APPLICATION NUMBER: US 08/459,504
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer P5(a)"
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-755-092-43

Query Match      67.4%; Score 12.8; DB 6; Length 32;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGTGACGTTACGGGG 18
Db 18 GGTGCGGTACAGGGG 3

RESULT 48
US-10-939-294A-19843
; Sequence 19843, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)
; CURRENT APPLICATION NUMBER: US/10/939,294A
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/502/731
; PRIOR FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 38895
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19843
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-19843

Query Match      67.4%; Score 12.8; DB 7; Length 32;
Best Local Similarity 87.5%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTGACGTTACGGG 16
Db 8 GGGGTGACGTCGCGG 23
```

RESULT 49

US-11-175-859-51905/c  
 ; Sequence 51905, Application US/11175859  
 ; Publication No. US20060024715A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Affymetrix, Inc.  
 ; APPLICANT: Liu, Guoying et al.  
 ; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
 ; FILE REFERENCE: 3690.1  
 ; CURRENT APPLICATION NUMBER: US/11/175,859  
 ; CURRENT FILING DATE: 2005-07-05  
 ; PRIOR APPLICATION NUMBER: US 60/585,352  
 ; PRIOR FILING DATE: 2004-07-02  
 ; NUMBER OF SEQ ID NOS: 116251  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 51905  
 ; LENGTH: 50  
 ; TYPE: DNA  
 ; ORGANISM: homo sapien  
 US-11-175-859-51905

Query Match 67.4%; Score 12.8; DB 11; Length 50;  
 Best Local Similarity 87.5%; Pred. No. 3.7e+03;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGG 16  
 ||| |||||  
 Db 42 GGGAGGACGTTTCAGGG 27

RESULT 50

US-10-310-914A-896490/c  
 ; Sequence 896490, Application US/10310914A  
 ; Publication No. US2006000322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shiler, Kvuzat  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310,914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 896490  
 ; LENGTH: 19  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-896490

Query Match 66.3%; Score 12.6; DB 7; Length 19;  
 Best Local Similarity 78.9%; Pred. No. 4.6e+03;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTGACGTTTCAGGGGGG 19  
 |||||  
 Db 19 GTGGTACGTCGAGGGGG 1

Search completed: February 16, 2006, 02:53:00  
 Job time : 181.124 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:51:58 ; Search time 575.802 Seconds  
(without alignments)  
2369.293 Million cell updates/sec

Title: US-09-669-187A-81

Perfect score: 24

Sequence: 1 ggggtccagcgtgcgcattggggg 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vl.\*

14: gb\_htg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	6	AX103889 Sequence
2	24	100.0	24	6	AX355412 Sequence
3	24	100.0	24	6	AX546942 Sequence
4	16.2	67.5	25	6	AX182410 Sequence
5	16	66.7	30	6	CB859706 Sequence
6	16	66.7	33	6	BD263032 Trans-Spe
7	16	66.7	33	6	AX217874 Sequence
8	15.2	63.3	35	6	AX630015 Sequence
9	15.2	63.3	35	6	AX351117 Sequence
10	15	62.5	16	6	AX103898 Sequence
11	15	62.5	16	6	AX355505 Sequence
12	15	62.5	16	6	AX546951 Sequence
13	15	62.5	27	6	AR004426 Sequence
14	15	62.5	27	6	I43661 Sequence 13
15	15	62.5	27	6	I86720 Sequence 8
16	15	62.5	40	6	AX754696 Sequence
17	15	62.5	50	8	HSTFE3ID3
18	14.8	61.7	20	6	AX463650 Sequence

[illegible]



c 238 13 54.2 35 6 BD265504 Mammalian  
c 239 13 54.2 35 6 AR370510 Sequence  
c 240 13 54.2 35 6 AR380981 Sequence  
c 241 13 54.2 35 6 AR442709 Sequence  
c 242 13 54.2 46 6 A98793 Sequence 26  
c 243 13 54.2 46 6 AR242321 Sequence  
c 244 13 54.2 48 6 AR117273 Sequence  
c 245 13 54.2 48 6 BD087162 Human thy  
c 246 13 54.2 48 6 AR257428 Sequence  
c 247 13 54.2 48 6 AR269373 Sequence  
c 248 13 54.2 50 6 CQ008484 Sequence  
c 249 12.8 53.3 18 6 AX460270 Sequence  
c 250 12.8 53.3 19 6 AX155585 Sequence  
c 251 12.8 53.3 20 6 AR293836 Sequence  
c 252 12.8 53.3 20 6 AX296687 Sequence  
c 253 12.8 53.3 23 6 I27136 Sequence 32  
c 254 12.8 53.3 24 6 I27121 Sequence 17  
c 255 12.8 53.3 24 6 AX289203 Sequence  
c 256 12.8 53.3 24 6 AX292054 Sequence  
c 257 12.8 53.3 24 6 AX444476 Sequence  
c 258 12.8 53.3 25 6 AX751162 Sequence  
c 259 12.8 53.3 25 6 AX751163 Sequence  
c 260 12.8 53.3 26 6 AR228693 Sequence  
c 261 12.8 53.3 29 6 AR117362 Sequence  
c 262 12.8 53.3 29 6 AR205141 Sequence  
c 263 12.8 53.3 29 6 AR223345 Sequence  
c 264 12.8 53.3 29 6 AR287846 Sequence  
c 265 12.8 53.3 30 6 AX166282 Sequence  
c 266 12.8 53.3 31 6 I19522 Sequence 4  
c 267 12.8 53.3 31 6 AX148321 Sequence  
c 268 12.8 53.3 31 6 BD017439 Transgeni  
c 269 12.8 53.3 33 6 E09065 DNA encodin  
c 270 12.8 53.3 36 6 BD188836 Hybrid pr  
c 271 12.8 53.3 36 6 BD188838 Hybrid pr  
c 272 12.8 53.3 36 6 BD188841 Hybrid pr  
c 273 12.8 53.3 36 6 BD188843 Hybrid pr  
c 274 12.8 53.3 36 6 BD188845 Hybrid pr  
c 275 12.8 53.3 39 6 BD233542 Targeted  
c 276 12.8 53.3 39 6 AR435711 Sequence  
c 277 12.8 53.3 39 6 AX006837 Sequence  
c 278 12.8 53.3 39 6 AX463645 Sequence  
c 279 12.8 53.3 39 6 AX463653 Sequence  
c 280 12.8 53.3 41 6 CS063847 Sequence  
c 281 12.8 53.3 41 6 AX699916 Sequence  
c 282 12.8 53.3 43 6 AX286326 Sequence  
c 283 12.8 53.3 49 6 AX288967 Sequence  
c 284 12.8 53.3 50 6 CQ002429 Sequence  
c 285 12.8 53.3 50 6 CQ003647 Sequence  
c 286 12.8 53.3 50 6 CQ003696 Sequence  
c 287 12.8 53.3 50 6 CQ006015 Sequence  
c 288 12.8 53.3 50 6 CQ009000 Sequence  
c 289 12.8 53.3 50 6 AX157284 Sequence  
c 290 12.6 52.5 20 6 AR170368 Sequence  
c 291 12.6 52.5 20 6 BD075110 MAGE-3 pe  
c 292 12.6 52.5 20 6 BD084642 RNase L a  
c 293 12.6 52.5 20 6 BD233818 Transcrip  
c 294 12.6 52.5 20 6 BD237168 MAGE-A3 p  
c 295 12.6 52.5 20 6 CS103773 Sequence  
c 296 12.6 52.5 20 6 AR221344 Sequence  
c 297 12.6 52.5 20 6 AR234713 Sequence  
c 298 12.6 52.5 20 6 AR241179 Sequence  
c 299 12.6 52.5 20 6 AR277764 Sequence  
c 300 12.6 52.5 20 6 AR492423 Sequence

ALIGNMENTS

RESULT 1  
AX103889 AX103889 Sequence 81 from Patent WO0122972.  
LOCUS AX103889 24 bp DNA linear PAT 30-APR-2001  
DEFINITION Sequence 81 from Patent WO0122972.  
ACCESSION AX103889

VERSION AX103889.1 GI:13920086  
KEYWORDS synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.  
TITLE Immunostimulatory nucleic acids  
JOURNAL Patent: WO 012972-A 81 05-APR-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical  
GmbH (DE)  
FEATURES Location/Qualifiers  
source 1..24  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 100.0%; Score 24; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGTCCAGCGTGGCCATGGGG 24  
|||||  
Db 1 GGGGTCCAGCGTGGCCATGGGG 24  
RESULT 2  
AX355412 AX355412 24 bp DNA linear PAT 06-FEB-2002  
LOCUS  
DEFINITION Sequence 440 from Patent WO0197843.  
ACCESSION AX355412  
VERSION AX355412.1 GI:18620080  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Weiner,G. and Hartmann,G.  
TITLE Methods for enhancing antibody-induced cell lysis and treating  
cancer  
JOURNAL Patent: WO 0197843-A 440 27-DEC-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
FEATURES Location/Qualifiers  
source 1..24  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic oligonucleotide  
chimeric phosphorothioate/phosphodiester backbone with  
phosphorothioate at 5' and 3' ends"  
ORIGIN  
Query Match 100.0%; Score 24; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGTCCAGCGTGGCCATGGGG 24  
|||||  
Db 1 GGGGTCCAGCGTGGCCATGGGG 24  
RESULT 3  
AX546942 AX546942 24 bp DNA linear PAT 01-MAR-2003  
LOCUS  
DEFINITION Sequence 81 from Patent WO02053141.  
ACCESSION AX546942  
VERSION AX546942.1 GI:25812086  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1

AUTHORS Bratzler,R.I.  
TITLE Inhibition of angiogenesis by nucleic acids  
JOURNAL Patent: WO 02053141-A 81 11-JUL-2002;  
Coley Pharmaceutical Group, Inc. (US)  
FEATURES  
source 1. .24  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic Sequence"  
  
ORIGIN  
Query Match 100.0%; Score 24; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGGTCCAGCGTGGCCCATGGGG 24  
|||||  
Db 1 GGGGTCCAGCGTGGCCCATGGGG 24  
  
RESULT 4  
AR182410  
LOCUS AR182410 25 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 1 from patent US 6338850.  
ACCESSION AR182410  
VERSION AR182410.1 GI:20225617  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Jevnikar,A.M., Ma,S. and Stiller,C.R.  
TITLE Methods and products for controlling the immune response of a  
mammal to glutamic acid decarboxylase  
JOURNAL Patent: US 6338850-A 1 15-JAN-2002;  
FEATURES  
source 1. .25  
/organism="unknown"  
/mol\_type="unassigned DNA"  
  
ORIGIN  
Query Match 67.5%; Score 16.2; DB 6; Length 25;  
Best Local Similarity 85.7%; Pred. No. 5.2e+04;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 GGGTCCAGCGTGGCCCATGGG 22  
|||||  
Db 2 GGATCCGGCGCGCCCATGGG 22  
  
RESULT 5  
CQ859706/c  
LOCUS CQ859706 30 bp DNA linear PAT 10-SEP-2004  
DEFINITION Sequence 2 from Patent WO2004072225.  
ACCESSION CQ859706  
VERSION CQ859706.1 GI:51981619  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Sharon,A. and Goldstein-Barhoom,S.  
TITLE Transgenic fungi expressing bcl-2 and methods of using bcl-2 or  
portions thereof for improving biomass production, survival,  
longevity, stress resistance and pathogenicity of fungi  
JOURNAL Patent: WO 2004072225-A 2 26-AUG-2004;  
Ramat at Tel Aviv University Ltd. (IL)  
FEATURES  
source 1. .30  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

ORIGIN  
/note="Single strand DNA oligonucleotide"  
  
Query Match 66.7%; Score 16; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 6e+04;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 CCAGCGTGGCCCATGG 21  
|||||  
Db 20 CCAGCGTGGCCCATGG 5  
  
RESULT 6  
BD263032/c  
LOCUS BD263032 33 bp DNA linear PAT 17-JUL-2003  
DEFINITION Trans-species transfer of apoptotic genes and transgenic plants  
developed thereby.  
ACCESSION BD263032  
VERSION BD263032.1 GI:33072800  
KEYWORDS JP 2002538769-A/5.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Dickman,M.B.  
TITLE Trans-species transfer of apoptotic genes and transgenic plants  
developed thereby  
JOURNAL Patent: JP 2002538769-A 5 19-NOV-2002;  
UNIVERSITY OF NEBRASKA LINCOLN  
COMMENT OS Artificial Sequence  
PN JP 2002538769-A/5  
PD 19-NOV-2002  
PR 29-OCT-1999 JP 2000579763  
PC 30-OCT-1998 US 60/106321,09-JUN-1999 US 60/138303 PI  
MARTIN B DICKMAN  
PC A01H57/00,C12N5/10,C12N15/09,C12Q1/68//(C12N5/10,C12R1:91), PC  
C12N15/00,  
PC C12N5/00, (C12N5/00,C12R1:91)  
CC PCR primer  
FH Key Location/Qualifiers  
FT source 1. .33  
/organism='Artificial Sequence'.  
FEATURES  
source 1. .33  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
  
ORIGIN  
Query Match 66.7%; Score 16; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 5.9e+04;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 CCAGCGTGGCCCATGG 21  
|||||  
Db 33 CCAGCGTGGCCCATGG 18  
  
RESULT 7  
AR217874/c  
LOCUS AR217874 33 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 11 from patent US 6417002.  
ACCESSION AR217874  
VERSION AR217874.1 GI:23317768  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Horlick,R.A. and Chelsky,D.  
TITLE Method for maintenance and selection of episomes  
JOURNAL Patent: US 6417002-A 11 09-JUL-2002;  
PharmacoPeia, Inc.; Cranbury, NJ

```

FEATURES
  source
    Location/Qualifiers
      1..33
        /organism="unknown"
        /mol_type="genomic DNA"
ORIGIN
  Query Match
    Best Local Similarity 66.7%; Score 16; DB 6; Length 33;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy
    6 CCAGCGTGGCCATGG 21
    |||||
  Db
    27 CCAGCGTGGCCATGG 12
    |||||
RESULT 8
AR630015/c
LOCUS
  DEFINITION Sequence 69 from patent US 6838556.
  ACCESSION AR630015
  VERSION AR630015.1 GI:59762210
  KEYWORDS
  SOURCE Unknown.
  ORGANISM Unknown.
  REFERENCE
    1 (bases 1 to 35)
    Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
    Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
    Sheppard,L.T., Kim,M.Y. and Bruce,T.W.
  TITLE Promoters for regulated gene expression
  JOURNAL Patent: US 6838556-A 69 04-JAN-2005;
  GENELABS TECHNOLOGIES, INC.; Redwood City, CA
FEATURES
  source
    Location/Qualifiers
      1..35
        /organism="unknown"
        /mol_type="genomic DNA"
ORIGIN
  Query Match
    Best Local Similarity 63.3%; Score 15.2; DB 6; Length 35;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
  Qy
    2 GGGTCCAGCGTGGCCATGG 21
    |||||
  Db
    28 GGGTCCAGCGGAGCCATGG 9
    |||||
RESULT 9
AX351117/c
LOCUS
  DEFINITION Sequence 69 from Patent WO0194600.
  ACCESSION AX351117
  VERSION AX351117.1 GI:18616471
  KEYWORDS
  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  ORGANISM
  REFERENCE
    1
    Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
    Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
    Sheppard,L.T., Lim,M.Y. and Bruce,T.W.
  TITLE Promoters for regulated gene expression
  JOURNAL Patent: WO 0194600-A 69 13-DEC-2001;
  GENELABS TECHNOLOGIES, INC. (US)
FEATURES
  source
    Location/Qualifiers
      1..35
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="primer"
ORIGIN
  Query Match
    Best Local Similarity 63.3%; Score 15.2; DB 6; Length 35;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
  Qy
    2 GGGTCCAGCGTGGCCATGG 21
    |||||
  Db
    28 GGGTCCAGCGGAGCCATGG 9
    |||||
RESULT 10
AX103898
LOCUS
  DEFINITION Sequence 90 from Patent WO0122972.
  ACCESSION AX103898
  VERSION AX103898.1 GI:13920095
  KEYWORDS
  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  ORGANISM
  REFERENCE
    1
    Krieg,A.M., Schetter,C. and Vollmer,J.C.
  AUTHORS Immunostimulatory nucleic acids
  TITLE Patent: WO 0122972-A 90 05-APR-2001;
  JOURNAL UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
  GmbH (DE)
FEATURES
  source
    Location/Qualifiers
      1..16
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
ORIGIN
  Query Match
    Best Local Similarity 62.5%; Score 15; DB 6; Length 16;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy
    5 TCCAGCGTGGCCAT 19
    |||||
  Db
    1 TCCAGCGTGGCCAT 15
    |||||
RESULT 11
AX355505
LOCUS
  DEFINITION Sequence 533 from Patent WO0197843.
  ACCESSION AX355505
  VERSION AX355505.1 GI:18620173
  KEYWORDS
  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  ORGANISM
  REFERENCE
    1
    Weiner,G. and Hartmann,G.
  AUTHORS Methods for enhancing antibody-induced cell lysis and treating
  TITLE cancer
  JOURNAL Patent: WO 0197843-A 533 27-DEC-2001;
  UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
  source
    Location/Qualifiers
      1..16
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic oligonucleotide
        chimeric phosphorothioate/phosphodiester backbone with
        phosphorothioate at 5' and 3' ends"
ORIGIN
  Query Match
    Best Local Similarity 62.5%; Score 15; DB 6; Length 16;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy
    5 TCCAGCGTGGCCAT 19
    |||||
  Db
    1 TCCAGCGTGGCCAT 15
    |||||

```

```

Best Local Similarity 85.0%; Pred. No. 1.3e+05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
  Qy
    2 GGGTCCAGCGTGGCCATGG 21
    |||||
  Db
    28 GGGTCCAGCGGAGCCATGG 9
    |||||
RESULT 10
AX103898
LOCUS
  DEFINITION Sequence 90 from Patent WO0122972.
  ACCESSION AX103898
  VERSION AX103898.1 GI:13920095
  KEYWORDS
  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  ORGANISM
  REFERENCE
    1
    Krieg,A.M., Schetter,C. and Vollmer,J.C.
  AUTHORS Immunostimulatory nucleic acids
  TITLE Patent: WO 0122972-A 90 05-APR-2001;
  JOURNAL UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
  GmbH (DE)
FEATURES
  source
    Location/Qualifiers
      1..16
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
ORIGIN
  Query Match
    Best Local Similarity 62.5%; Score 15; DB 6; Length 16;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy
    5 TCCAGCGTGGCCAT 19
    |||||
  Db
    1 TCCAGCGTGGCCAT 15
    |||||
RESULT 11
AX355505
LOCUS
  DEFINITION Sequence 533 from Patent WO0197843.
  ACCESSION AX355505
  VERSION AX355505.1 GI:18620173
  KEYWORDS
  SOURCE
    synthetic construct
    other sequences; artificial sequences.
  ORGANISM
  REFERENCE
    1
    Weiner,G. and Hartmann,G.
  AUTHORS Methods for enhancing antibody-induced cell lysis and treating
  TITLE cancer
  JOURNAL Patent: WO 0197843-A 533 27-DEC-2001;
  UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
  source
    Location/Qualifiers
      1..16
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic oligonucleotide
        chimeric phosphorothioate/phosphodiester backbone with
        phosphorothioate at 5' and 3' ends"
ORIGIN
  Query Match
    Best Local Similarity 62.5%; Score 15; DB 6; Length 16;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Qy
    5 TCCAGCGTGGCCAT 19
    |||||
  Db
    1 TCCAGCGTGGCCAT 15
    |||||

```

[illegible]



ORIGIN

Query Match 60.8%; Score 14.6; DB 6; Length 47;  
Best Local Similarity 81.0%; Pred. No. 2.1e+05;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCCATGG 21  
Db 10 GGGTCCCGGTGGCCCATGG 30

RESULT 21  
CS019648/c  
LOCUS CS019648 26 bp DNA linear PAT 23-FEB-2005  
DEFINITION Sequence 1 from Patent WO2005012357.  
ACCESSION CS019648  
VERSION CS019648.1 GI:60220655  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Milmer, J. and Jiang, M.  
TITLE Bcl-2 splicing variants  
JOURNAL Patent: WO 2005012357-A 1 10-FEB-2005;  
Milmer, Jo (GB)  
FEATURES Location/Qualifiers  
source 1..26  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
/note="Primer"

ORIGIN

Query Match 60.0%; Score 14.4; DB 6; Length 26;  
Best Local Similarity 93.8%; Pred. No. 2.8e+05;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCATGG 21  
Db 20 CCAGCGTGGCCCATGC 5

RESULT 22  
CQ902189  
LOCUS CQ902189 29 bp DNA linear PAT 16-NOV-2004  
DEFINITION Sequence 129 from Patent EP1475441.  
ACCESSION CQ902189  
VERSION CQ902189.1 GI:55784068  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Aujame, L., Bouchardon, A., Renaud-Mongenie, G., Rokbi, B., Nassif, X., Tinsley, C. and Perrin, A.  
TITLE Specific nucleic acids and polypeptide from pathogenic strains of Neisseria  
JOURNAL Patent: EP 1475441-A 129 10-NOV-2004;  
Aventis Pasteur (FR); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM) (FR)  
FEATURES Location/Qualifiers  
source 1..29  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence: amorce de PCR"

ORIGIN

Query Match 60.0%; Score 14.4; DB 6; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCCATGGGG 24  
Db 2 GGGATCCAACTGCTTCATGGGTG 25

RESULT 23  
AR628538  
LOCUS AR628538 29 bp DNA linear PAT 14-FEB-2005  
DEFINITION Sequence 127 from patent US 6835384.  
ACCESSION AR628538  
VERSION AR628538.1 GI:59753857  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Aujame, L., Bouchardon, A., Renaud-Mongenie, G., Rokbi, B., Nassif, X., Tinsley, C. and Perrin, A.  
TITLE Nucleic acids and polypeptides specific of the neisseria genus pathogenic strains  
JOURNAL Patent: US 6835384-A 127 28-DEC-2004;  
Aventis Pasteur and Institut National de la Sante et de la Recherche Medicale (INSERM); Lyons; FRX;  
FEATURES Location/Qualifiers  
source 1..29  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 60.0%; Score 14.4; DB 6; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCCATGGGG 24  
Db 2 GGGATCCAACTGCTTCATGGGTG 25

RESULT 24  
AX024184  
LOCUS AX024184 29 bp DNA linear PAT 15-SEP-2000  
DEFINITION Sequence 127 from Patent FR2785293.  
ACCESSION AX024184  
VERSION AX024184.1 GI:10184495  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Nassif, X., Tinsley, C., Aujame, L., Perrin, A., Rokbi, B., Bouchardon, A. and Renaud, M.G.  
JOURNAL Patent: FR 2785293-A 127 05-MAY-2000;  
PASTEUR MERIEUX SERUMS VACC (FR)  
FEATURES Location/Qualifiers  
source 1..29  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="amorce de"

ORIGIN

Query Match 60.0%; Score 14.4; DB 6; Length 29;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCCATGGGG 24  
Db 2 GGGATCCAACTGCTTCATGGGTG 25

RESULT 25  
BD002993/c

LOCUS BD002993 35 bp DNA linear PAT 31-JAN-2002  
DEFINITION A method for determining DNA methyltransferase.  
ACCESSION BD002993  
VERSION BD002993.1 GI:18630954  
KEYWORDS JP 2000232889-A/2.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Aonuma, M.  
TITLE A method for determining DNA methyltransferase  
JOURNAL Patent: JP 2000232889-A 2 29-AUG-2000;  
DALIHI PHARMACEUTICAL CO LTD  
OS Artificial Sequence  
COMMENT PN JP 2000232889-A/2  
PD 29-AUG-2000  
PF 30-JUL-1999 JP 1999216640  
PR MASASHI AONUMA  
PI C12N15/09, C12N9/10, C12N11/14, C12Q1/48, C12N15/00 CC  
PC Location/Qualifiers  
FH Key 1..35  
FT source /organism='Artificial Sequence'.  
FEATURES  
source 1..35  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
ORIGIN  
Query Match 60.0%; Score 14.4; DB 6; Length 35;  
Best Local Similarity 75.0%; Pred. No. 2.7e+05;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 GGGTCCAGCGTGGCCATGGGG 24  
Db 26 GCGGCTCGCGTGGCCAGCGGG 3  
RESULT 26  
LOCUS BD002995/c 35 bp DNA linear PAT 31-JAN-2002  
DEFINITION A method for determining DNA methyltransferase.  
ACCESSION BD002995  
VERSION BD002995.1 GI:18630956  
KEYWORDS JP 2000232889-A/4.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Aonuma, M.  
TITLE A method for determining DNA methyltransferase  
JOURNAL Patent: JP 2000232889-A 4 29-AUG-2000;  
DALIHI PHARMACEUTICAL CO LTD  
OS Artificial Sequence  
COMMENT PN JP 2000232889-A/4  
PD 29-AUG-2000  
PF 30-JUL-1999 JP 1999216640  
PR MASASHI AONUMA  
PI C12N15/09, C12N9/10, C12N11/14, C12Q1/48, C12N15/00 CC  
PC Location/Qualifiers  
FH Key 1..35  
FT source /organism='Artificial Sequence'.  
FEATURES  
source 1..35  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
ORIGIN  
Query Match 60.0%; Score 14.4; DB 6; Length 35;  
Best Local Similarity 75.0%; Pred. No. 2.7e+05;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 GGGTCCAGCGTGGCCATGGGG 24  
Db 26 GCGGCTCGCGTGGCCAGCGGG 3  
RESULT 26  
LOCUS BD002995/c 35 bp DNA linear PAT 31-JAN-2002  
DEFINITION A method for determining DNA methyltransferase.  
ACCESSION BD002995  
VERSION BD002995.1 GI:18630956  
KEYWORDS JP 2000232889-A/4.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Aonuma, M.  
TITLE A method for determining DNA methyltransferase  
JOURNAL Patent: JP 2000232889-A 4 29-AUG-2000;  
DALIHI PHARMACEUTICAL CO LTD  
OS Artificial Sequence  
COMMENT PN JP 2000232889-A/4  
PD 29-AUG-2000  
PF 30-JUL-1999 JP 1999216640  
PR MASASHI AONUMA  
PI C12N15/09, C12N9/10, C12N11/14, C12Q1/48, C12N15/00 CC  
PC Location/Qualifiers  
FH Key 1..35  
FT source /organism='Artificial Sequence'.  
FEATURES  
source 1..35  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
ORIGIN  
Query Match 60.0%; Score 14.4; DB 6; Length 35;  
Best Local Similarity 75.0%; Pred. No. 2.7e+05;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 GGGTCCAGCGTGGCCATGGGG 24  
Db 26 GCGGCTCGCGTGGCCAGCGGG 3

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 GGGTCCAGCGTGGCCATGGGG 24  
Db 26 GCGGCTCGCGTGGCCAGCGGG 3  
RESULT 27  
LOCUS CQ008520/c 50 bp DNA linear PAT 16-JAN-2004  
DEFINITION Sequence 7160 from Patent WO0147944.  
ACCESSION CQ008520  
VERSION CQ008520.1 GI:41015226  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Shimkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0147944-A 7160 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES  
source 1..50  
/organism='Homo sapiens'  
/mol\_type='unassigned DNA'  
/db\_xref='taxon:9606'  
misc\_feature 25..26  
/note='Nucleotide deleted between bases 25 and 26'  
Accession number cg40388639'  
ORIGIN  
Query Match 60.0%; Score 14.4; DB 6; Length 50;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 GGGTCCAGCGTGGCCATGGGG 24  
Db 33 GGGGCCAGCGTGGCATGGGG 10  
RESULT 28  
LOCUS BD194701 19 bp DNA linear PAT 17-JUL-2003  
DEFINITION Lineage-restricted neuronal precursors.  
ACCESSION BD194701  
VERSION BD194701.1 GI:33004447  
KEYWORDS JP 2002515071-A/14.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Rao, M.S., Proschel, M.M. and Kalyani, A.J.  
TITLE Lineage-restricted neuronal precursors  
JOURNAL Patent: JP 2002515071-A 14 21-MAY-2002;  
UNIVERSITY OF UTAH RESEARCH FOUNDATION  
COMMENT OS Rattus norvegicus (rat)  
PN JP 2002515071-A/14  
PD 21-MAY-2002  
PF 03-JUL-1998 JP 1999507430  
PR 04-JUL-1997 US 08/909435, 02-JUL-1998 US 09/109858 PI  
MAHENDRA S RAO, MARGOT MAYER PROSCHEL, ANJALI J KALYANI PC  
A61K48/00, A61K35/30, C12N5/00, C12N5/06, C12N5/08 CC  
LINEAGE-RESTRICTED NEURONAL PRECURSORS  
FH Key Location/Qualifiers  
FT source 1..19  
/organism='Rattus norvegicus (rat)'.  
FEATURES  
Location/Qualifiers

```
source      1. .19
            /organism="Rattus norvegicus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10116"

ORIGIN
Query Match      59.2%; Score 14.2; DB 6; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.6e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  3  GGTCCAGCGTGGCCATGG 21
      ||||| ||||| |||||
Db  1  GGTCCAGCAATTGGCCATGG 19

RESULT 29
AR580293
LOCUS      AR580293
DEFINITION Sequence 14 from patent US 6787353.
ACCESSION AR580293
VERSION    AR580293.1 GI:56610412
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Rao,M.S., Mayer-Proschel,M. and Kalyani,A.J.
TITLE       Lineage-restricted neuronal precursors and methods of isolation
JOURNAL     Patent: US 6787353-A 14 07-SEP-2004;
            University of Utah Research Foundation; Salt Lake City, UT
FEATURES   source
            Location/Qualifiers
            1. .19
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      59.2%; Score 14.2; DB 6; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.6e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  3  GGTCCAGCGTGGCCATGG 21
      ||||| ||||| |||||
Db  1  GGTCCAGCAATTGGCCATGG 19

RESULT 30
AX839895/c
LOCUS      AX839895
DEFINITION Sequence 9 from Patent EPI348964.
ACCESSION  AX839895
VERSION     AX839895.1 GI:39978426
KEYWORDS    .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    1
REFERENCE    Cochran,S.Y., Yamagami,K.M. and Ohashi,Y.M.
AUTHORS      Schizophrenia related gene
TITLE        Patent: EP 1348964-A 9 01-OCT-2003;
JOURNAL      Mitsubishi Pharma Corporation (JP)
FEATURES     source
            Location/Qualifiers
            1. .45
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: oligonucleotide
            (45mer) used for in s i tu hybridization for Kv3.3 mRNA"

ORIGIN
Query Match      59.2%; Score 14.2; DB 6; Length 45;
Best Local Similarity 84.2%; Pred. No. 3.1e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy  4  GTCCAGCGTGGCCATGG 22
      ||||| ||||| |||||
Db  37 GTTCAGCGGGCGCCAGGG 19

RESULT 31
I96090
LOCUS      I96090
DEFINITION Sequence 9 from patent US 5734033.
ACCESSION  I96090
VERSION     I96090.1 GI:3940560
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Reed,J.
TITLE        Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL      Patent: US 5734033-A 9 31-MAR-1998;
FEATURES     source
            Location/Qualifiers
            1. .17
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  6  CCAGCGTGGCCAT 19
      ||||| ||||| |||||
Db  4  CCAGCGTGGCCAT 17

RESULT 32
I96091
LOCUS      I96091
DEFINITION Sequence 10 from patent US 5734033.
ACCESSION  I96091
VERSION     I96091.1 GI:3940561
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Reed,J.
TITLE        Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL      Patent: US 5734033-A 10 31-MAR-1998;
FEATURES     source
            Location/Qualifiers
            1. .17
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  6  CCAGCGTGGCCAT 19
      ||||| ||||| |||||
Db  1  CCAGCGTGGCCAT 14

RESULT 33
AR052619
LOCUS      AR052619
DEFINITION Sequence 17 from patent US 5831066.
ACCESSION  AR052619
VERSION     AR052619.1 GI:5975983
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Reed,J.
TITLE        Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL      Patent: US 5831066-A 10 31-MAR-1998;
FEATURES     source
            Location/Qualifiers
            1. .17
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  6  CCAGCGTGGCCAT 19
      ||||| ||||| |||||
Db  1  CCAGCGTGGCCAT 14

RESULT 33
AR052619
LOCUS      AR052619
DEFINITION Sequence 17 from patent US 5831066.
ACCESSION  AR052619
VERSION     AR052619.1 GI:5975983
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Reed,J.
TITLE        Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL      Patent: US 5831066-A 10 31-MAR-1998;
FEATURES     source
            Location/Qualifiers
            1. .17
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
REFERENCE 1 (bases 1 to 18)
AUTHORS   Reed,J.C.
TITLE      Regulation of bcl-2 gene expression
JOURNAL    Patent: US 5831066-A 17 03-NOV-1998;
FEATURES   Location/Qualifiers
           source
           1..18
           /organism="unknown"
           /mol_type="unassigned DNA"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
6 CCAGCGTGGCCCAT 19
|||||
Db
5 CCAGCGTGGCCCAT 18
|||||
RESULT 34
AR052624
LOCUS      AR052624
DEFINITION Sequence 24 from patent US 5831066.
ACCESSION AR052624
VERSION    AR052624.1 GI:5975988
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS     Reed,J.C.
TITLE        Regulation of bcl-2 gene expression
JOURNAL      Patent: US 5831066-A 24 03-NOV-1998;
FEATURES     Location/Qualifiers
           source
           1..18
           /organism="unknown"
           /mol_type="unassigned DNA"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
6 CCAGCGTGGCCCAT 19
|||||
Db
5 CCAGCGTGGCCCAT 18
|||||
RESULT 35
AR116926
LOCUS      AR116926
DEFINITION Sequence 1 from patent US 6140051.
ACCESSION AR116926
VERSION    AR116926.1 GI:14097832
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS     Brown,L.R. and Xu,C.
TITLE        Fluorescent dibenzazole derivatives and methods related thereto
JOURNAL      Patent: US 6140051-A 1 31-OCT-2000;
FEATURES     Location/Qualifiers
           source
           1..18
           /organism="unknown"
           /mol_type="unassigned DNA"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
6 CCAGCGTGGCCCAT 19
|||||
Db
5 CCAGCGTGGCCCAT 18
|||||
RESULT 36
AR140496
LOCUS      AR140496
DEFINITION Sequence 55 from patent US 6207646.
ACCESSION AR140496
VERSION    AR140496.1 GI:14482992
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS     Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.
TITLE        Immunostimulatory nucleic acid molecules
JOURNAL      Patent: US 6207646-A 55 27-MAR-2001;
FEATURES     Location/Qualifiers
           source
           1..18
           /organism="unknown"
           /mol_type="unassigned DNA"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
6 CCAGCGTGGCCCAT 19
|||||
Db
5 CCAGCGTGGCCCAT 18
|||||
RESULT 37
AR146347
LOCUS      AR146347
DEFINITION Sequence 59 from patent US 6218371.
ACCESSION AR146347
VERSION    AR146347.1 GI:15109536
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS     Krieg,A.M. and Weiner,G.
TITLE        Methods and products for stimulating the immune system using
JOURNAL      immunotherapeutic oligonucleotides and cytokines
JOURNAL      Patent: US 6218371-A 59 17-APR-2001;
FEATURES     Location/Qualifiers
           source
           1..18
           /organism="unknown"
           /mol_type="unassigned DNA"
ORIGIN
Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy
6 CCAGCGTGGCCCAT 19
|||||
Db
5 CCAGCGTGGCCCAT 18
|||||
RESULT 38
AR146392
LOCUS      AR146392
DEFINITION Sequence 104 from patent US 6218371.
ACCESSION AR146392
VERSION    AR146392.1 GI:15109581
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
```

```

REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Weiner,G.
TITLE Methods and products for stimulating the immune system using
JOURNAL immunotherapeutic oligonucleotides and cytokines
PATENT: US 6218371-A 104 17-APR-2001;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 CCAGCGTGGCCCAT 19
Db 5 CCAGCGTGGCCCAT 18
|||||
RESULT 39
LOCUS AR154716 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 45 from patent US 6239116.
ACCESSION AR154716
VERSION AR154716.1 GI:15122769
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Kline,J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6239116-A 45 29-MAY-2001;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 CCAGCGTGGCCCAT 19
Db 5 CCAGCGTGGCCCAT 18
|||||
RESULT 40
LOCUS AR167448 18 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 14 from patent US 6287591.
ACCESSION AR167448
VERSION AR167448.1 GI:17903228
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sample,S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansell,S.M.,
Cullis,P., Scherret,P. and Debever,D.
TITLE Charged therapeutic agents encapsulated in lipid particles
containing four lipid components
JOURNAL Patent: US 6287591-A 14 11-SEP-2001;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;

```

```

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 CCAGCGTGGCCCAT 19
Db 5 CCAGCGTGGCCCAT 18
|||||
RESULT 41
LOCUS BD069938 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Use of nucleic acids containing unethylated CPG dinucleotide in
the treatment of LPS-associated disorders.
ACCESSION BD069938
VERSION BD069938.1 GI:22615541
KEYWORDS JP 2001513776-A/27.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schwartz,D.A. and Krieg,A.M.
TITLE Use of nucleic acids containing unethylated CPG dinucleotide in
the treatment of LPS-associated disorders
JOURNAL Patent: JP 2001513776-A 27 04-SEP-2001;
COMMENT UNIVERSITY OF IOWA RESEARCH FOUNDATION
OS Artificial Sequence
PN JP 2001513776-A/27
PD 04-SEP-2001
PF 25-FEB-1998 JP 1998537810
PR 28-FEB-1997 US 60/039405
PI DAVID A SCHWARTZ,ARTHUR M KRIEG
PC A61K49/00,C07H21/02,C07H21/04,A01N43/04
CC synthetic oligonucleotide
FH Key Location/Qualifiers
FT source 1..18
    /organism='Artificial Sequence'.
FEATURES
    source
        1..18
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match 58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e+05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 CCAGCGTGGCCCAT 19
Db 5 CCAGCGTGGCCCAT 18
|||||
RESULT 42
LOCUS BD076451 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Combined antisense library.
ACCESSION BD076451
VERSION BD076451.1 GI:22622054
KEYWORDS JP 2001519170-A/45.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Riley,T.A., Brown,B.D. and Arnold,L.J.
TITLE Combined antisense library
JOURNAL Patent: JP 2001519170-A 45 23-OCT-2001;
COMMENT OASIS BIOSCIENCES INC
OS Artificial Sequence
PN JP 2001519170-A/45
PD 23-OCT-2001
PF 28-SEP-1998 JP 2000515030
PR 02-OCT-1997 US 60/060673,18-AUG-1998 US
TIMOTHY A RILEY,BOB D BROWN,D LYLE J ARNOLD
PC C12Q1/68,C07H21/04,C12N15/09,C12P19/34,C12N15/00 CC

```



BD190420  
LOCUS BD190420 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Microemulsions with Adsorbed Macromolecules and Microparticles.  
ACCESSION BD190420  
VERSION BD190420.1 GI:33000159  
KEYWORDS JP 2002537102-A/4.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Barackman,J., Simph,M., Ugozoli,M., Kazazu,J., Donnelly,J.,  
Ott,G.S. and Ohagan,D.  
TITLE Microemulsions with Adsorbed Macromolecules and Microparticles  
JOURNAL Patent: JP 2002537102-A 4 05-NOV-2002;  
Chiron Corporation  
COMMENT OS Artificial Sequence  
PN JP 2002537102-A/4  
PD 05-NOV-2002  
PF 09-FEB-2000 JP 2000600618  
PR 29-JUL-1999 US 60/146391,28-OCT-1999 US 60/161997, PR  
26-FEB-1999 US 60/121858  
PI john barackman,manmohan simph,mildred ugozoli,jina kazazu,john  
donnelly,  
PI gary s ott,derek ohagan  
CC Oligonucleotide Location/Qualifiers.  
FH Key Location/Qualifiers  
FEATURES  
source 1. .18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 58.3%; Score 14; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.4e+05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 CCAGCGTGGCCCAT 19  
Db 5 CCAGCGTGGCCCAT 18  
RESULT 47  
LOCUS BD192469 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Compositions and methods for the delivery of oligonucleotides via  
the alimentary canal.  
ACCESSION BD192469  
VERSION BD192469.1 GI:33002208  
KEYWORDS JP 2002510319-A/34.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Teng,C.L. and Hardee,G.  
TITLE Compositions and methods for the delivery of oligonucleotides via  
the alimentary canal  
JOURNAL Patent: JP 2002510319-A 34 02-APR-2002;  
ISIS PHARMACEUTICALS INC  
COMMENT OS Artificial Sequence  
PN JP 2002510319-A/34  
PD 02-APR-2002  
PF 01-JUL-1998 JP 1999507295  
PR 01-JUL-1997 US 08/866829  
PI CHING LEOU TENG,GREG HARDEE  
PC C1201/68,A61K9/127,A61K48/00,C07H21/04  
CC Description of Artificial Sequence: Novel Sequence FH Key  
Location/Qualifiers.  
FEATURES  
source 1. .18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"

/db\_xref="taxon:32630"  
ORIGIN  
Query Match 58.3%; Score 14; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.4e+05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 CCAGCGTGGCCCAT 19  
Db 5 CCAGCGTGGCCCAT 18  
RESULT 48  
LOCUS BD205569 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Method of controlling hematopoiesis by using CpG oligonucleotide.  
ACCESSION BD205569  
VERSION BD205569.1 GI:33015339  
KEYWORDS JP 2002514397-A/59.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Wagner,H. and Lipford,G.  
TITLE Method of controlling hematopoiesis by using CpG oligonucleotide  
JOURNAL Patent: JP 2002514397-A 59 21-MAY-2002;  
CORY PHARMACEUTICALS GMBH,CORY PHARMACEUTICALS GROUP INC  
COMMENT OS Artificial Sequence  
PN JP 2002514397-A/59  
PD 21-MAY-2002  
PF 14-MAY-1999 JP 2000547969  
PR 14-MAY-1998 US 60/085516,02-FEB-1999 US 09/241653 PI  
HERMANN WAGNER,GRAYSON LIPFORD  
PC C12N15/09,A61K31/70,A61K39/39,C07H21/04//A61K45/00,C12N15/00  
CC Synthetic Sequence  
FH Key Location/Qualifiers  
FT source 1. .18  
/organism='Artificial Sequence'.  
FEATURES  
source 1. .18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 58.3%; Score 14; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.4e+05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 CCAGCGTGGCCCAT 19  
Db 5 CCAGCGTGGCCCAT 18  
RESULT 49  
LOCUS BD205614 18 bp DNA linear PAT 17-JUL-2003  
DEFINITION Method of controlling hematopoiesis by using CpG oligonucleotide.  
ACCESSION BD205614  
VERSION BD205614.1 GI:33015384  
KEYWORDS JP 2002514397-A/104.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Wagner,H. and Lipford,G.  
TITLE Method of controlling hematopoiesis by using CpG oligonucleotide  
JOURNAL Patent: JP 2002514397-A 104 21-MAY-2002;  
CORY PHARMACEUTICALS GMBH,CORY PHARMACEUTICALS GROUP INC  
COMMENT OS Artificial Sequence  
PN JP 2002514397-A/104  
PD 21-MAY-2002  
PF 14-MAY-1999 JP 2000547969

PR 14-MAY-1998 US 60/085516,02-FEB-1999 US 09/241653 PI  
HERMANN WAGNER,GRAYSON LIPFORD  
PC C12N15/09,A61K31/70,A61K39/39,C07H21/04//A61K45/00,C12N15/00  
CC Synthetic Sequence  
FH Key Location/Qualifiers  
FT source 1..18  
FT Location/Qualifiers  
1..18  
/organism="Artificial Sequence".  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

FEATURES  
source

ORIGIN

Query Match 58.3%; Score 14; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred.No. 4.4e+05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 CCAGCGTGGCCAT 19  
|||||  
Db 5 CCAGCGTGGCCAT 18

RESULT 50  
BD222609 18 bp DNA linear PAT 17-JUL-2003  
LOCUS  
DEFINITION Compositions of CPG and saponin adjuvants and uses thereof.  
ACCESSION BD222609  
VERSION BD222609.1 GI:33032379  
KEYWORDS JP 2002522510-A/1.  
SOURCE Quillaja saponaria  
ORGANISM Quillaja saponaria  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Quillajaaceae; Quillaja.  
1 (bases 1 to 18)  
REFERENCE  
AUTHORS Kensil,C.A.  
TITLE Compositions of CPG and saponin adjuvants and uses thereof  
JOURNAL Patent: JP 2002522510-A 1 23-JUL-2002;  
COMMENT AQUILA BIOPHARMACEUTICALS INC  
OS Quillaja saponaria  
PN JP 2002522510-A/1  
PD 23-JUL-2002  
PF 06-AUG-1999 JP 2000564661  
PR 10-AUG-1998 US 60/095913,08-APR-1999 US 60/128608 PI  
CHARLOTTE A KENSIL  
PC A61K39/39,A61K39/00,C12N15/09,C12N15/00  
CC Compositions of CPG and saponin adjuvants and uses thereof FH  
Key Location/Qualifiers  
FT source 1..18  
FT Location/Qualifiers  
1..18  
/organism="Quillaja saponaria"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32244"

FEATURES  
source

ORIGIN

Query Match 58.3%; Score 14; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred.No. 4.4e+05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 CCAGCGTGGCCAT 19  
|||||  
Db 5 CCAGCGTGGCCAT 18

Search completed: February 15, 2006, 18:55:44  
Job time : 587.802 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:25:23 ; Search time 180.893 Seconds  
(without alignments)  
884.241 Million cell updates/sec

Title: US-09-669-187A-81

Perfect score: 24

Sequence: 1 ggggtccagcgtgcgcattggggg 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

N\_Geneseq\_21.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	4	AAF98956
2	24	100.0	24	6	ABSF77597
3	24	100.0	24	6	ABL39036
4	24	100.0	24	9	ACD99389
5	24	100.0	24	9	ADB36458
6	24	100.0	24	13	ADU89397
7	17.2	71.7	26	2	AAQ86577
8	16	66.7	30	13	ADR29366
9	16	66.7	33	3	AAA50259
10	16	66.7	33	3	AA48984
11	15.2	63.3	35	6	ABK29920
12	15	62.5	16	6	AAF98965
13	15	62.5	16	6	ABSF77606
14	15	62.5	16	6	ABL39111
15	15	62.5	16	9	ACD99398
16	15	62.5	16	9	ADB36467
17	15	62.5	16	13	ADU89406
18	15	62.5	25	9	ACI96181
19	15	62.5	27	2	AAT18388

20	15	62.5	28	14	ADY71779	Ady71779 Signal se
21	15	62.5	28	14	ADY71781	Ady71781 Control o
22	15	62.5	40	10	ADF70717	Adf70717 Human dop
23	14.8	61.7	20	6	ABN86431	Abn86431 Translati
24	14.6	60.8	25	9	ACI35454	AcI35454 Human mic
25	14.6	60.8	25	9	ACI87918	AcI87918 Human mic
26	14.6	60.8	25	9	ACI55188	AcI55188 Human mic
27	14.6	60.8	25	9	ACI87302	AcI87302 Human mic
28	14.6	60.8	47	3	AAA30408	Aaa30408 EGF sequ
29	14.6	60.8	47	10	ADD14864	Add14864 Ligand ge
30	14.4	60.0	18	12	ADP86181	Adp86181 Cpg immun
31	14.4	60.0	18	12	ADP86182	Adp86182 Cpg immun
32	14.4	60.0	26	14	ADM88846	Adm88846 Human Bcl
33	14.4	60.0	29	3	AAA15383	Aaa15383 PCR prime
34	14.4	60.0	31	10	ADF28077	Adf28077 Caspase-x
35	14.4	60.0	32	6	ABA92890	AbA92890 Human 5'
36	14.4	60.0	34	6	ABK90294	Abk90296 Bcl-2-tar
37	14.4	60.0	34	6	ABK90296	Abk90296 Bcl-2-tar
38	14.4	60.0	34	6	ABK90352	Abk90352 Bcl-2/CRE
39	14.4	60.0	34	10	ADF50458	Adf50458 PCR prime
40	14.4	60.0	41	12	ADK17713	Adk17713 Cytochrom
41	14.4	60.0	50	4	AAL33952	Aal33952 Human SNP
42	14.2	59.2	19	4	AAC88236	Aac88236 Murine li
43	14.2	59.2	25	9	ACI94928	AcI94928 Human mic
44	14.2	59.2	25	9	ACI94310	AcI94310 Human mic
45	14.2	59.2	31	12	ADK43158	Adk43158 Human N-a
46	14.2	59.2	33	2	AAV05322	Aav05322 PCR prime
47	14.2	59.2	38	14	AE855627	Aeb55627 Hamster B
48	14.2	59.2	45	11	ADX31048	Adx31048 Rat volta
49	14	58.3	17	2	AAV19660	Aav19660 Human bcl
50	14	58.3	17	2	AAV19659	Aav19659 Human bcl
51	14	58.3	18	2	AAQ86659	Aaq86659 Bcl-2 ant
52	14	58.3	18	2	AAV52545	Aav52545 Unmethyla
53	14	58.3	18	2	AAV28181	Aav28181 Antisense
54	14	58.3	18	2	AAV27719	Aav27719 Immunosti
55	14	58.3	18	2	AAV19667	Aav19667 Human bcl
56	14	58.3	18	2	AAZ41948	Aaz41948 IL-12 sec
57	14	58.3	18	2	AAZ41905	Aaz41905 IL-12 sec
58	14	58.3	18	2	AAV78803	Aav78803 HPV fusio
59	14	58.3	18	2	AAV99434	Aav99434 Antisense
60	14	58.3	18	2	AAZ31944	Aaz31944 Cpg adjuv
61	14	58.3	18	2	AAZ27536	Aaz27536 Synthetic
62	14	58.3	18	2	AAV18702	Aav18702 Target bc
63	14	58.3	18	2	AAV88537	Aav88537 Cytosine-
64	14	58.3	18	2	AAV33514	Aav33514 BCL2-targ
65	14	58.3	18	2	AAV23693	Aav23693 Deletion
66	14	58.3	18	3	AAZ60975	Aaz60975 Nucleotid
67	14	58.3	18	3	AAZ48024	Aaz48024 Immune re
68	14	58.3	18	3	AAZ47981	Aaz47981 Immune re
69	14	58.3	18	3	AAA14470	Aaa14470 Phosphoro
70	14	58.3	18	3	AAZ87997	Aaz87997 BBTB-labe
71	14	58.3	18	3	AAZ47850	Aaz47850 Immunosti
72	14	58.3	18	3	AAA38517	Aaa38517 Oligonuc
73	14	58.3	18	3	AAV90450	Aav90450 Cpg adjuv
74	14	58.3	18	3	AAZ99003	Aaz99003 Cpg motif
75	14	58.3	18	3	AAZ98660	Aaz98660 Human Bcl
76	14	58.3	18	3	AAZ93264	Aaz93264 Cpg immun
77	14	58.3	18	3	AAZ47680	Aaz47680 Parasitic
78	14	58.3	18	3	AAZ47643	Aaz47643 Parasitic
79	14	58.3	18	3	AAA91620	Aaa91620 Human Bcl
80	14	58.3	18	3	AAV60278	Aav60278 Immunosti
81	14	58.3	18	3	AAV65037	Aav65037 Bcl2 anti
82	14	58.3	18	3	AAV64137	Aav64137 Immunosti
83	14	58.3	18	4	AAH50615	Aah50615 Natural k
84	14	58.3	18	4	AAH50615	Aah50615 Anti-bcl
85	14	58.3	18	4	AAH60923	Aah60923 Cpg oligo
86	14	58.3	18	4	AAH19305	Aah19305 Cpg immun
87	14	58.3	18	4	AAF98832	Aaf98832 Immunosti
88	14	58.3	18	4	AAF59502	Aaf59502 Immunosti
89	14	58.3	18	4	AAF98930	Aaf98930 Immunosti
90	14	58.3	18	4	AAF98929	Aaf98929 Immunosti
91	14	58.3	18	4	AAF98866	Aaf98866 Immunosti
92	14	58.3	18	4	AAF98885	Aaf98885 Immunosti

93	14	58.3	18	4	AAA92362	Aaa92362 CG motif	166	14	58.3	18	13	ADR69265	Adr69265 CpG immun
94	14	58.3	18	5	AAS08980	Aas08980 CpG-conta	167	14	58.3	18	13	ADR61963	Adt61963 Mitogenic
95	14	58.3	18	5	AAf27748	Aaf27748 P. faicip	168	14	58.3	18	13	ADT04172	Adt04172 Novel imm
96	14	58.3	18	6	ABQ88341	Abq88341 Immunosti	169	14	58.3	18	13	ADT93913	Adt93913 Antisense
97	14	58.3	18	6	ABK90280	Abk90280 Bcl-2-tar	170	14	58.3	18	13	ADU70267	Adu70267 Immunosti
98	14	58.3	18	6	ABK90285	Abk90285 Bcl-2-tar	171	14	58.3	18	13	ADU70021	Adu70021 Immunosti
99	14	58.3	18	6	ABL01615	AbL01615 bcl-2 tar	172	14	58.3	18	13	ADU89317	Adu89317 Allergic
100	14	58.3	18	6	ALA44699	Ala44699 Human bcl	173	14	58.3	18	13	ADU89407	Adu89407 Allergic
101	14	58.3	18	6	ABS77607	Abs77607 Angiogene	174	14	58.3	18	13	ADU89371	Adu89371 Allergic
102	14	58.3	18	6	ABS77570	Abs77570 Angiogene	175	14	58.3	18	13	ADU89370	Adu89370 Allergic
103	14	58.3	18	6	ABS77571	Abs77571 Angiogene	176	14	58.3	18	13	ADV78745	Adv78745 Antisense
104	14	58.3	18	6	ABS77517	Abs77517 Angiogene	177	14	58.3	18	13	ADW50636	Adw50636 Human Bcl
105	14	58.3	18	6	ABL39123	AbL39123 Immunosti	178	14	58.3	18	13	ADW11410	Adw11410 Bcl-2 ant
106	14	58.3	18	6	ABL39324	AbL39324 Immunosti	179	14	58.3	18	14	ADW12541	Adw12541 Human bcl
107	14	58.3	18	6	ABA97468	AbA97468 Bcl-2 tar	180	14	58.3	18	14	ADW13853	Adw13853 Optimized
108	14	58.3	18	6	ABV73939	Abv73939 Methylate	181	14	58.3	18	14	ADW13846	Adw13846 Bcl-2 ORF
109	14	58.3	18	6	ABV73938	Abv73938 CpG oligo	182	14	58.3	18	14	ADW29230	Adw29230 Immunosti
110	14	58.3	18	6	ALA43435	Aal43435 Immunosti	183	14	58.3	18	14	ADW40254	Adw40254 Human bcl
111	14	58.3	18	6	ABV74424	Abv74424 Immunosti	184	14	58.3	18	14	ADY53646	Ady53646 Anti-canc
112	14	58.3	18	6	ALA44489	Ala44489 CpG motif	185	14	58.3	18	14	ADY39638	Ady39638 Oligodeox
113	14	58.3	18	6	ABQ78541	Abq78541 Antisense	186	14	58.3	18	14	ADY71778	Ady71778 Control o
114	14	58.3	18	6	ABQ78538	Abq78538 Antisense	187	14	58.3	18	14	ADY84967	Ady84967 CpG oligo
115	14	58.3	18	6	ABN88303	Abn88303 Immunosti	188	14	58.3	18	14	ADZ39824	Adz39824 Immunosti
116	14	58.3	18	6	AD22796	Aad22796 Human bcl	189	14	58.3	18	14	ADZ39839	Adz39839 Immunosti
117	14	58.3	18	6	ABL58454	AbL58454 CpG immun	190	14	58.3	18	14	ADZ77762	Adz77762 CpG adjuv
118	14	58.3	18	6	ALA39240	Ala39240 Murine To	191	14	58.3	18	14	ADZ77752	Adz77752 CpG adjuv
119	14	58.3	18	6	ABS70564	AbS70564 Dendritic	192	14	58.3	18	14	ADZ88533	Adz88533 S-CpG ODN
120	14	58.3	18	6	ABL53546	AbL53546 Cpr oligo	193	14	58.3	18	14	ADZ58562	Adz58562 Phosphoro
121	14	58.3	18	6	ABL53544	AbL53544 Cpr oligo	194	14	58.3	18	14	AEA16639	Aea16639 CpG immun
122	14	58.3	18	6	ABL54169	AbL54169 Oligonucl	195	14	58.3	18	14	ADZ84124	Adz84124 Human bcl
123	14	58.3	18	6	ABL54148	AbL54148 Bcl-2 ant	196	14	58.3	18	14	AE828241	Aeb28241 Human Bcl
124	14	58.3	18	8	ABZ76751	Abz76751 Phosphoro	197	14	58.3	18	14	AE807505	Aeb07505 Novel vir
125	14	58.3	18	8	ACC59107	Acc59107 CpG oligo	198	14	58.3	18	14	AE850092	Aeb50092 Oligonucl
126	14	58.3	18	8	ABZ80168	Abz80168 Immunosti	199	14	58.3	18	14	AE850092	Aeb50092 Oligonucl
127	14	58.3	18	8	ACC59006	Acc59006 Human bcl	200	14	58.3	19	2	AAZ06730	Aaz06730 NK lytic
128	14	58.3	18	8	ABX89852	Abx89852 Cancer me	201	14	58.3	20	4	AAV74246	Aav74246 CpG-N mot
129	14	58.3	18	8	ABZ22867	Abz22867 Phosphoro	202	14	58.3	20	4	AAF98962	Aaf98962 Immunosti
130	14	58.3	18	9	ACA92708	AcA92708 Immunosti	203	14	58.3	20	4	AAC86407	Aac86407 Human bcl
131	14	58.3	18	9	ACD99315	AcD99315 Immunosti	204	14	58.3	20	6	ABL77603	AbL77603 Angiogene
132	14	58.3	18	9	ACD99399	AcD99399 Immunosti	205	14	58.3	20	6	ABL39325	AbL39325 Immunosti
133	14	58.3	18	9	ACC58501	Acc58501 Oligonucl	206	14	58.3	20	9	ACD99395	AcD99395 Immunosti
134	14	58.3	18	9	ACC58516	Acc58516 Oligonucl	207	14	58.3	20	9	ADB36464	AdB36464 Immunosti
135	14	58.3	18	9	ADA24232	Ada24232 Human bcl	208	14	58.3	20	13	ADU89403	Adu89403 Allergic
136	14	58.3	18	9	ADB36468	AdB36468 Immunosti	209	14	58.3	21	3	AAC65064	Aac65064 Human bcl
137	14	58.3	18	9	ADB36431	AdB36431 Immunosti	210	14	58.3	21	14	ADV65824	Adv65824 Antisense
138	14	58.3	18	9	ADB36432	AdB36432 Immunosti	211	14	58.3	22	2	AAQ49817	Aaq49817 Bcl-2 ant
139	14	58.3	18	9	ADB36387	AdB36387 Immunosti	212	14	58.3	22	2	AAQ49816	Aaq49816 Bcl-2 ant
140	14	58.3	18	10	ADC24658	Adc24658 Antisense	213	14	58.3	22	6	ABK90353	Abk90353 Bcl-2 tar
141	14	58.3	18	10	ADC33583	Adc33583 Human bcl	214	14	58.3	23	6	ADF39399	Adf39399 Human Bcl
142	14	58.3	18	10	AAD60214	Aad60214 Oligonucl	215	14	58.3	28	6	ABL35450	AbL35450 Immunosti
143	14	58.3	18	10	ADF82814	Adf82814 Immunosti	216	14	58.3	28	14	ADY71780	Ady71780 Control o
144	14	58.3	18	10	ADF82829	Adf82829 Immunosti	217	14	58.3	30	3	AAC63979	Aac63979 Icelandic
145	14	58.3	18	10	ADG68147	Adg68147 Umethylya	218	14	58.3	32	14	AE828476	Aeb28476 Phosphodi
146	14	58.3	18	10	ACF36817	AcF36817 Immunosti	219	14	58.3	35	2	AAQ86644	Aaq86644 Bcl-2 tra
147	14	58.3	18	10	ABX76040	Abx76040 Immunosti	220	14	58.3	35	2	AAV19652	Aav19652 Human bcl
148	14	58.3	18	10	ACA58705	AcA58705 Gastric u	221	14	58.3	35	6	ABK90265	Abk90265 Bcl-2-tar
149	14	58.3	18	11	ADM41180	Adm41180 Human ant	222	14	58.3	35	6	ABQ78523	Abq78523 Antisense
150	14	58.3	18	12	ADE901170	Ade901170 Human bcl	223	14	58.3	35	6	ABL54150	AbL54150 Bcl-2 ant
151	14	58.3	18	12	ADE39674	Ade39674 Oligonucl	224	14	58.3	35	13	ADT93919	Adt93919 Antisense
152	14	58.3	18	12	ADE39689	Ade39689 Oligonucl	225	14	58.3	35	14	ADW13831	Adw13831 Bcl-2 gen
153	14	58.3	18	12	ADF42925	Adf42925 Methylate	226	14	58.3	36	4	AAH45307	Aah45307 Human Bcl
154	14	58.3	18	12	ADF42910	Adf42910 Methylate	227	14	58.3	36	10	ADM10311	Adm10311 Human epi
155	14	58.3	18	12	ADT01087	Adt01087 Immunosti	228	14	58.3	40	2	AAO53418	Aao53418 Human dop
156	14	58.3	18	12	ADL64033	AdL64033 CpG DNA o	229	14	58.3	40	12	ADO70419	Ado70419 Human Bcl
157	14	58.3	18	12	ADL63958	AdL63958 CpG DNA o	230	14	58.3	40	12	ADO70436	Ado70436 Human Bcl
158	14	58.3	18	12	ADL97920	AdL97920 Immunosti	231	14	58.3	50	6	ABZ04678	Abz04678 Human leu
159	14	58.3	18	12	ADN11025	Adn11025 CpG oligo	232	13.8	57.5	30	3	AAZ46938	Aaz46938 Human sac
160	14	58.3	18	12	ADM99056	Adm99056 Immunosti	233	13.8	57.5	45	5	AAH26512	Aah26512 Low densi
161	14	58.3	18	12	ADO04772	Ado04772 CpG oligo	234	13.8	57.5	45	6	ABK70067	Abk70067 Antibody
162	14	58.3	18	12	ADQ07602	Adq07602 Umethylya	235	13.8	57.5	45	10	ADL18019	Adl18019 Anti-lect
163	14	58.3	18	12	ADP86189	Adp86189 CpG immun	236	13.8	57.5	45	11	ADL35283	Adl35283 Anti-Fcga
164	14	58.3	18	12	ADQ26939	Adq26939 Human Bcl	237	13.8	57.5	47	3	AAZ69280	Aaz69280 Human map
165	14	58.3	18	12	ADQ07472	Adq07472 Immunosti	238	13.6	56.7	21	2	AAT59612	Aat59612 Human cys



c 239	13.6	56.7	21	3	AAZ35659 Human cys	Az335659 Human cys	DT	12-JUN-2001 (first entry)
c 240	13.6	56.7	21	13	ADU41858 Knock-dow	Adu41858 Knock-dow	XX	Immunostimulatory nucleic acid #72.
c 241	13.6	56.7	28	9	ACC59319 Rat MCH-R	Acc59319 Rat MCH-R	DE	
c 242	13.6	56.7	30	13	ADS51886 Peptide c	Ad51886 Peptide c	XX	Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
c 243	13.6	56.7	31	3	AAA54027 Primer us	Aaa54027 Primer us	XX	immunostimulatory; tumour; viral infection; bacterial infection;
c 244	13.6	56.7	34	8	ABX93713 Human thr	Abx93713 Human thr	KW	fungal infection; parasitic infection; cancer; asthma;
c 245	13.6	56.7	34	13	ADT92200 Nucleotid	Adt92200 Nucleotid	KW	infectious disease; allergy; immune deficiency; phosphorothioate; ss.
c 246	13.6	56.7	36	14	ADY96801 Human imm	Ady96801 Human imm	KW	
c 247	13.6	56.7	36	11	ADZ51806 PCR prime	Adz51806 PCR prime	XX	Synthetic.
c 248	13.4	55.8	25	9	ACT96180 Human mic	Act96180 Human mic	OS	
c 249	13.4	55.8	26	14	ADV16247 DNA bindi	Adv16247 DNA bindi	XX	
c 250	13.4	55.8	27	6	ABK89362 Consensus	Abk89362 Consensus	FN	WO200122972-A2.
c 251	13.4	55.8	27	8	ABT17195 Transcrip	Abt17195 Transcrip	XX	
c 252	13.4	55.8	27	10	ABT17194 Transcrip	Abt17194 Transcrip	PD	05-APR-2001.
c 253	13.4	55.8	27	10	ADC60806 Cis eleme	Adc60806 Cis eleme	XX	25-SEP-2000; 2000WO-US026383.
c 254	13.4	55.8	27	10	ADC60807 Cis eleme	Adc60807 Cis eleme	XX	
c 255	13.4	55.8	27	10	ADF48576 Cis-eleme	Adf48576 Cis-eleme	XX	25-SEP-1999; 99US-0156113P.
c 256	13.4	55.8	27	10	ADF48577 Cis-eleme	Adf48577 Cis-eleme	PR	27-SEP-1999; 99US-0156135P.
c 257	13.4	55.8	27	13	ADN48288 Thermococ	Adn48288 Thermococ	PR	23-AUG-2000; 2000US-0227436P.
c 258	13.4	55.8	28	4	AAH88128 ATT beta	Aah88128 ATT beta	PR	(IOWA ) UNIV IOWA RES FOUND.
c 259	13.4	55.8	30	6	ABK97988 Cell-TRAP	Abk97988 Cell-TRAP	XX	(COLE-) COLEY PHARM GMBH.
c 260	13.4	55.8	30	6	ABK98241 Nucleic a	Abk98241 Nucleic a	PA	
c 261	13.4	55.8	33	5	AAI65834 Primer fo	Aai65834 Primer fo	PA	Krieg AM, Schetter C, Vollmer J;
c 262	13.4	55.8	35	2	AAT99806 Primer h5	Aat99806 Primer h5	PI	WPI; 2001-273485/28.
c 263	13.4	55.8	35	12	ADN48288 Thermococ	Adn48288 Thermococ	XX	Vaccinating against tumors, infectious diseases, allergies and asthma
c 264	13.4	55.8	37	2	AAQ78306 Multiple	Aaq78306 Multiple	XX	using immunostimulatory Py-rich and TG nucleic acids.
c 265	13.4	55.8	38	2	AAQ78307 Multiple	Aaq78307 Multiple	DR	Disclosure; Page 40; 338pp; English.
c 266	13.4	55.8	38	2	AAQ78307 Primer KK	Aaq78307 Primer KK	XX	The present invention relates to a method for stimulating an immune
c 267	13.4	55.8	38	2	AAQ78307 Primer KK	Aaq78307 Primer KK	XX	response. The method comprises administering an immunostimulatory nucleic
c 268	13.4	55.8	40	3	AAZ95823 Polynucle	Aaz95823 Polynucle	CC	acid to a non-rodent subject in sufficient quantity to stimulate an
c 269	13.4	55.8	40	14	ADW05171 Elongatio	Adw05171 Elongatio	CC	immune response. The present sequence is one such immunostimulatory
c 270	13.4	55.8	41	6	ABA02131 Human ins	Aba02131 Human ins	CC	nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
c 271	13.4	55.8	41	6	ABA02132 Human ins	Aba02132 Human ins	CC	(py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
c 272	13.4	55.8	41	6	AAI43702 Human zin	Aai43702 Human zin	CC	against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
c 273	13.4	55.8	41	6	AAI43701 Human zin	Aai43701 Human zin	CC	and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
c 274	13.4	55.8	43	2	AAT13004 Adrenergi	Aat13004 Adrenergi	CC	haemophilus, campylobacter, clostridium, Escherichia coli and/or
c 275	13.4	55.8	43	2	AAT13008 Adrenergi	Aat13008 Adrenergi	CC	staphylococcus), fungal antigens and/or parasitic antigens. The method is
c 276	13.4	55.8	43	2	AAV33512 Human G-p	Aav33512 Human G-p	CC	also useful for preventing cancer, asthma, infectious disease, allergy or
c 277	13.4	55.8	43	3	AAZ39529 Human adr	Aaz39529 Human adr	CC	immune deficiency. The present sequence can also be used to redirect a
c 278	13.4	55.8	43	3	AAZ39533 Human adr	Aaz39533 Human adr	CC	Th2 to a Th1 immune response and to activate immune cells. Note: the
c 279	13.4	55.8	43	6	ABX14072 3' PCR pr	Abx14072 3' PCR pr	CC	present sequence may have a phosphorothioate backbone
c 280	13.4	55.8	43	6	ABX14068 3' PCR pr	Abx14068 3' PCR pr	XX	Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;
c 281	13.4	55.8	43	12	ADH51574 Human G-p	Adh51574 Human G-p	XX	Query Match 100.0%; Score 24; DB 4; Length 24;
c 282	13.4	55.8	43	12	ADH51570 Human G-p	Adh51570 Human G-p	XX	Best Local Similarity 100.0%; Pred. No. 0.58;
c 283	13.4	55.8	45	14	AEA31420 Human DNA	Aea31420 Human DNA	XX	Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
c 284	13.4	55.8	50	4	AAI32200 Human SNP	Aai32200 Human SNP	XX	
c 285	13.4	55.8	50	4	AAH90486 Human clo	Aah90486 Human clo	XX	
c 286	13.4	55.8	50	8	ACC47738 Green flu	Acc47738 Green flu	XX	
c 287	13.2	55.0	19	10	ADF84373 Human ABL	Adf84373 Human ABL	XX	
c 288	13.2	55.0	19	10	ADF84692 Human ABL	Adf84692 Human ABL	XX	
c 289	13.2	55.0	20	12	ADP22678 Golden ha	Adp22678 Golden ha	XX	
c 290	13.2	55.0	25	9	ACI97973 Human mic	Act97973 Human mic	XX	
c 291	13.2	55.0	29	2	AAV15798 Primer fo	Aav15798 Primer fo	XX	
c 292	13.2	55.0	33	4	AAH21729 Corynebac	Aah21729 Corynebac	XX	
c 293	13.2	55.0	36	14	ADY96800 Human imm	Ady96800 Human imm	XX	
c 294	13.2	55.0	43	6	ABS63505 Human Bcl	Abs63505 Human Bcl	XX	
c 295	13.2	55.0	43	6	ABS63509 Human Bcl	Abs63509 Human Bcl	XX	
c 296	13	54.2	16	14	ABE28235 Human Bcl	Abe28235 Human Bcl	XX	
c 297	13	54.2	17	6	ABK90362 Bcl-2-tar	Abk90362 Bcl-2-tar	XX	
c 298	13	54.2	17	14	ABE28226 Human Bcl	Abe28226 Human Bcl	XX	
c 299	13	54.2	18	2	AAV11591 Liposomal	Aav11591 Liposomal	XX	
c 300	13	54.2	18	14	ABE28186 Human Bcl	Abe28186 Human Bcl	XX	

## ALIGNMENTS

RESULT 1

AAF98956

ID AAF98956 standard; DNA; 24 BP.

XX

AC

AAF98956;

XX

Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;

diabetic retinopathy; retinopathy of prematurity; macular degeneration;

corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

ABS77597;

13-DEC-2002 (first entry)

Angiogenesis inhibitory oligonucleotide #81.

RESULT 2

ABS77597

ID ABS77597 standard; DNA; 24 BP.

XX

AC

ABS77597;

XX

DT

DE

XX

XX

XX

KW

KW

KW

KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX  
OS Synthetic.  
XX  
PN WO200253141-A2.  
XX  
XX  
PD 11-JUL-2002.  
XX  
XX PF 14-DEC-2001; 2001WO-US048458.  
XX  
XX PR 14-DEC-2000; 2000US-0255534P.  
XX  
PA (COLE-) COLEY PHARM GROUP INC.  
XX  
XX PI Bratzler RL;  
XX  
XX WPI; 2002-566690/60.  
XX  
XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.  
XX  
XX Claim 2; Page 21; 276pp; English.  
XX  
CC The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX  
SQ Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 24; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTCCAGCGTCGCCATGGGG 24  
| | | | | | | | | | | | | | | | | | | | | |  
DB 1 GGGGTCCAGCGTCGCCATGGGG 24  
| | | | | | | | | | | | | | | | | | | | | |  
RESULT 3  
ABL39036  
ID ABL39036 standard; DNA; 24 BP.  
XX  
XX ABL39036;  
AC  
XX  
DT 16-APR-2002 (first entry)  
XX  
DE Immunostimulatory nucleic acid SEQ ID NO: 440.  
XX  
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; ss.  
XX  
OS Synthetic.  
XX  
XX WO200197843-A2.  
PN  
XX  
PD 27-DEC-2001.  
XX  
XX 22-JUN-2001; 2001WO-US020154.  
PF  
XX

PR 22-JUN-2000; 2000US-0213346P.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA  
XX  
PI Weiner G, Hartmann G;  
XX  
XX WPI; 2002-154611/20.  
DR  
XX  
XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer.  
XX  
XX Disclosure; Page 207; 312pp; English.  
XX  
XX The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention  
XX  
XX Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 24; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTCCAGCGTCGCCATGGGG 24  
| | | | | | | | | | | | | | | | | | | | | |  
DB 1 GGGGTCCAGCGTCGCCATGGGG 24  
| | | | | | | | | | | | | | | | | | | | | |  
RESULT 4  
ACD99389  
ID ACD99389 standard; DNA; 24 BP.  
XX  
XX ACD99389;  
AC  
XX  
DT 25-SEP-2003 (first entry)  
XX  
DE Immunostimulatory nucleic acid #75.  
XX  
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX  
OS Synthetic.  
XX  
XX US2003050268-A1.  
PN  
XX  
XX 13-MAR-2003.  
PD  
XX  
XX 29-MAR-2002; 2002US-00112653.  
PF  
XX  
XX 29-MAR-2001; 2001US-0279642P.  
PR  
XX  
XX (KRIE/) KRIEG A M.  
PA (BERG/) BERG D J.  
XX  
XX Krieg AM, Berg DJ;  
PI  
XX  
XX WPI; 2003-521815/49.  
DR  
XX

PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX  
XX  
PS Disclosure; Page 10; 229pp; English.  
XX  
CC The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
XX Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 24; DB 9; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTCCAGCGTGGCCATGGGG 24  
DB 1 GGGGTCCAGCGTGGCCATGGGG 24  
  
RESULT 5  
ADB36458  
ID ADB36458 standard; DNA; 24 BP.  
XX  
XX ADB36458;  
XX  
XX 04-DEC-2003 (first entry)  
XX  
XX Immunostimulatory nucleic acid #72.  
DE  
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
XX hypo-responsive subject; immunostimulatory.  
KW  
XX Synthetic.  
OS  
XX US2003087848-A1.  
PN  
XX 08-MAY-2003.  
XX  
XX 02-FEB-2001; 2001US-00776479.  
XX  
XX 03-FEB-2000; 2000US-0179991P.  
PR  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
XX  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
XX nucleic acid alone or in combination with an asthma/allergy medicament.  
PT  
XX Disclosure; Page 6; 221pp; English.  
PS  
XX The invention relates to a method of treating or preventing allergy or  
XX asthma which comprises administering to a subject a poly-G nucleic acid  
XX in an aerosol formulation. The methods and compositions of the present  
XX invention are useful for diagnosing and/or treating asthma and allergy  
XX especially in a hypo-responsive subject. The present sequence represents  
XX an immunostimulatory nucleic acid of the invention.  
XX  
XX Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 24; DB 9; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTCCAGCGTGGCCATGGGG 24  
DB 1 GGGGTCCAGCGTGGCCATGGGG 24  
  
RESULT 6  
ADU89397  
ID ADU89397 standard; DNA; 24 BP.  
XX  
XX ADB89397;  
XX  
XX 10-FEB-2005 (first entry)  
DT  
XX Allergic response suppressor oligonucleotide #81.  
DE  
XX ss; antiasthmatic; antiallergic; dermatologic; antiinflammatory;  
KW antibacterial; virucide; immunoglobulin E antagonist; allergy;  
KW immunostimulatory; asthma; rhinitis; urticaria; dermatitis;  
KW bacterial infection; viral infection.  
XX  
XX Synthetic.  
OS  
XX US2004235774-A1.  
PN  
XX 25-NOV-2004.  
XX  
XX 23-APR-2004; 2004US-00831778.  
PP  
XX 03-FEB-2000; 2000US-0179991P.  
PR  
XX 02-FEB-2001; 2001US-00776479.  
XX  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2004-833006/82.  
XX  
XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
XX dermatitis, in a subject, comprises administering a first and second dose  
XX of an immunostimulatory nucleic acid.  
PT  
XX Disclosure; SEQ ID NO 81; 235pp; English.  
PS  
XX The invention relates to a method of suppressing a symptom of an allergic  
XX response in a subject by administering a first and second dose of an  
XX immunostimulatory nucleic acid that comprises a nucleotide sequence  
XX comprising 5'-cg-3', and where the second dose is administered from 1 day  
XX to 8 weeks after the first dose. The methods and compositions of the  
XX present invention are useful for the treatment or prevention of asthma  
XX and allergy, including rhinitis, urticaria and atopic dermatitis, using  
XX an immunostimulatory nucleic acid alone or in combination with other  
XX medicaments. They can also be used in preventing bacterial and viral  
XX infections. This sequence represents an oligonucleotide used in the  
XX method of the invention.  
XX  
XX Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 24; DB 13; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTCCAGCGTGGCCATGGGG 24  
DB 1 GGGGTCCAGCGTGGCCATGGGG 24  
  
RESULT 7  
AAQ86577  
ID AAQ86577 standard; DNA; 26 BP.  
XX

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTCCAGCGTGGCCATGGGG 24  
DB 1 GGGGTCCAGCGTGGCCATGGGG 24  
  
RESULT 6  
ADU89397  
ID ADU89397 standard; DNA; 24 BP.  
XX  
XX ADB89397;  
XX  
XX 10-FEB-2005 (first entry)  
DT  
XX Allergic response suppressor oligonucleotide #81.  
DE  
XX ss; antiasthmatic; antiallergic; dermatologic; antiinflammatory;  
KW antibacterial; virucide; immunoglobulin E antagonist; allergy;  
KW immunostimulatory; asthma; rhinitis; urticaria; dermatitis;  
KW bacterial infection; viral infection.  
XX  
XX Synthetic.  
OS  
XX US2004235774-A1.  
PN  
XX 25-NOV-2004.  
XX  
XX 23-APR-2004; 2004US-00831778.  
PP  
XX 03-FEB-2000; 2000US-0179991P.  
PR  
XX 02-FEB-2001; 2001US-00776479.  
XX  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2004-833006/82.  
XX  
XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
XX dermatitis, in a subject, comprises administering a first and second dose  
XX of an immunostimulatory nucleic acid.  
PT  
XX Disclosure; SEQ ID NO 81; 235pp; English.  
PS  
XX The invention relates to a method of suppressing a symptom of an allergic  
XX response in a subject by administering a first and second dose of an  
XX immunostimulatory nucleic acid that comprises a nucleotide sequence  
XX comprising 5'-cg-3', and where the second dose is administered from 1 day  
XX to 8 weeks after the first dose. The methods and compositions of the  
XX present invention are useful for the treatment or prevention of asthma  
XX and allergy, including rhinitis, urticaria and atopic dermatitis, using  
XX an immunostimulatory nucleic acid alone or in combination with other  
XX medicaments. They can also be used in preventing bacterial and viral  
XX infections. This sequence represents an oligonucleotide used in the  
XX method of the invention.  
XX  
XX Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 24; DB 13; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGTCCAGCGTGGCCATGGGG 24  
DB 1 GGGGTCCAGCGTGGCCATGGGG 24  
  
RESULT 7  
AAQ86577  
ID AAQ86577 standard; DNA; 26 BP.  
XX

```

XX AC AAQ86577;
XX DT 25-MAR-2003 (revised)
XX DT 25-SEP-1995 (first entry)
XX DE Alpha-amylase signal sequence primer.
XX KW Barley; Hordeum vulgare; alpha-amylase; signal peptide; PCR; primer;
XX KW polymerase chain reaction; major histocompatibility complex; MHC;
XX KW transgenic plant; allograft rejection suppression; plasmid pSM155;
XX KW tobacco; Nicotiana tabacum; ss.
XX OS Synthetic.
XX XX WO9508347-A1.
XX PN 30-MAR-1995.
XX PD 21-SEP-1994; 94WO-CA000530.
XX PF 21-SEP-1993; 93GB-00019429.
XX PR (UNLO ) UNIV HOSPITAL LONDON HEALTH ASSOC.
XX PA Jevnikar AM, Ma S, Stiller CR;
XX PI WPI; 1995-139392/18.
XX DR Expressing a mammalian antigen in transformed plants to provide a source
XX PT of plant material - for oral or enteral admin. to a mammal to produce
XX PT tolerance to the antigen.
XX XX Example 2; Page 17; 41pp; English.
XX PS The signal sequence was isolated from barley alpha-amylase cDNA by PCR
XX CC using the primers given in AAQ86577-78. The product was cloned into
XX CC pBluescriptII together with a mouse MHC II alpha chain mature peptide-
XX CC encoding sequence to obtain plasmid pSM155, for expression in tobacco cv.
XX CC SRI transformants. (Updated on 25-MAR-2003 to correct PN field.) (Updated
XX CC on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 26 BP; 4 A; 8 C; 12 G; 2 T; 0 U; 0 Other;
Query Match 71.7%; Score 17.2; DB 2; Length 26;
Best Local Similarity 86.4%; Pred. No. 5.e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GGGTCCAGCGTGGCCCATGGG 23
Db 2 GGATCCGGCGCGCCCATGGG 23
RESULT 8
ID ADR29366/c
XX AC ADR29366;
XX DT 18-NOV-2004 (first entry)
XX DE Human Bcl-2 PCR primer SEQ ID NO:2.
XX KW filamentous fungus; Bcl-2; herbicide;
XX KW Colletotrichum gloeosporioides f.sp. aescynomene; food production;
XX KW drug production; paper; pulp industry; agriculture; bioremediation;
XX KW human; PCR; primer; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2004072225-A2.
XX XX

```

---

```

PD XX 26-AUG-2004.
XX PF 10-FEB-2004; 2004WO-IL000132.
XX PR 12-FEB-2003; 2003US-0446513P.
XX XX (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
XX XX Sharon A, Goldstein-Barhoom S;
XX XX WPI; 2004-625842/60.
XX DR Novel filamentous fungus having exogenous polynucleotide expressing Bcl-2
XX PT polypeptide, and exhibiting accelerated growth compared to wild-type
XX PT filamentous fungus, useful for eradicating unwanted weed growing in crop
XX PT field.
XX PS Disclosure; SEQ ID NO 2; 57pp; English.
XX XX The present invention describes a filamentous fungus (I) comprising an
XX CC exogenous polynucleotide capable of expressing a Bcl-2 polypeptide or its
XX CC active portion, and exhibiting accelerated growth as compared to a wild-
XX CC type filamentous fungus. Also described: (1) enhancing (M1) growth of
XX CC filamentous fungus, involving providing the filamentous fungus with a Bcl
XX CC -2 polypeptide or its active portion, and so enhancing the growth of the
XX CC filamentous fungus; (2) enhancing (M2) the viability and/or pathogenicity
XX CC of a filamentous fungus stored at sub-optimal temperature; (3) increasing
XX CC (M3) the resistance of a filamentous fungus to stress; (4) a fungal
XX CC culture medium (II) suitable for growth of fungus, comprising Bcl-2
XX CC polypeptide or its active portion and a carbon source; and (5) a
XX CC filamentous fungus comprising a first exogenous polynucleotide encoding
XX CC Bcl-2 or its active portion, and a second exogenous polynucleotide
XX CC encoding a suicide gene. Bcl-2 has herbicide activities. (I) is
XX CC Colletotrichum gloeosporioides f.sp. aescynomene. (M1) is useful for
XX CC eradicating an unwanted weed growing in a crop field, which involves
XX CC spreading (I) in the crop field which is pathogenic to the unwanted weed.
XX CC The filamentous fungi are useful in industrial applications, such as food
XX CC and drug production, paper and pulp industry, agriculture and
XX CC bioremediation. (I) remains viable in storage for a time period longer
XX CC than the wild-type filamentous fungus when grown on solid media. (I)
XX CC exhibits increased resistance to temperature, oxidative and/or radiation
XX CC stress, as compared to the wild-type filamentous fungus. The present
XX CC sequence represents a PCR primer for the human Bcl-2 gene, which is used
XX CC in the exemplification of the present invention.
XX SQ Sequence 30 BP; 7 A; 8 C; 13 G; 2 T; 0 U; 0 Other;
Query Match 66.7%; Score 16; DB 13; Length 30;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CCAGCGTGGCCCATGG 21
Db 20 CCAGCGTGGCCCATGG 5
RESULT 9
AA50259/c
ID AAA50259 standard; DNA; 33 BP.
XX AC AAA50259;
XX XX 07-NOV-2000 (first entry)
XX DT Bcl2 gene 5' PCR primer.
XX DE Bcl2 gene; human; episome; transfection; selection; gene therapy;
XX KW PCR primer; ss.
XX OS Homo sapiens.
XX OS WO200047778-A1.
XX PN
XX XX

```

```

PD 17-AUG-2000.
XX
XX
XX 11-FEB-2000; 2000WO-US003547.
XX
XX 11-FEB-1999; 99US-00249585.
XX
XX (PHAR-) PHARMACOPEIA INC.
XX
XX Horlick RA, Chelsky D;
XX
XX WPI; 2000-515062/46.
XX
XX Stably transfecting eukaryotic cells with at least one episome for the
XX production of a desired protein in vitro and for gene therapy.
XX
XX Example 1; Page 29; 53pp; English.
XX
XX The present 5' primer was used with the 3' primer given in AAA50260 for
XX the PCR amplification of Bcl2 DNA, introducing a 5' BsiWI site and a 3'
XX NheI site. The PCR product was incorporated into an episome to
XX demonstrate a method of the invention. The method relates to the
XX maintenance and selection of episomes in transfecting eukaryotic cells in
XX vitro or in vivo, e.g. for gene therapy. It involves transfecting the
XX cells with an episome under conditions in which cells that survive are
XX successfully transfecting with the episome. The resulting cells express a
XX first protein whose expression causes cell death and a second protein
XX whose expression prevents cell death resulting from expression of the
XX first protein. In an example of the method, bcl2 and bad, and dff45 and
XX cide-1, were used as kill antagonist and kill agonist pairs in episomes
XX used to transfect 293E cells. The method allows the rapid establishment
XX of eukaryotic cells that stably and reliably express a gene of interest
XX
XX Sequence 33 BP; 9 A; 9 C; 10 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 16; DB 3; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 6 CCAGCGTGGCCATGG 21
XX Db 27 CCAGCGTGGCCATGG 12
XX
XX RESULT 10
XX AAA48984/C
XX ID AAA48984 standard; DNA; 33 BP.
XX AC AAA48984;
XX
XX 28-NOV-2000 (first entry)
XX
XX Mutagenic PCR primer Bcl2-5 targeted to anti-apoptotic gene bcl-2.
XX
XX Apoptosis; bcl-2; resistance; bacterial; viral; pathogens; PCR primer;
XX human; ss.
XX
XX Homo sapiens.
XX
XX WO200026391-A2.
XX
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025522.
XX
XX 30-OCT-1998; 98US-0106321P.
XX
XX 09-JUN-1999; 99US-0138303P.
XX
XX (UTNE-) UNIV NEBRASKA-LINCOLN.
XX
XX Dickman MB;
XX
XX WPI; 2000-365634/31.
XX
XX
XX
XX Transgenic plants with improved resistance characteristics comprising
XX nucleic acids encoding apoptotic proteins.
XX
XX Example 3; Page 58; 109pp; English.
XX
XX The present invention relates to the use of apoptotic genes in the the
XX production of transgenic plants with improved resistance characteristics.
XX The present sequence is the mutagenic PCR primer Bcl2-5. This primer was
XX used with primer Bcl2-3 (AAA48985) to introduce a 5' NcoI site and a 3'
XX XbaI site in the human apoptotic gene bcl-2. Specifically the primer
XX introduced an Ala residue between the Met (position 1) and His (position
XX 2) residues of the native protein. The altered bcl-2 sequence was used in
XX the creation of the final vector used to transform plants. The improved
XX resistance characteristics of the plants helps protect against bacterial,
XX viral and other pathogens. Resistance to abiotic challenges may also be
XX conferred
XX
XX Sequence 33 BP; 3 A; 9 C; 12 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 16; DB 3; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 2e+03;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 6 CCAGCGTGGCCATGG 21
XX Db 33 CCAGCGTGGCCATGG 18
XX
XX RESULT 11
XX ABK29920/C
XX ID ABK29920 standard; DNA; 35 BP.
XX
XX AC ABK29920;
XX
XX 23-APR-2002 (first entry)
XX
XX Human epidermal growth factor receptor 2 (Her2), primer #2.
XX
XX Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
XX HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
XX vanH promoter; androgen receptor promoter; AR promoter;
XX human epidermal growth factor receptor 2 promoter; her2 promoter;
XX beta lactamase promoter; B1a promoter; transgene; cancer; breast cancer;
XX colon cancer; immunological disorder; prostate cancer; cytostatic;
XX autoimmune disease; HBV pre-S promoter; HBV-X promoter;
XX Enterococcus infection; immunosuppressive; antibacterial; antiviral;
XX gene expression modulator; multiple sclerosis; MS;
XX chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
XX systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
XX familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
XX transgenic; ds.
XX
XX Homo sapiens.
XX
XX WO200194600-A2.
XX
XX 13-DEC-2001.
XX
XX 06-JUN-2001; 2001WO-US018343.
XX
XX 06-JUN-2000; 2000US-0209549P.
XX
XX (GENE-) GENELABS TECHNOLOGIES INC.
XX
XX Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;
XX Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;
XX Lim MY, Bruce TW;
XX
XX WPI; 2002-130595/17.
XX
XX New nucleic acid regulatory sequences, which are able to regulate
XX expression of a gene operably linked to a promoter, useful for regulating
XX the expression of transgenes and for treating e.g., cancer and

```



CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth.  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention

XX  
SQ Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
| | | | |  
Db 1 TCCAGCGTGC GCCAT 15

RESULT 14  
ABL39111  
ID ABL39111 standard; DNA; 16 BP.

XX ABL39111;

XX 16-APR-2002 (first entry)

XX Immunostimulatory nucleic acid SEQ ID NO: 533.

XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
XX angiogenesis; metastasis; cytostatic; ss.

XX Synthetic.

XX WO200197843-A2.

XX 27-DEC-2001.

XX 22-JUN-2001; 2001WO-US020154.

XX 22-JUN-2000; 2000US-0213346P.

XX (IOWA ) UNIV IOWA RES FOUND.

XX Weiner G, Hartmann G;

XX WPI; 2002-154611/20.

XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer.

XX Disclosure; Page 231; 312pp; English.

XX The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The

CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention

XX Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
| | | | |  
Db 1 TCCAGCGTGC GCCAT 15

RESULT 15  
ACD99398

ID ACD99398 standard; DNA; 16 BP.

XX ACD99398;

XX 25-SEP-2003 (first entry)

XX Immunostimulatory nucleic acid #84.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
XX antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
XX psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX Synthetic.

XX US2003050268-A1.

XX 13-MAR-2003.

XX 29-MAR-2002; 2002US-00112653.

XX 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIEG A M.

XX (BERG/) BERG D J.

XX Krieg AM, Berg DJ;

XX WPI; 2003-521815/49.

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.

XX Disclosure; Page 10; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid

XX Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
| | | | |  
Db 1 TCCAGCGTGC GCCAT 15

RESULT 16

```
ADB36467
ID  ADB36467 standard; DNA; 16 BP.
XX
XX  AC  ADB36467;
XX
XX  DT  04-DEC-2003 (first entry)
XX
XX  DE  Immunostimulatory nucleic acid #81.
XX
XX  KW  de; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX  KW  hypo-responsive subject; immunostimulatory.
XX  OS  Synthetic.
XX
XX  FN  US2003087848-A1.
XX
XX  PD  08-MAY-2003.
XX
XX  PF  02-FEB-2001; 2001US-00776479.
XX
XX  PR  03-FEB-2000; 2000US-0179991P.
XX
XX  PA  (BRAT/) BRATZLER R L.
XX  PA  (PETE/) PETERSEN D M.
XX  PA  (FOUR/) FOURON Y.
XX
XX  PI  Bratzler RL, Petersen DM, Fouron Y;
XX
XX  WI  WPI; 2003-657977/62.
XX
XX  PT  Treating and/or preventing allergy or asthma using an immunostimulatory
XX  PT  nucleic acid alone or in combination with an asthma/allergy medicament.
XX
XX  PS  Disclosure; Page 6; 221pp; English.
XX
XX  CC  The invention relates to a method of treating or preventing allergy or
XX  CC  asthma which comprises administering to a subject a poly-G nucleic acid
XX  CC  in an aerosol formulation. The methods and compositions of the present
XX  CC  invention are useful for diagnosing and/or treating asthma and allergy
XX  CC  especially in a hypo-responsive subject. The present sequence represents
XX  CC  an immunostimulatory nucleic acid of the invention.
XX
XX  SQ  Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGGCCCAT 19
Db 1 TCCAGCGTGGCCCAT 15

RESULT 17
ADU89406
ID  ADU89406 standard; DNA; 16 BP.
XX
XX  AC  ADU89406;
XX
XX  DT  10-FEB-2005 (first entry)
XX
XX  DE  Allergic response suppressor oligonucleotide #90.
XX
XX  KW  ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;
XX  KW  antibacterial; virucide; immunoglobulin E antagonist; allergy;
XX  KW  immunostimulator; asthma; rhinitis; urticaria; dermatitis;
XX  KW  bacterial infection; viral infection.
XX  OS  Synthetic.
XX
XX  FN  US2004235774-A1.
XX
XX  PD  25-NOV-2004.

Query Match 62.5%; Score 15; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGGCCCAT 19
Db 1 TCCAGCGTGGCCCAT 15

RESULT 18
ACI96181/c
ID  ACI96181 standard; DNA; 25 BP.
XX
XX  AC  ACI96181;
XX
XX  DT  14-OCT-2003 (first entry)
XX
XX  DE  Human microarray DNA oligonucleotide SEQ ID NO 96172.
XX
XX  KW  EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX  KW  genetic variation; biallelic marker; polymorphism; human;
XX  KW  cross-species comparison.
XX  OS  Homo sapiens.
XX
XX  FN  US2003104410-A1.
XX
XX  PD  05-JUN-2003.
XX
XX  PF  15-MAR-2002; 2002US-00098263.
XX
XX  PR  16-MAR-2001; 2001US-0276759P.
XX
XX  PA  (AFFY-) AFFYMETRIX INC.
XX
XX  PI  Mittmann MP;
XX
XX  WI  WPI; 2003-567953/53.

The invention relates to a method of suppressing a symptom of an allergic
response in a subject by administering a first and second dose of an
immunostimulatory nucleic acid that comprises a nucleotide sequence
comprising 5'-cg-3', and where the second dose is administered from 1 day
to 8 weeks after the first dose. The methods and compositions of the
present invention are useful for the treatment or prevention of asthma
and allergy, including rhinitis, urticaria and atopic dermatitis, using
an immunostimulatory nucleic acid alone or in combination with other
medicaments. This can also be used in preventing bacterial and viral
infections. This sequence represents an oligonucleotide used in the
method of the invention.

Sequence 16 BP; 3 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 13; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGGCCCAT 19
Db 1 TCCAGCGTGGCCCAT 15
```



PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 96172; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying allelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX SQ Sequence 25 BP; 3 A; 9 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 9; Length 25;  
Best Local Similarity 78.3%; Pred. No. 5.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GGGGTCCAGCTGCGCCATGGG 23  
||| ||||| ||| ||||| |||||  
Db 24 GGAGTCCACAGTCCGCCACGGG 2

RESULT 19

AAT18388/c

ID AAT18388 standard; DNA; 27 BP.

AC AAT18388;

XX 08-DEC-1996 (first entry)

XX Human Bcl-2 forward DNA primer.

XX Fas-associated protein; tumour necrosis factor receptor; PTP-BAS;  
KW apoptosis; FAP; cell surface protein; autoimmune disease; HIV virus;  
KW hybridoma; cell death; DNA primer; PCR; polymerase chain reaction; ss.

XX Synthetic.

XX WO9534661-A1.

XX 21-DEC-1995.

XX 14-JUN-1995; 95WO-US007583.

PR 14-JUN-1994; 94US-00259514.

PR 27-MAR-1995; 95US-00410804.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

XX Reed JC, Sato T;

DR WPI; 1996-049689/05.

XX New Fas associated proteins PTP-BAS types 4 and 5 - involved in

PT programmed cell death, used for modulating apoptosis, e.g. for treating  
PT cancer, and for identifying other modulators.

PS Disclosure; Page 42; 84pp; English.

XX The cDNA sequence encoding the cytoplasmic domain of human Fas (AA 191-  
CC 335) was modified by PCR mutagenesis using this primer along with the  
CC corresponding reverse primer (AAT18389) and another forward (AAT18386)  
CC and reverse (AAT18387) primer set. It was then subcloned in frame into  
CC plasmid pEG202 to produce plasmid pEG/Fas(191-135). The cDNA sequence for  
CC the cytoplasmic domain of human Fas was then subcloned into the EcoRI  
CC site of pEG202, in-frame with the upstream LexA sequences

XX SQ Sequence 27 BP; 7 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 CCACGCTGCGCCATG 20  
||| ||||| ||||| |||||  
Db 21 CCACGCTGCGCCATG 7

RESULT 20

ADY71779

ID ADY71779 standard; DNA; 28 BP.

XX AC ADY71779;

XX 02-JUN-2005 (first entry)

XX Signal sequence-containing oligonucleotide #5.

XX Cellular transport; ss.

XX Synthetic.

XX WO2005024033-A2.

XX 17-MAR-2005.

XX 10-SEP-2004; 2004WO-EP010162.

XX 11-SEP-2003; 2003EP-00020437.

XX (UYSC-) UNIV SCHLESWIG-HOLSTEIN.

XX Sczakiel G, Hopert A, Wuensche W, Overhoff M;

XX WPI; 2005-223387/23.

XX New nucleic acid promoting transmembrane transport of nucleic acids,  
PT useful for treating genetically based disorders.

XX Example 3; Page 11; 23pp; English.

XX The invention relates to a nucleic acid comprising a first nucleotide  
CC sequence having at least one signal sequence unit or a mixture of units,  
CC the signal sequence causing a transmembrane transport of the nucleic acid  
CC in a biological system. The invention also relates to a vector containing  
CC the nucleic acid, a host organism containing at least the nucleic acid or  
CC the vector, a method of producing the nucleic acid or the vector, a  
CC pharmaceutical composition comprising the nucleic acid, the vector or the  
CC host organism and optionally a pharmaceutical carrier and/or diluent or  
CC a kit comprising the nucleic acid, the vector or the host organism. The  
CC nucleotide sequence further contains at least one second nucleotide  
CC linked and/or forming a complex with the first and/or second nucleotide  
CC sequence, where the covalently linked and/or complexed components are  
CC biologically active. The nucleic acid, vector or host organism is useful  
CC for preparing a pharmaceutical composition for treating genetically based  
CC disorders. This sequence represents a signal sequence-containing

CC oligonucleotide used in the scope of the invention.

XX Sequence 28 BP; 3 A; 9 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 14; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCATG 20

Db 5 CCAGCGTGGCCCATG 19

RESULT 21

ADY71781  
ID ADY71781 standard; DNA; 28 BP.

XX AC ADY71781;

XX 02-JUN-2005 (first entry)

DE Control oligonucleotide #18.

XX Cellular transport; ss.

XX Synthetic.

XX W02005024033-A2.

XX 17-MAR-2005.

XX 10-SEP-2004; 2004WO-EP010162.

XX 11-SEP-2003; 2003EP-00020437.

XX (UYSC-) UNIV SCHLESWIG-HOLSTEIN.

XX Sczakiel G, Hopert A, Wuensche W, Overhoff M;

XX WPI; 2005-223387/23.

XX New nucleic acid promoting transmembrane transport of nucleic acids,  
PT useful for treating genetically based disorders.

XX Example 3; Page 11; 23pp; English.

XX The invention relates to a nucleic acid comprising a first nucleotide  
CC sequence having at least one signal sequence unit or a mixture of units,  
CC the signal sequence causing a transmembrane transport of the nucleic acid  
CC in a biological system. The invention also relates to a vector containing  
CC the nucleic acid, a host organism containing at least the nucleic acid or  
CC the vector, a method of producing the nucleic acid or the vector, a  
CC pharmaceutical composition comprising the nucleic acid, the vector or the  
CC host organism and optionally a pharmaceutical carrier and/or diluent and  
CC a kit comprising the nucleic acid, the vector or the host organism. The  
CC nucleotide sequence further contains at least one second nucleotide  
CC sequence to be transported and/or one or more components covalently  
CC linked and/or forming a complex with the first and/or second nucleotide  
CC sequence, where the covalently linked and/or complexed components are  
CC biologically active. The nucleic acid, vector or host organism is useful  
CC for preparing a pharmaceutical composition for treating genetically based  
CC disorders. This sequence represents an oligonucleotide used in the scope  
CC of the invention.

XX Sequence 28 BP; 6 A; 10 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 14; Length 28;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCATG 20

Db 5 CCAGCGTGGCCCATG 19

RESULT 22

ADF70717/C

ID ADF70717 standard; DNA; 40 BP.

XX AC ADF70717;

XX 12-FEB-2004 (first entry)

XX Human dopamine transporter enhancer SEQ ID NO:1.

XX human; ds; dopamine transporter; DAT; enhancer; expression vector;  
KW reporter gene; antiparkinsonian; neuroleptic; antidepressant;  
KW Parkinson's disease; schizophrenia.

XX Homo sapiens.

XX GB2381525-A.

XX 07-MAY-2003.

XX 01-NOV-2001; 2001GB-00026268.

XX 01-NOV-2001; 2001GB-00026268.

XX (TCS-) TCS CELLWORKS LTD.

XX Quinn J;

XX WPI; 2003-432825/41.

XX Novel expression vector comprising reporter gene and a reporter gene-  
PT transcription promoting enhancer sequence that has a variable number of  
PT tandem repeat and is found in 3'non-coding region of human dopamine  
PT transporter.

XX Claim 1; SEQ ID NO 1; 52pp; English.

XX The invention relates to a novel expression vector comprising an enhancer  
CC sequence and a reporter gene. The enhancer sequence comprises a variable  
CC number of tandem repeat (VNTR) and is found in the 3' non-coding region  
CC of the human dopamine transporter (DAT) gene. The enhancer sequence is  
CC capable of promoting the transcription of the reporter gene. An  
CC expression vector of the invention has antiparkinsonian, neuroleptic, and  
CC antidepressant activity, and may act as a dopamine transporter gene  
CC expression regulator, that increases or decreases dopamine levels. The  
CC expression vector is useful for identifying a compound capable of  
CC regulating the expression of a target gene (preferably human dopamine  
CC transporter gene) that comprises an enhancer sequence. A compound of the  
CC invention is useful for treating Parkinson's disease and schizophrenia  
CC that are associated with reduced and increased levels of dopamine,  
CC respectively. The present sequence is used in the exemplification of the  
CC invention.

XX Sequence 40 BP; 8 A; 15 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 62.5%; Score 15; DB 10; Length 40;  
Best Local Similarity 78.3%; Pred. No. 5.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCCATGGGG 23

Db 32 GGGGCCCTGCATGCGTCTGGGG 10

RESULT 23

ABN86431

ID ABN86431 standard; DNA; 20 BP.

XX AC ABN86431;

XX 21-OCT-2002 (first entry)

```
XX DE Translational consensus WAP-EPO with NotI modification sequence.
XX KW Therapeutic; erythropoietin; EPO; transgenic; WAP; ss.
XX OS Synthetic.
XX PN EP1217072-A2.
XX PD 26-JUN-2002.
XX PP 07-DEC-2001; 2001EP-00128498.
XX PR 07-DEC-2000; 2000CZ-00004569.
XX PA (BIOP-) BIOPHARM VU BIOFARMACIE A VETERINARNICH.
XX PI Mikus T, Maly P;
XX WI; 2002-550408/59.
XX DR Preparing vectors for therapeutic protein production in transgenic
XX PT animals, based on utilization of modified translational Kozak consensus
XX PT to connect promoter regulatory sequences with coding structural gene
XX PT fragments.
XX PS Disclosure; Fig 1; 32pp; English.
XX CC The invention relates to the preparation of an expression vector for the
XX CC therapeutic protein production, characterized by the utilization of
XX CC sequence motifs for restriction endonucleases NotI or NcoI to connect the
XX CC gene segments (including promoter regulatory regions) with the gene
XX CC segments (including structural fragments of the gene coding the required
XX CC protein). The method is useful for preparing an expression vector for
XX CC therapeutic protein production, in particular human erythropoietin (EPO).
XX CC The vector produced by the method is useful for EPO expression in
XX CC suitable transfected eukaryotic cells or in the mammary gland of
XX CC transgenic organisms. The present sequence represents a translational
XX CC consensus WAP-EPO sequence with NotI modification
XX SQ Sequence 20 BP; 3 A; 7 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 61.7%; Score 14.8; DB 6; Length 20;
Best Local Similarity 88.9%; Pred. No. 6.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 6 CCAGCGTGGCCCATGGGG 23
Db 3 CCAGCGCGCCCATGGGG 20
RESULT 24
ACI35454
ID ACI35454 standard; DNA; 25 BP.
XX AC ACI35454;
XX DT 13-OCT-2003 (first entry)
XX DE Human microarray DNA oligonucleotide SEQ ID NO 35445.
XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.
XX OS Homo sapiens.
XX PN US2003104410-A1.
XX PD 05-JUN-2003.
XX PF 15-MAR-2002; 2002US-00098263.
XX PR 15-MAR-2002; 2002US-00098263.
XX XX

PR 16-MAR-2001; 2001US-0276759P.
XX (AFFY-) AFFYMETRIX INC.
XX PI Mittmann MP;
XX WI; 2003-567953/53.
XX DR New array of nucleic acid probes, useful for in situ hybridization, in
XX PT Southern, Northern or dot-blot hybridization to identify or detect the
XX PT sequence or specific mutations of any gene.
XX PS Claim 1; SEQ ID NO 35445; 9pp; English.
XX CC The invention discloses a microarray comprising a plurality of nucleic
XX CC acid probes including one of 2,018,500 fully defined sequences, or its
XX CC perfect match, perfect mismatch, antisense match or antisense mismatch.
XX CC Also disclosed is a method of gene expression analysis. The array is used
XX CC in monitoring gene expression levels by hybridisation to a DNA library,
XX CC in analysis of genetic variation or in hybridisation of tag-labelled
XX CC compounds. The nucleic acid probes are specifically designed for analysis
XX CC of at least one target sequence. The method of analysis comprises
XX CC hybridising at least one or more nucleic acids to at least two or more
XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid
XX CC probes are attached to a solid support. The analysis comprises monitoring
XX CC gene expression levels, identifying biallelic markers or polymorphisms,
XX CC or family members of a gene and a cross-species comparison. Each of the
XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid
XX CC probes is useful in situ hybridisation, in Southern, Northern or dot-
XX CC blot hybridisation to identify or detect the sequence or specific
XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX CC primer extensions or in screening cDNA or genomic libraries or subclones
XX CC for additional subclones containing segments of DNA that have been
XX CC isolated and previously sequenced. The sequence presented is one of the
XX CC nucleic acid probes incorporated in the microarray. Note: The sequence
XX CC data for this patent can also be obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html
XX SQ Sequence 25 BP; 2 A; 7 C; 9 G; 7 T; 0 U; 0 Other;
Query Match 60.8%; Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4 GTCCAGCGTGGCCCATGGGG 24
Db 1 GTCCACTGTGCTCCATGGGTG 21
RESULT 25
ACI87918
ID ACI87918 standard; DNA; 25 BP.
XX AC ACI87918;
XX DT 14-OCT-2003 (first entry)
XX DE Human microarray DNA oligonucleotide SEQ ID NO 87909.
XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX KW genetic variation; biallelic marker; polymorphism; human;
XX KW cross-species comparison.
XX OS Homo sapiens.
XX PN US2003104410-A1.
XX PD 05-JUN-2003.
XX PF 15-MAR-2002; 2002US-00098263.
XX PR 16-MAR-2001; 2001US-0276759P.
XX XX
```

```

PA (AFFY-) AFFYMETRIX INC.
XX Mittmann MP;
PI WPI; 2003-567953/53.
XX New array of nucleic acid probes, useful for in situ hybridization, in
DR Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX Claim 1; SEQ ID NO 87909; 9pp; English.
XX The invention discloses a microarray comprising a plurality of nucleic
XX acid probes including one of 2,018,500 fully defined sequences, or its
XX perfect match, perfect mismatch, antisense match or antisense mismatch.
XX Also disclosed is a method of gene expression analysis. The array is used
XX in monitoring gene expression levels by hybridisation to a DNA library,
XX in analysis of genetic variation or in hybridisation of tag-labelled
XX compounds. The nucleic acid probes are specifically designed for analysis
XX of at least one target sequence. The method of analysis comprises
XX hybridising at least one or more nucleic acids to at least two or more
XX nucleic acid probes and detecting the hybridisation. The nucleic acid
XX probes are attached to a solid support. The analysis comprises monitoring
XX gene expression levels, identifying biallelic markers or polymorphisms,
XX or family members of a gene and a cross-species comparison. Each of the
XX nucleic acids further comprises a tag sequence. The array of nucleic acid
XX probes is useful in situ hybridisation, in Southern, Northern or dot-
XX blot hybridisation to identify or detect the sequence or specific
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX primer extensions or in screening cDNA or genomic libraries or subclones
XX for additional subclones containing segments of DNA that have been
XX isolated and previously sequenced. The sequence presented is one of the
XX nucleic acid probes incorporated in the microarray. Note: The sequence
XX data for this patent can also be obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 3 A; 7 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GTCACGGCTGCGCCATGGGG 24
DB 3 GTCCACTGTGCTCCATGGGTG 23

RESULT 26
ACI55188
ID ACI55188 standard; DNA; 25 BP.
XX
XX ACI55188;
XX
XX 13-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 55179.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; biallelic marker; polymorphism; human;
XX cross-species comparison.
XX
XX Homo sapiens.
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX (AFFY-) AFFYMETRIX INC.
XX Mittmann MP;
XX

```

---

```

PI Mittmann MP;
XX WPI; 2003-567953/53.
XX New array of nucleic acid probes, useful for in situ hybridization, in
DR Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX Claim 1; SEQ ID NO 55179; 9pp; English.
XX The invention discloses a microarray comprising a plurality of nucleic
XX acid probes including one of 2,018,500 fully defined sequences, or its
XX perfect match, perfect mismatch, antisense match or antisense mismatch.
XX Also disclosed is a method of gene expression analysis. The array is used
XX in monitoring gene expression levels by hybridisation to a DNA library,
XX in analysis of genetic variation or in hybridisation of tag-labelled
XX compounds. The nucleic acid probes are specifically designed for analysis
XX of at least one target sequence. The method of analysis comprises
XX hybridising at least one or more nucleic acids to at least two or more
XX nucleic acid probes and detecting the hybridisation. The nucleic acid
XX probes are attached to a solid support. The analysis comprises monitoring
XX gene expression levels, identifying biallelic markers or polymorphisms,
XX or family members of a gene and a cross-species comparison. Each of the
XX nucleic acids further comprises a tag sequence. The array of nucleic acid
XX probes is useful in situ hybridisation, in Southern, Northern or dot-
XX blot hybridisation to identify or detect the sequence or specific
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX primer extensions or in screening cDNA or genomic libraries or subclones
XX for additional subclones containing segments of DNA that have been
XX isolated and previously sequenced. The sequence presented is one of the
XX nucleic acid probes incorporated in the microarray. Note: The sequence
XX data for this patent can also be obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 3 A; 7 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GTCACGGCTGCGCCATGGGG 24
DB 4 GTCCACTGTGCTCCATGGGTG 24

RESULT 27
ACI87302
ID ACI87302 standard; DNA; 25 BP.
XX
XX ACI87302;
XX
XX 14-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 87293.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; biallelic marker; polymorphism; human;
XX cross-species comparison.
XX
XX Homo sapiens.
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX (AFFY-) AFFYMETRIX INC.
XX Mittmann MP;
XX

```

```

DR WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 87293; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
XX Sequence 25 BP; 3 A; 7 C; 7 G; 8 T; 0 U; 0 Other;
SQ
Query Match 60.8%; Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%; Pred. No. 8.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 GTCCAGCGTGCAGCCATGGGG 24
DB 3 GTCCACTGTGCTCCATGGGTG 23
RESULT 28
AAA30408
ID AAA30408 standard; DNA; 47 BP.
XX
XX AAA30408;
XX
XX 15-SEP-2003 (revised)
DT 11-SEP-2000 (first entry)
XX
XX EGF sequence biotinylated PCR primer Anchor1M9f.
XX
XX Phage display; biopanning; fusion protein; antibacterial;
KW ligand internalisation; cell transduction; library screening;
KW gene therapy; PCR primer; ss.
XX
XX Enterobacteria phage M13.
XX
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /note= "biotinylated"
FT
XX W0200029555-A1.
XX
XX 25-MAY-2000.
XX
XX 29-OCT-1999; 99WO-US025361.
XX
XX 17-NOV-1998; 98US-00193445.
PR 17-NOV-1998; 98US-00195379.
PR
PR 26-FEB-1999; 99US-00258689.
XX
XX (SELE-) SELECTIVE GENETICS INC.
XX
XX Larocca D, Baird A, Kassner P;
XX
XX WPI; 2000-387775/33.
XX
XX Selecting internalized ligands displayed on a genetic package by
PT contacting them with a cell, where each package carries a gene encoding a
PT detectable product expressed on internalization, useful for identifying
PT ligands for gene therapy.
XX
XX Example 19; Page 65; 112pp; English.
XX
XX The present sequence is a PCR primer used to amplify the EGF sequence in
CC COS cells infected with non-targeted M13 phage and EGF-phage. The
CC amplification primers have sequences located on each side of the EGF
CC sequence in the gene III coding sequence. The PCR products were digested
CC with restriction endonucleases and ligated into a new phage vector and
CC used to transform competent bacterial cells by electroporation. Plaques
CC were analysed via PCR using oligonucleotides which included the present
CC sequence. Four rounds of selection were sufficient to enrich the targeted
CC EGF-phage to 100%. This selection procedure is a useful example of a
CC novel method of selecting internalising ligands displayed on a genetic
CC package. The package carries a gene encoding a detectable product
CC expressed on internalisation. The method is referred to as Ligand
CC Identification Via Expression or LIVE (RTM). The method identifies
CC ligands that may be useful as antibacterial agents or in gene therapy.
CC The method is also useful for studying protein-protein interactions that
CC lead to cell transduction and identifying cells which are transduced by
CC the ligands. (Updated on 15-SEP-2003 to standardise OS field)
XX
XX Sequence 47 BP; 6 A; 10 C; 18 G; 13 T; 0 U; 0 Other;
SQ
Query Match 60.8%; Score 14.6; DB 3; Length 47;
Best Local Similarity 81.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GGGGTCCAGCGTGCAGCCATGG 21
DB 10 GGGTTCCTCCGCTGGCGATGG 30
RESULT 29
ADD14864
ID ADD14864 standard; DNA; 47 BP.
XX
XX ADD14864;
XX
XX 01-JAN-2004 (first entry)
DT
XX
XX Ligand gene III fusion PCR primer #1.
DE
XX
XX Transgene expression; gene delivery; anti-bacterial agent; cancer;
KW restenosis; antibacterial; cytostatic; vasotropic; PCR; primer; ss.
XX
XX Synthetic.
XX
XX US2002068272-A1.
XX
XX 06-JUN-2002.
XX
XX 24-MAY-2001; 2001US-00866073.
XX
XX 29-OCT-1999; 99WO-US025361.
PR
XX (LARO/) LARocca D.
PA (KASS/) KASSNER P.
PA (BAIR/) BAIRD A.
XX
XX Larocca D, Kassner P, Baird A;
XX

```

DR WPI; 2003-776567/73.

XX Genetic package display method useful for detecting and identifying

PT protein-protein interactions that facilitate internalization and

PT transgene expression.

XX

PS Example 19; Page 24; 47pp; English.

XX

CC The invention relates to a method for selecting ligands that internalise

CC and facilitate transgene expression, comprising displaying on a phage

CC carrying a transgene encoding a detectable product, and recovering a

CC nucleic acid molecule encoding the ligands from the cell expressing the

CC detectable product. The methods are useful in selecting and identifying

CC ligands displayed on a phage that internalise and facilitate transgene

CC expression, and also in identifying transduction facilitating peptides.

CC Internalising ligands identified by the methods are useful in gene

CC delivery methods and as anti-bacterial agents. The ligands and anti-

CC ligands identified are useful in the treatment of e.g., cancer and

CC restenosis. The method is also useful in that it allows identification of

CC molecules that are targets for new discovery. This sequence represents a

CC PCR primer used to amplify a ligand gene III fusion of the invention.

XX

SQ Sequence 47 BP; 6 A; 10 C; 18 G; 13 T; 0 U; 0 Other;

Query Match 60.8%; Score 14.6; DB 10; Length 47;

Best Local Similarity 81.0%; Pred. No. 8.3e+03;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTCCCGCGTGGCGATGG 21

Db 10 GGGTCCCGCGTGGCGATGG 30

RESULT 30

ADP86181

ID ADP86181 standard; DNA; 18 BP.

XX

AC ADP86181;

XX

DT 09-SEP-2004 (first entry)

XX

CC CpG immunostimulatory oligonucleotide #52.

XX

CC CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;

XX viral infection; bacterial infection; cancer; lymphoma;

XX intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;

XX carcinoma; sarcoma; gene therapy; phosphorothioate; ss.

XX

OS Unidentified.

XX

PH Key Location/Qualifiers

FT modified\_base 1..18

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

XX

PN WO2004053104-A2.

XX

PD 24-JUN-2004.

XX

PF 11-DEC-2003; 2003WO-US039775.

XX

PR 11-DEC-2002; 2002US-0432409P.

XX

PR 25-SEP-2003; 2003US-0506108P.

XX

PA (COLE-) COLEY PHARM GROUP INC.

XX

PA (COLE-) COLEY PHARM GMBH.

XX

PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;

XX

XX WPI; 2004-487902/46.

DR

XX New oligonucleotides, useful for treating allergy or asthma, viral and

PT bacterial infections, and cancer, e.g. biliary tract cancer, breast

PT bacterial infections, and cancer, e.g. biliary tract cancer, breast

PT cancer, cervical cancer.

XX

PS Example; SEQ ID NO 52; 104pp; English.

XX

CC The invention relates to a class of CpG immunostimulatory

CC oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that

CC are useful for stimulating an immune response. Oligonucleotides and

CC compositions of the invention are useful for treating allergy or asthma,

CC viral and bacterial infections and cancer e.g. biliary tract cancer,

CC breast cancer, cervical cancer, choriocarcinoma, colon cancer;

CC endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms,

CC liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma,

CC neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer,

CC rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain

CC and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer,

CC Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer,

CC testicular cancer, as well as other carcinomas and sarcomas. The

CC invention is also useful in gene therapy. The present sequence is a CpG

CC immunostimulatory oligonucleotide.

XX

SQ Sequence 18 BP; 2 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 12; Length 18;

Best Local Similarity 93.8%; Pred. No. 1e+04;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GTCAGCGTGCGCCAT 19

Db 3 GTCAGCGTGCGCCAT 18

RESULT 31

ADP86182

ID ADP86182 standard; DNA; 18 BP.

XX

AC ADP86182;

XX

DT 09-SEP-2004 (first entry)

XX

CC CpG immunostimulatory oligonucleotide #53.

XX

CC CpG immunostimulatory oligonucleotide; immune response; allergy; asthma;

XX viral infection; bacterial infection; cancer; lymphoma;

XX intraepithelial neoplasm; melanoma; neuroblastoma; Hodgkin's lymphoma;

XX carcinoma; sarcoma; gene therapy; phosphorothioate; ss.

XX

OS Unidentified.

XX

PH Key Location/Qualifiers

FT modified\_base 1..18

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "Phosphorothioate backbone"

XX

PN WO2004053104-A2.

XX

PD 24-JUN-2004.

XX

PF 11-DEC-2003; 2003WO-US039775.

XX

PR 11-DEC-2002; 2002US-0432409P.

XX

PR 25-SEP-2003; 2003US-0506108P.

XX

PA (COLE-) COLEY PHARM GROUP INC.

XX

PA (COLE-) COLEY PHARM GMBH.

XX

PI Krieg AM, Jurk M, Vollmer J, Uhlmann E;

XX

XX WPI; 2004-487902/46.

DR

XX New oligonucleotides, useful for treating allergy or asthma, viral and

PT bacterial infections, and cancer, e.g. biliary tract cancer, breast

cancer, cervical cancer.

Example; SEQ ID NO 53; 104pp; English.

The invention relates to a class of CpG immunostimulatory oligonucleotides containing a 5'TCG motif or a CG at or the 5' end that are useful for stimulating an immune response. Oligonucleotides and compositions of the invention are useful for treating allergy or asthma, viral and bacterial infections and cancer e.g. biliary tract cancer, breast cancer, cervical cancer, choriocarcinoma, colon cancer, endometrial cancer, gastric cancer, lymphomas, intraepithelial neoplasms, liver cancer, lung cancer (e.g. small cell and non-small cell), melanoma, neuroblastomas, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, sarcomas, thyroid cancer, renal cancer, bone cancer, brain and CNS cancer, connective tissue cancer, oesophageal cancer, eye cancer, Hodgkin's lymphoma, larynx cancer, oral cavity cancer, skin cancer, testicular cancer, as well as other carcinomas and sarcomas. The invention is also useful in gene therapy. The present sequence is a CpG immunostimulatory oligonucleotide.

Sequence 18 BP; 2 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 12; Length 18;  
Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GTCCAGCGTGGCCCAT 19  
| | | | | | | | | | | | | | | |  
Db 3 GCCCAGCGTGGCCCAT 18

RESULT 32  
ADW88846/C  
ID ADW88846 standard; DNA; 26 BP.  
XX AC ADW88846;  
XX DT 21-APR-2005 (first entry)  
XX DE Human Bcl-2 RT-PCR primer Bcl-2up.  
XX cytosatic; gene therapy; apoptosis modulation; pharmaceutical; cancer;  
KW cytosatic; neoplasm; Bcl-2; reverse transcriptase PCR; RT-PCR; primer;  
KW ss.  
XX Homo sapiens.  
OS WO2005012357-A1.  
FN 10-FEB-2005.  
PD 30-JUL-2004; 2004WO-GB003326.  
PF 31-JUL-2003; 2003GB-00017988.  
PR (MILM/) MILMER J.  
XX PA Milmer J, Jiang M;  
XX WIPI; 2005-123281/13.  
XX Regulating apoptosis in a cell, useful for treating cancer, comprises  
PT targeting an abnormally or alternatively spliced mRNA, an abnormally or  
PT alternatively structured mRNA, or a product of either.  
XX Disclosure; Page 14; 35pp; English.  
XX The invention describes a method of regulating apoptosis in a cell  
CC comprising targeting an abnormally or alternatively spliced mRNA, an  
CC abnormally or alternatively structured mRNA, or a product of either. Also  
CC described are: a nucleotide construct with a nucleotide sequence which is  
CC homologous to mRNA transcribed from an abnormally spliced gene; an agent  
CC selected from small molecule or protein; polypeptide; peptide; aptamer;

chemical; antibody; nucleic acid; polypeptide or nucleotide probe, which agent interacts with or binds with a protein expressed by an abnormally spliced mRNA for use as a medicament or for the manufacture of a medicament for the treatment of cancerous cell growth; a pharmaceutical composition comprising a nucleotide construct such as siRNA, anti-sense RNA, shRNA or miRNA; or the agent cited above, and a pharmaceutical diluent or carrier; a DNA or RNA expression vector comprising an expression cassette including the nucleotide sequence selected from: the nucleic acid sequence of the abnormally spliced gene element as given in the specification; a nucleic acid molecule which hybridizes to the nucleic acid sequence of (a); and a nucleic acid molecule which has a nucleic acid sequence which is degenerate because of the genetic code to the sequences in (a) and (b) and any sequence which is complementary to any of the above sequences, where the expression cassette is transcriptionally linked to a promoter sequence. The method is useful for regulating apoptosis in a cell or for treating cancer. The agent or nucleotide construct is useful as a medicament or for the manufacture of a medicament for the treatment of cancerous cell growth. In addition, the nucleotide construct is a means for silencing the expression of an abnormally spliced gene for use as a medicament for treating cancerous cell growth. The DNA or RNA expression vector is used as a delivery means for a molecule that is used in the targeting of an abnormally spliced mRNA or its product. This sequence represents a reverse transcriptase PCR primer used to isolate alternatively spliced Bcl-2 polynucleotides.

Sequence 26 BP; 6 A; 8 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 14; Length 26;  
Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCATGG 21  
| | | | | | | | | | | | | | | |  
Db 20 CCAGCGTGGCCCATCG 5

RESULT 33  
AAA15383  
ID AAA15383 standard; DNA; 29 BP.  
XX AC AAA15383;  
XX DT 04-SEP-2000 (first entry)  
XX DE PCR primer for a Neisseria pathogenic strain DNA sequence.  
XX Pathogenic strain; Neisseria; vaccine; Neisseria infection; PCR primer;  
KW ss.  
XX Neisseria meningitidis.  
OS WO200026375-A2.  
FN 11-MAY-2000.  
PD 28-OCT-1999; 99WO-FR002643.  
PF 30-OCT-1998; 98FR-00013693.  
PR (INMR) PASTEUR MERIEUX SERUMS & VACCINS SA.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
XX Aujaume L, Bouchardon A, Renauld-Mongenie G, Rokbi B, Nassif X;  
XX Tinsley C, Perrin A;  
XX WIPI; 2000-365622/31.  
XX New polypeptide specific for pathogenic Neisseria useful in therapeutic or preventative vaccines and for diagnosis.  
XX Example 1; Page 30; 187pp; French.  
XX The present sequence represents a PCR primer that was used to amplify DNA

CC encoding a protein that is specific for pathogenic strains of *Neisseria*.  
CC The polynucleotides, polypeptides, or their antigenic fragments, are used  
CC in vaccines to treat or protect against *Neisseria* infections, are used  
CC particularly by *N. meningitidis*. The polynucleotide sequence is also used  
CC for recombinant production of the polypeptide and to produce attenuated  
CC *Neisseria* strains that overexpress it, or express it in a non-toxic  
CC mutant form

XX Sequence 29 BP; 5 A; 8 C; 8 G; 8 T; 0 U; 0 Other;  
SQ

Query Match 60.0%; Score 14.4; DB 3; Length 29;  
Best Local Similarity 75.0%; Pred. No. 1e+04;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCCATGGGG 24  
||| ||| ||| ||| ||| ||| |||  
DB 2 GGGATCCACCTGCTTCATGGGTG 25

RESULT 34  
ADF28077/c  
ID ADF28077 standard; cDNA; 31 BP.  
XX  
XX ADF28077;  
AC  
XX  
XX 12-FEB-2004 (first entry)  
DT  
XX  
XX Caspase-resistant Bcl-2 5'-end terminal fragment.

DE  
XX  
XX Bcl-2; endothelial cell; mutant; vascularisation; human; antidiabetic;  
KW antiulcer; vulnery; cardiovascular; cell therapy; ss.

XX Synthetic.

OS  
XX WO2003087337-A2.

PN  
XX 23-OCT-2003.

XX  
XX 14-APR-2003; 2003WO-US011371.

XX  
XX 12-APR-2002; 2002US-0371677P.

XX (UYUA ) UNIV YALE.

XX Bothwell ALM, Pober JS, Schechner JS;

XX WPI; 2003-833725/77.

XX  
XX New engineered human skin equivalent that becomes perfused in vivo after  
PT engraftment on an immunodeficient animal, useful for treating conditions  
PT involving impaired angiogenesis, e.g. diabetes, chronic leg ulcers or  
PT wounds.

XX Example 2; SEQ ID NO 3; 144pp; English.

XX  
XX The invention relates to an engineered human skin equivalent, where the  
CC skin equivalent becomes perfused in vivo after engraftment on an  
CC immunodeficient animal. The method involves implanting onto a skin  
CC surface wound of an animal a construct prepared by a method comprising:  
CC preparing a solution comprising collagen and fibronectin; suspending  
CC endothelial cells in the solution where the suspended endothelial cells  
CC comprise a nucleic acid encoding a caspase-resistant Bcl-2 polypeptide;  
CC adjusting the solution of step (b) to about pH 7.0-8.0; and warming the  
CC solution of step (c) to about 25-40 °deg;C to form a three-dimensional  
CC gel. The method of endothelial cell transplantation promotes  
CC vascularisation of human skin equivalents in vivo. Administration can be  
CC orthotopic or subcutaneous. The engineered human skin equivalents and  
CC methods are useful in treating diseases or conditions involving impaired  
CC angiogenesis, such as diabetes, chronic leg ulcers, wounds,  
CC cardiovascular disease or burns. The present sequence represents a  
CC Caspase-resistant Bcl-2 5'-end terminal fragment

XX Sequence 31 BP; 7 A; 10 C; 8 G; 6 T; 0 U; 0 Other;  
SQ

Query Match 60.0%; Score 14.4; DB 10; Length 31;  
Best Local Similarity 93.8%; Pred. No. 1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 AGCGTGGCCCATGGGG 23  
||||| ||||| ||||| |||||  
DB 31 AGCGTGGCCCATGGTG 16

RESULT 35  
ABA92890/c  
ID ABA92890 standard; DNA; 32 BP.

XX ABA92890;

XX 03-APR-2002 (first entry)

XX Human 5' end of Bcl-2 DNA SEQ ID NO:3.

XX Human; D34A caspase-resistant Bcl-2; Bcl-2; mutant; vasotropic;  
KW vascularisation; angiogenesis; tissue transplantation; grafting;  
KW organ transplantation; gene; ss.

XX Homo sapiens.

PN WO200193880-A1.

XX 13-DEC-2001.

XX 05-JUN-2001; 2001WO-US018034.

XX 05-JUN-2000; 2000US-0208931P.

PR 30-MAR-2001; 2001US-0279797P.

XX (UYUA ) UNIV YALE.

XX Bothwell ALM, Pober JS, Schechner JS, Zheng L;

XX WPI; 2002-130568/17.

XX New synthetic composition comprising collagen, fibronectin and cells,  
PT useful for forming cultured endothelial cells for tissue/organ  
PT transplantation or grafting onto recipients with impaired  
PT vascularization.

XX Example 2; Page 55; 99pp; English.

XX  
XX The present invention describes a synthetic composition, which comprises  
CC collagen, fibronectin and at least one cell. Also described are: (1) a  
CC construct prepared by a method (M1) comprising: (a) preparing a solution  
CC comprising collagen and fibronectin; (b) suspending endothelial cells in  
CC the solution of step (a), where the suspended endothelial cells comprise  
CC a nucleic acid encoding a caspase-resistant Bcl-2 polypeptide; and (c)  
CC polymerising the collagen within the solution of step (b) to form a three  
CC dimensional gel; (2) a method (M2) of animal implantation comprising  
CC implanting into an animal the construct produced by the method of (1);  
CC (3) a method (M3) for forming endothelial cells into tubes within a  
CC matrix; (4) a method (M4) of producing endothelial cell tubules in vivo;  
CC (5) a method (M5) of promoting vascularisation in a tissue or an organ,  
CC or in animal; (6) methods (M6) for identifying genes or gene products  
CC involved in the process of vascularisation; (7) a method (M7) of  
CC identifying an agent, which modulates vascularisation or vascular  
CC remodeling; and (8) the endothelial cell tubules produced by the method  
CC of (M4). The synthetic composition has vasotropic activity. The  
CC composition is useful in methods for forming cultured endothelial cells  
CC into tubes or forming cultured endothelial cells into tubes within a  
CC three-dimensional gel. This is particularly useful in the grafting of  
CC engineered skin onto recipients with impaired vascularisation or impaired  
CC angiogenesis, or in all aspects of tissue and organ transplantation and  
CC grafting. The present sequence represents the 5' end of human Bcl-2,  
CC which is used in an example from the present invention

XX



SQ Sequence 32 BP; 7 A; 10 C; 9 G; 6 T; 0 U; 0 Other;  
 Query Match 60.0%; Score 14.4; DB 6; Length 32;  
 Best Local Similarity 93.8%; Pred. No. 1e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 AGCGTGGCCATGGGG 23  
 |||||  
 DB 32 AGCGTGGCCATGGTG 17  
 |||||

RESULT 36  
 ABK90294  
 ID ABK90294 standard; DNA; 34 BP.  
 XX  
 AC ABK90294;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Bcl-2/CRE hybrid antisense oligonucleotide #1.  
 XX  
 KW Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE;  
 KW CAMP response element; bacterial infection; viral infection;  
 KW inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;  
 KW autoimmune disorder; parasitic infection; virucide; hyperplasia;  
 KW tumorigenesis; hepatitis B infection; human.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..34  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 XX  
 PN WO200257480-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 22-JAN-2002; 2002WO-US001967.  
 XX  
 PR 22-JAN-2001; 2001US-0263244P.  
 XX  
 PA (GENT-) GENTA INC.  
 XX  
 PI Klem RE;  
 XX  
 DR WPI; 2002-590754/63.  
 XX  
 PT Hybrid oligomer comprises a cyclic AMP response element sequence and a  
 PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for  
 PT preventing or treating cell-proliferative disorders e.g., cancer.  
 XX  
 PS Disclosure; Page 25; 78pp; English.  
 XX  
 CC The invention relates to a hybrid oligomer comprising a cyclic AMP  
 CC response element (CRE) sequence and a sequence that hybridizes to the bcl  
 CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of  
 CC cancer cells in vitro, which comprises contacting the cancer cells with a  
 CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;  
 CC (2) treating or preventing cancer in a human, which comprises  
 CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE  
 CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid  
 CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a  
 CC carrier. The pharmaceutical composition of the invention is useful for  
 CC preventing or treating cell-proliferative disorders e.g., cancer,  
 CC hyperplasia or tumorigenesis and also bacterial infection, viral  
 CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,  
 CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and  
 CC bcl-2 antisense oligomer are also useful for preventing or treating  
 CC hepatitis B virus infection. The hybrid oligomers can also be used for  
 CC screening candidate transcription factors or other molecules e.g., gene  
 CC regulatory proteins or for diagnostic assays. The present sequence is a  
 CC Bcl-2/CRE hybrid antisense oligonucleotide  
 XX  
 SQ Sequence 34 BP; 6 A; 12 C; 8 G; 8 T; 0 U; 0 Other;  
 Query Match 60.0%; Score 14.4; DB 6; Length 34;

Best Local Similarity 93.8%; Pred. No. 1e+04; Mismatches 0; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCCATGG 21  
 |||||  
 DB 13 CCAGCGTGGCCATGG 28  
 |||||

RESULT 37  
 ABK90296  
 ID ABK90296 standard; DNA; 34 BP.  
 XX  
 AC ABK90296;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Bcl-2-targeting antisense oligonucleotide BK1-PS.  
 XX  
 KW Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE;  
 KW CAMP response element; bacterial infection; viral infection;  
 KW inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;  
 KW autoimmune disorder; parasitic infection; virucide; hyperplasia;  
 KW tumorigenesis; hepatitis B infection; human.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..34  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 XX  
 PN WO200257480-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 22-JAN-2002; 2002WO-US001967.  
 XX  
 PR 22-JAN-2001; 2001US-0263244P.  
 XX  
 PA (GENT-) GENTA INC.  
 XX  
 PI Klem RE;  
 XX  
 DR WPI; 2002-590754/63.  
 XX  
 PT Hybrid oligomer comprises a cyclic AMP response element sequence and a  
 PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for  
 PT preventing or treating cell-proliferative disorders e.g., cancer.  
 XX  
 PS Example 1; Page 58; 78pp; English.  
 XX  
 CC The invention relates to a hybrid oligomer comprising a cyclic AMP  
 CC response element (CRE) sequence and a sequence that hybridizes to the bcl  
 CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of  
 CC cancer cells in vitro, which comprises contacting the cancer cells with a  
 CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;  
 CC (2) treating or preventing cancer in a human, which comprises  
 CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE  
 CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid  
 CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a  
 CC carrier. The pharmaceutical composition of the invention is useful for  
 CC preventing or treating cell-proliferative disorders e.g., cancer,  
 CC hyperplasia or tumorigenesis and also bacterial infection, viral  
 CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,  
 CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and  
 CC bcl-2 antisense oligomer are also useful for preventing or treating  
 CC hepatitis B virus infection. The hybrid oligomers can also be used for  
 CC screening candidate transcription factors or other molecules e.g., gene  
 CC regulatory proteins or for diagnostic assays. The present sequence is a  
 CC Bcl-2 antisense oligonucleotide  
 XX

SQ Sequence 34 BP; 6 A; 12 C; 8 G; 8 T; 0 U; 0 Other;  
 Query Match 60.0%; Score 14.4; DB 6; Length 34;  
 Best Local Similarity 93.8%; Pred. No. 1e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 CCAGCGTGGCCCATGG 21  
 DB 13 CCAGCGTGGCCCATGG 28  
 RESULT 38  
 ABK90352  
 ID ABK90352 standard; DNA; 34 BP.  
 AC ABK90352;  
 XX 21-OCT-2002 (first entry)  
 DE Bcl-2/CRE hybrid antisense oligonucleotide BK7-DE.  
 XX Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE;  
 KW cAMP response element; bacterial infection; viral infection;  
 KW inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;  
 KW autoimmune disorder; parasitic infection; virucide; hyperplasia;  
 KW tumourigenesis; hepatitis B infection; human.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200257480-A2.  
 XX 25-JUL-2002.  
 XX 22-JAN-2002; 2002WO-US001967.  
 XX 22-JAN-2001; 2001US-0263244P.  
 XX (GENT-) GENTA INC.  
 XX Klem RE;  
 XX WPI; 2002-590754/63.  
 XX Hybrid oligomer comprises a cyclic AMP response element sequence and a  
 PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for  
 PT preventing or treating cell-proliferative disorders e.g., cancer.  
 XX Example 1; Page 58; 78pp; English.  
 XX The invention relates to a hybrid oligomer comprising a cyclic AMP  
 CC response element (CRE) sequence and a sequence that hybridizes to the bcl  
 CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of  
 CC cancer cells in vitro, which comprises contacting the cancer cells with a  
 CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;  
 CC (2) treating or preventing cancer in a human, which comprises  
 CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE  
 CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid  
 CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a  
 CC carrier. The pharmaceutical composition of the invention is useful for  
 CC preventing or treating cell-proliferative disorders e.g., cancer,  
 CC hyperplasia or tumourigenesis and also bacterial infection, viral  
 CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,  
 CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and  
 CC bcl-2 antisense oligomer are also useful for preventing or treating  
 CC hepatitis B virus infection. The hybrid oligomers can also be used for  
 CC screening candidate transcription factors or other molecules e.g., gene  
 CC regulatory proteins or for diagnostic assays. The present sequence is a  
 CC Bcl-2/CRE hybrid antisense oligonucleotide  
 XX  
 SQ Sequence 34 BP; 6 A; 12 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 60.0%; Score 14.4; DB 6; Length 34;

Best Local Similarity 93.8%; Pred. No. 1e+04;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 CCAGCGTGGCCCATGG 21  
 DB 13 CCAGCGTGGCCCATGG 28  
 RESULT 39  
 ADF50458/C  
 ID ADF50458 standard; DNA; 34 BP.  
 XX ADF50458;  
 XX 12-FEB-2004 (first entry)  
 DE PCR primer used to amplify human GPCR G2A cDNA (SeqID 138).  
 XX human; PCR; primer; ss; transformation; endocrine cell line;  
 KW expression cloning system; bioactive peptide; GPCR ligand.  
 XX Homo sapiens.  
 OS WO2003087366-A1.  
 PN 23-OCT-2003.  
 XX 16-APR-2003; 2003WO-JP004840.  
 XX 16-APR-2002; 2002JP-00113030.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Sasaki K, Miura K, Saeki S, Yoshizawa M, Kishimoto K, Kunitomo H;  
 PI Nishi T, Obinata M;  
 XX WPI; 2003-833737/77.  
 XX Endocrine cell lines originated from mammalian hypothalamus and  
 PT pancreatic islet, applicable in expression cloning systems of bioactive  
 PT peptide precursor genes, and in screening G protein-coupled receptor  
 PT ligands.  
 XX Example 22; SEQ ID NO 138; 316pp; Japanese.  
 XX This invention relates to a novel method for obtaining a DNA that encodes  
 CC a peptide acting as agonist, antagonist or inverse agonist on a target  
 CC receptor. Specifically, it comprises transformation of endocrine cell  
 CC lines originating from mammalian hypothalamus and pancreatic islets,  
 CC culturing the transformants and contacting with cells expressing the  
 CC target receptor. The identification of those cells with a response  
 CC reaction can be used for selecting a transformant cell line with the  
 CC appropriate target activity that is expressing the novel transformed DNA.  
 CC Accordingly, the present invention describes novel cell lines that are  
 CC applicable in expression cloning systems of bioactive peptide precursor  
 CC genes, and in screening GPCR ligands for use as drugs including agonists,  
 CC antagonists and inverse agonists i.e. activators and inhibitors. Such  
 CC cell lines can provide a highly sensitive and convenient GPCR ligand  
 CC assay system. This oligonucleotide sequence is a PCR primer used to  
 CC amplify human GPCR cDNA of the invention.  
 XX Sequence 34 BP; 8 A; 14 C; 9 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 60.0%; Score 14.4; DB 10; Length 34;  
 Best Local Similarity 75.0%; Pred. No. 1e+04;  
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 GGGGTCCAGCGTGGCCCATGGGG 24  
 DB 27 GGGGTCTCTGGCGCGCCCAATGTGG 4  
 RESULT 40

```

ADK17713/c
ID ADK17713 standard; DNA; 41 BP.
AC ADK17713;
XX
XX 06-MAY-2004 (first entry)
XX
XX Cytochrome P450 gene polymorphism detecting oligo, SEQ ID No 27.
XX
XX detection; gene polymorphism; cytochrome P450; drug evaluation; safety;
XX drug screening; single nucleotide polymorphism; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX variation replace(21,T)
XX /*tag= a
XX /standard_name="single nucleotide polymorphism"
XX
XX WO2003102181-A1.
XX
XX 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-JP006750.
XX
XX 30-MAY-2002; 2002JP-00158237.
XX (RIKE ) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
XX
XX WPI; 2004-043114/04.
XX
XX Detecting gene polymorphism particularly of cytochrome P450- encoded gene
XX with specific oligonucleotides, applicable obtaining gene information,
XX evaluation of drugs and screening drug candidates.
XX
XX Claim 1; SEQ ID NO 27; 144pp; Japanese.
XX
XX The invention relates to a novel method for detecting gene polymorphisms
XX of a gene that encodes cytochrome P450. The method involves using an
XX oligonucleotide and/or a primer selected from those having sequences with
XX at least 13 bases, including the base at position-21 in the base
XX sequences represented by the oligos of 40-41 base pairs, or their
XX complementary sequences, provided in the specification. The method is
XX applicable in obtaining gene information, evaluation of drugs including
XX safety and therapeutic efficacy, and screening drug candidates. This
XX polynucleotide sequence represents one of the 40-41 base pair long oligos
XX used in the gene polymorphism detection method of the invention.
XX
XX Sequence 41 BP; 12 A; 13 C; 11 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 60.0%; Score 14.4; DB 12; Length 41;
XX Best Local Similarity 93.8%; Pred. No. 1e+04;
XX Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 GGGGTCCAGCGTGGCG 16
XX ||| |||||
XX 35 GGGATCCAGCGTGGCG 20
XX
XX RESULT 41
XX AAL33952/c
XX ID AAL33952 standard; DNA; 50 BP.
XX
XX AC AAL33952;
XX
XX 24-JAN-2002 (first entry)
XX
XX Human SNP oligonucleotide #7160.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuoprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
XX

```

---

```

KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX Homo sapiens.
XX
XX OS
XX WO200147944-A2.
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.
XX
XX 28-DEC-1999; 99US-0173419P.
XX 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX
XX WPI; 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.
XX
XX Claim 1; Page 3440; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiopoietin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
XX protein coupled receptors and thioesterases. The present sequence is one
XX such oligonucleotide. The oligonucleotides and the peptides encoded by
XX them may be used in the prevention, diagnosis and treatment of diseases
XX associated with inappropriate expression of the proteins listed above.
XX Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukaemia), diseases of the nervous system and an infection of pathogenic
XX organisms
XX
XX Sequence 50 BP; 8 A; 24 C; 13 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 60.0%; Score 14.4; DB 4; Length 50;
XX Best Local Similarity 75.0%; Pred. No. 1e+04;
XX Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX 1 GGGGTCCAGCGTGGCGCATGGGG 24
XX ||| |||||
XX 33 GGGGGCCAGCGTGGCATGGGG 10
XX
XX RESULT 42
XX AAC88236
XX ID AAC88236 standard; DNA; 19 BP.
XX
XX AC AAC88236;
XX
XX 02-MAR-2001 (first entry)
XX
XX Murine lineage-restricted precursor cell population PCR primer #14.
XX
XX Mouse; lineage restricted precursor cell; neuron-restricted precursor;
XX NRP; glial-restricted precursor; GRP; mouse neural tube; transplantation;
XX antibody; PCR primer; ss.
XX
XX Mus sp.

```

```

XX WO200068359-A1.
PN
XX
XX 16-NOV-2000.
PD
XX
XX 05-MAY-2000; 2000WO-US012446.
PF
XX
XX 07-MAY-1999; 99US-0133159P.
XX
XX (UTAH ) UNIV UTAH RES FOUND.
PA
XX
XX Mujtaba T, Rao MS;
PI
XX
XX WPI; 2001-024863/03.
DR
XX
XX New pure populations of neuron- or glial-restricted precursor cells and
PT neuroepithelial stem cells from mouse neural tubes or embryonic stem
PT cells for developing new drugs or techniques that enhance survival of
PT transplanted cell.
XX
XX Example 8; Page 22; 37pp; English.
PS
XX
XX The present invention provides populations of lineage-restricted
XX precursor cells from mouse neural tube and mouse embryonic stem cells.
XX These populations are of neuron-restricted precursor cells (NRPs) and
XX glial-restricted precursor cells (GRPs). These cell populations are
XX useful in the development of new transplant techniques, for
XX transplantation in diseases where neuronal or glial degeneration has
XX occurred, in the identification of drugs which enhance the survival and
XX proliferation of transplanted cells, to identify genes specific to
XX selected stages of development, and in the generation of cell-specific
XX antibodies
XX
XX Sequence 19 BP; 3 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 59.2%; Score 14.2; DB 4; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GGTCCAGCGTGGCCATGG 21
DB 1 GGTCCAGCAATTGCCATGG 19
RESULT 43
ACI94928
ID ACI94928 standard; DNA; 25 BP.
XX
XX ACI94928;
AC
XX
XX 14-OCT-2003 (first entry)
DT
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 94919.
DE
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
OS
XX
XX US2003104410-A1.
PN
XX
XX 05-JUN-2003.
PD
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
PA
XX
XX Mittmann MP;
PI
XX
XX WPI; 2003-567953/53.
DR
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 94919; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
XX acid probes including one of 2,018,500 fully defined sequences, or its
XX perfect match, perfect mismatch, antisense match or antisense mismatch.
XX Also disclosed is a method of gene expression analysis. The array is used
XX in monitoring gene expression levels by hybridisation to a DNA library,
XX in analysis of genetic variation or in hybridisation of tag-labelled
XX compounds. The nucleic acid probes are specifically designed for analysis
XX of at least one target sequence. The method of analysis comprises
XX hybridising at least one or more nucleic acids to at least two or more
XX nucleic acid probes and detecting the hybridisation. The nucleic acid
XX probes are attached to a solid support. The analysis comprises monitoring
XX gene expression levels, identifying biallelic markers or polymorphisms,
XX or family members of a gene and a cross-species comparison. Each of the
XX nucleic acids further comprises a tag sequence. The array of nucleic acid
XX probes is useful in in situ hybridisation, in Southern, Northern or dot-
XX blot hybridisation to identify or detect the sequence or specific
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX primer extensions or in screening cDNA or genomic libraries or subclones
XX for additional subclones containing segments of DNA that have been
XX isolated and previously sequenced. The sequence presented is one of the
XX nucleic acid probes incorporated in the microarray. Note: The sequence
XX data for this patent can also be obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html
XX
XX Sequence 25 BP; 3 A; 9 C; 6 G; 7 T; 0 U; 0 Other;
SQ
Query Match 59.2%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 GTCCAGCGTGGCCATGGG 22
DB 6 GTCCACTGTGCTCCATGGG 24
RESULT 44
ACI94310
ID ACI94310 standard; DNA; 25 BP.
XX
XX ACI94310;
AC
XX
XX 14-OCT-2003 (first entry)
DT
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 94301.
DE
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
OS
XX
XX US2003104410-A1.
PN
XX
XX 05-JUN-2003.
PD
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
PA
XX
XX Mittmann MP;
PI
XX
XX WPI; 2003-567953/53.
DR
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in

```

PT Southern, Northern or dot-blot hybridization to identify or detect the  
 XX sequence or specific mutations of any gene.  
 XX Claim 1; SEQ ID NO 94301; 9pp; English.  
 XX The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library.  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying allelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
 XX  
 XX Sequence 25 BP; 3 A; 9 C; 6 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 59.2%; Score 14.2; DB 9; Length 25;  
 Best Local Similarity 84.2%; Pred. No. 1.2e+04;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 GTCCAGCTGTCGCCATGG 22  
 ||||| ||||| ||||| |||||  
 Db 6 GTCCACTGTGCTCCATGG 24  
 RESULT 45  
 ADK43158  
 ID ADK43158 standard; DNA; 31 BP.  
 XX  
 AC ADK43158;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human N-acetylglucosamine transferase NGalNAC-T1 PCR primer #3.  
 XX  
 KW oligosaccharide; N-acetylglucosamine; N-acetylglucosamine;  
 KW beta1-4 linkage; human; N-acetylglucosamine transferase; NGalNAC-T1; ss;  
 KW PCR; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004016790-A1.  
 XX  
 PD 26-FEB-2004.  
 XX  
 PF 13-AUG-2003; 2003WO-JP010309.  
 XX  
 PR 14-AUG-2002; 2002JP-00236292.  
 XX  
 XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 FA (AMSH) AMERSHAM BIOSCIENCES KK.  
 XX  
 PI Narimatsu H, Gotoh M, Sato T;  
 XX  
 DR WPI; 2004-203801/19.  
 XX  
 XX New isolated protein having specified amino acid sequence for enzyme used  
 PT in producing oligosaccharides.  
 PT

XX Example 1; SEQ ID NO 16; 79pp; English.  
 XX  
 CC The invention relates to an isolated N-acetylglucosamine transferase  
 CC protein. The protein is useful for enzyme used in producing  
 CC oligosaccharides. The inventive isolated protein has the activity of  
 CC transferring N-acetylglucosamine to N-acetylglucosamine via beta1-4  
 CC linkage. The present sequence represents human N-acetylglucosamine  
 CC transferase, NGalNAC-T1, PCR primer.  
 XX  
 SQ Sequence 31 BP; 4 A; 12 C; 10 G; 5 T; 0 U; 0 Other;  
 Query Match 59.2%; Score 14.2; DB 12; Length 31;  
 Best Local Similarity 84.2%; Pred. No. 1.2e+04;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGGGTCCAGCTGCGCCAT 19  
 ||||| ||||| ||||| |||||  
 Db 13 GGGGTCCAGCTGCGCCAT 31  
 RESULT 46  
 AAV05322/c  
 ID AAV05322 standard; DNA; 33 BP.  
 XX  
 AC AAV05322;  
 XX  
 DT 22-MAY-1998 (first entry)  
 XX  
 DE PCR primer 1 used in RT-PCR to amplify bcl-2 cDNA.  
 XX  
 KW bcl-2 gene; anti-apoptotic gene; prevention; cell death; treatment;  
 KW neurodegenerative disease; disease; Huntington's; Parkinson's;  
 KW Alzheimer's; retroviral vector; LNXS; LNCX; live packaging cell;  
 KW biocompatible capsule; release; viral vector; implant; gene therapy;  
 KW tumour; PCR primer; amplify; ss.  
 OS Synthetic.  
 OS Mammalia.  
 XX  
 FH Key Location/Qualifiers  
 FT RBS 10..16  
 FT /\*tag= a  
 FT /note= "Kozak sequence which enhances translation  
 FT efficiency of bcl-2"  
 XX  
 XX WO9744065-A2.  
 XX  
 PD 27-NOV-1997.  
 XX  
 PF 20-MAY-1997; 97WO-US008463.  
 XX  
 PR 20-MAY-1996; 96US-00650726.  
 XX  
 XX (CYTO-) CYTOTHERAPEUTICS INC.  
 XX  
 XX Hamang JP, Aebischer P;  
 PI WPI; 1998-018231/02.  
 XX  
 DR Capsule containing packaging cells that produce viral vectors for gene  
 XX therapy - used as replaceable implants in treatment of cancer,  
 XX atherosclerosis etc., providing localised, long-term vector delivery.  
 XX  
 XX Example 5; Page 33; 45pp; English.  
 XX  
 CC PCR primers AAV05322-23 are used in a reverse transcription polymerase  
 CC PCR reaction (RT-PCR) to amplify bcl-2 cDNA from human, rat, or mouse  
 CC thymus total RNA. Bcl-2 genes are anti-apoptotic genes whose products  
 CC prevent unwanted death of certain cell populations, and are useful for  
 CC treating neurodegenerative diseases such as Huntington's, Parkinson's or  
 CC Alzheimer's disease. The PCR product was ligated into retroviral vectors  
 CC LNXS and LNCX, to produce retroviral vectors LNXS-bcl-2 and LNCX-bcl-2.



```

XX AAV19660;
AC
XX 25-MAR-2003 (revised)
DT 12-JUN-1998 (first entry)
XX
XX Human bcl-2 antisense oligonucleotide 6.
DE
XX Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW cancer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX US5734033-A.
FN
XX 31-MAR-1998.
PD
XX
XX 24-MAR-1994; 94US-00217082.
PF
XX
XX 22-DEC-1988; 88US-00288692.
PR
XX 21-FEB-1992; 92US-00840716.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
FA
XX
XX Reed J;
PI
XX
XX WPI; 1998-229881/20.
DR
XX
XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful for
PT treating cancers, e.g. lymphoma(s) and some leukaemia(s).
XX
XX Claim 6; Col 14; 21pp; English.
PS
XX
XX This antisense oligonucleotide is complementary to the translation
CC initiation site of the human bcl-2 mRNA. The bcl-2 antisense
CC oligonucleotides are phosphorothioate derivatives and can straddle
CC strategic sites such as the translation initiation site, donor and
CC acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of a
CC functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukaemias. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
XX Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 58.3%; Score 14; DB 2; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+04;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 6 CCAGCGTGGCCCAT 19
XX |||||
XX Db 1 CCAGCGTGGCCCAT 14
XX
XX RESULT 50
XX AAV19659
XX ID AAV19659 standard; DNA; 17 BP.
XX
XX AAV19659;
AC
XX
XX 25-MAR-2003 (revised)
DT 12-JUN-1998 (first entry)
XX
XX Human bcl-2 antisense oligonucleotide 5.
DE
XX Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
KW cancer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX
XX

```

```

PN US5734033-A.
XX
XX 31-MAR-1998.
PD
XX
XX 24-MAR-1994; 94US-00217082.
PF
XX
XX 22-DEC-1988; 88US-00288692.
PR
XX 21-FEB-1992; 92US-00840716.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Reed J;
DI
XX
XX WPI; 1998-229881/20.
DR
XX
XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful for
PT treating cancers, e.g. lymphoma(s) and some leukaemia(s).
XX
XX Claim 6; Col 14; 21pp; English.
PS
XX
XX This antisense oligonucleotide is complementary to the translation
CC initiation site of the human bcl-2 mRNA. The bcl-2 antisense
CC oligonucleotides are phosphorothioate derivatives and can straddle
CC strategic sites such as the translation initiation site, donor and
CC acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of a
CC functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukaemias. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
XX Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 58.3%; Score 14; DB 2; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+04;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 6 CCAGCGTGGCCCAT 19
XX |||||
XX Db 4 CCAGCGTGGCCCAT 17
XX
XX Search completed: February 15, 2006, 18:07:05
XX Job time : 189.893 secs

```

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:07:43 ; Search time 1596.3 Seconds  
(without alignments)  
703.434 Million cell updates/sec

Title: US-09-669-187A-81

Perfect score: 24  
Sequence: 1 ggggtccagcgtgcgcattggggg 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gse1:\*  
10: gb\_gse2:\*  
11: gb\_gse3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	62.5	50	1	AU107435
2	15	62.5	50	1	AU107436
3	14.8	61.7	49	1	AJ796516
C 4	14.4	60.0	46	1	AA878878
C 5	14.2	59.2	47	6	CF661152
C 6	14.2	59.2	49	1	AA993146
C 7	13.6	56.7	49	1	A1098584
C 8	13.6	56.7	50	1	AU102746
C 9	13.4	55.8	37	10	CU517576
C 10	13.4	55.8	40	1	A1800161
11	13.4	55.8	43	1	AA863355
12	13	54.2	33	9	A2434579
13	13	54.2	38	3	B1548958
14	13	54.2	50	1	AU104320
15	13	54.2	50	1	AU105443
16	13	54.2	50	1	AU107884
17	13	54.2	50	1	AU107885
18	13	54.2	50	1	AU107886
C 19	13	54.2	50	8	R85071
20	12.8	53.3	34	2	BF384787
21	12.8	53.3	37	1	A1755616
22	12.8	53.3	38	3	B1597957

C 23	12.8	53.3	39	1	AJ683869
C 24	12.8	53.3	40	9	AZ998247
25	12.8	53.3	41	3	B1561395
26	12.8	53.3	44	9	A2444974
27	12.8	53.3	48	9	AZ510921
28	12.8	53.3	49	1	AA903627
29	12.8	53.3	50	1	AU106561
30	12.8	53.3	50	2	BB616279
C 31	12.8	53.3	50	9	AZ983659
C 32	12.8	53.3	50	10	CL521622
C 33	12.6	52.5	28	9	AZ829200
C 34	12.6	52.5	45	9	AK216071
C 35	12.6	52.5	45	9	CC183529
C 36	12.6	52.5	45	10	CG728115
37	12.6	52.5	48	3	B1906001
C 38	12.6	52.5	49	1	A1254752
39	12.6	52.5	49	1	A1434488
40	12.6	52.5	49	1	AA594397
41	12.6	52.5	49	10	CZ295110
C 42	12.6	52.5	49	11	CR900779
43	12.6	52.5	50	6	CB221472
44	12.4	51.7	23	9	AZ619403
C 45	12.4	51.7	37	1	A1619702
46	12.4	51.7	45	9	AZ434030
C 47	12.4	51.7	46	10	CL210842
48	12.4	51.7	47	9	BZ585242
49	12.4	51.7	48	5	BW590752
C 50	12.4	51.7	49	1	AA906151
C 51	12.4	51.7	49	1	A1788892
C 52	12.4	51.7	49	2	BE376178
C 53	12.4	51.7	49	10	CZ169359
C 54	12.4	51.7	49	10	CL211000
55	12.4	51.7	50	1	AU102361
56	12.2	50.8	24	9	AZ582169
57	12.2	50.8	35	9	AZ369507
58	12.2	50.8	46	1	AA231183
59	12.2	50.8	46	1	AV949324
60	12.2	50.8	47	10	BX893758
C 61	12.2	50.8	50	10	CG710772
C 62	12.2	50.8	50	10	CG894689
C 63	12.2	50.8	50	11	DE037319
C 64	12	50.0	28	10	AJ595885
C 65	12	50.0	29	3	BP917129
C 66	12	50.0	30	10	AJ590951
C 67	12	50.0	34	1	AA971412
68	12	50.0	34	1	A1270065
69	12	50.0	40	3	BP870432
70	12	50.0	40	3	BP938418
71	12	50.0	42	3	B1546340
C 72	12	50.0	46	1	A1033006
C 73	12	50.0	46	1	A1814794
C 74	12	50.0	46	8	H49581
75	12	50.0	50	1	AU106897
76	12	50.0	50	1	AU107574
77	11.8	49.2	25	1	A1153891
78	11.8	49.2	25	1	A1608697
C 79	11.8	49.2	29	1	AJ667773
80	11.8	49.2	29	9	AZ346074
81	11.8	49.2	32	9	AZ797835
C 82	11.8	49.2	36	10	CZ469516
C 83	11.8	49.2	41	2	BG251287
C 84	11.8	49.2	41	9	BH630222
C 85	11.8	49.2	42	10	CL520164
C 86	11.8	49.2	43	10	CL520165
C 87	11.8	49.2	43	1	A1801617
C 88	11.8	49.2	44	8	CA003443
C 89	11.8	49.2	45	2	BG700027
C 90	11.8	49.2	45	7	CV722146
91	11.8	49.2	45	9	BH753340
C 92	11.8	49.2	46	1	AA761099
93	11.8	49.2	46	2	BG115566
94	11.8	49.2	46	9	BH612517
95	11.8	49.2	48	9	BH747445

AJ683869	AJ683869
AZ998247	AZ998247
B1561395	2M0355P03
AZ444974	1M0240A01
AZ510921	1M0355P08
AA903627	OKS902.8
AU106561	AU106561
BB616279	BB616279
AZ983659	2M0263J03
CL521622	SAL3H08 F
AZ829200	2M0106N11
AK216071	Mus muscu
CC183529	XE347 Bay
CG728115	1119098B0
B1906001	603062308
A1254752	qt89f07.x
A1434488	ti45e03.x
AA594397	nl93g10.8
CZ295110	Sus scrofa
CR900779	Sus scrofa
CB221472	1DU013A09
AZ619403	1M0451E09
A1619702	ty52a05.x
AZ434030	1M0220B14
BZ585242	3590.1.30
BW590752	BW590752
AA906151	oj82h01.8
A1788892	uk55c11.x
BE376178	60128534
CZ169359	W136C07 G
CL211000	W139D04 G
AU102361	AU102361
AZ582169	1M0374F20
AZ369507	1M0120E11
AA231183	mw33f06.r
AV949324	AV949324
BX893758	Arabidops
CG710772	1119018G1
CG894689	0394733-0
DE037319	Branchios
AJ595885	Arabidops
BP917129	BP917129
AJ590951	Arabidops
AA971412	op92c11.8
A1270065	qt91f01.x
BP870432	73-Ad-2-7
BP938418	73-Ad-2-7
B1546340	603188832
A1033006	ox22e05.8
A1814794	wk65h12.x
H49581	yo23b02.81
AU106897	AU106897
AU107574	AU107574
A1153891	ud50c12.r
A1608697	tw26b02.x
AJ667773	AJ667773
AZ346074	1M0081L05
AZ797835	2M0054116
CZ469516	c04788-3p
BG251287	602366120
BH630222	1007087E0
CL520164	SAJ3E11 F
CL520165	SAJ3G11 F
A1801617	to91g08.x
CA003443	iv37e10.9
BG700027	602681027
CV722146	YBH--06-J
BH753340	SALK_0287
AA761099	ny13h09.8
BG115566	602317256
BH612517	SALK_0328
BH747445	SALK_0087

96 11.8 49.2 49 1 AI457484 AI457484 tL37h02.x  
97 11.8 49.2 50 1 AI0106874 AI0106874  
98 11.6 48.3 21 9 AZ352290 AZ352290 1M0090M10  
99 11.6 48.3 22 11 TA140A04P AL466405 T. brucei  
100 11.6 48.3 26 9 AQ025266 EP(3)3084  
101 11.6 48.3 34 9 A2389322 A2389322 1M0149G18  
102 11.6 48.3 35 9 AZ497161 A2497161 1M0333G22  
103 11.6 48.3 36 3 B1861680 B1861680 603389356  
104 11.6 48.3 37 8 H39876 H39876 yo57f03.r1  
105 11.6 48.3 43 1 AA514418 AA514418 nf61e03.s  
106 11.6 48.3 43 10 AG194532 AG194532 Pan trogl  
107 11.6 48.3 44 2 BG035308 BG035308 602324932  
108 11.6 48.3 45 9 A2465441 A2465441 1M0275D21  
109 11.6 48.3 46 1 AA989668 AA989668 am71f03.s  
110 11.6 48.3 48 1 AA535087 AA535087 nf84d09.s  
111 11.6 48.3 48 9 A2826757 A2826757 2M0102B17  
112 11.6 48.3 48 9 CC183089 CC183089 XG518 Bay  
113 11.6 48.3 48 9 CC25220 CC25220 XM220 Bay  
114 11.6 48.3 49 1 AA627090 AA627090 ng66e10.s  
115 11.6 48.3 49 1 AA937999 AA937999 o078d03.s  
116 11.6 48.3 49 2 BF218814 BF218814 601882326  
117 11.6 48.3 49 6 CF299145 CF299145 7LEAF--03  
118 11.6 48.3 49 8 H22280 H22280 Y136B03.r1  
119 11.6 48.3 50 1 AA836763 AA836763 of37b12.s  
120 11.6 48.3 50 1 AA847284 AA847284 oe81h02.s  
121 11.6 48.3 50 1 AA918433 AA918433 om38a02.s  
122 11.6 48.3 50 1 AA995631 AA995631 os02e09.s  
123 11.6 48.3 50 1 A1016948 A1016948 ou27e02.x  
124 11.6 48.3 50 1 AU103357 AU103357  
125 11.6 48.3 50 1 AU103358 AU103358  
126 11.6 48.3 50 1 AU103359 AU103359  
127 11.6 48.3 50 1 AU103361 AU103361  
128 11.6 48.3 50 1 AU103492 AU103492  
129 11.6 48.3 50 1 AU103984 AU103984  
130 11.6 48.3 50 1 AA594651 AA594651 nl95g09.s  
131 11.6 48.3 50 11 CR397545 CR397545 Arabidops  
132 11.4 47.5 25 1 AA961707 AA961707 or40e08.s  
133 11.4 47.5 28 9 A2774408 A2774408 2M0003P09  
134 11.4 47.5 30 9 A2854289 A2854289 2M0157M17  
135 11.4 47.5 30 11 TA341A10Q AL493292 T. brucei  
136 11.4 47.5 31 8 H04278 H04278 Y750a08.s1  
137 11.4 47.5 34 2 BG250817 BG250817 602363234  
138 11.4 47.5 37 10 CZ467241 CZ467241 c01543c-5  
139 11.4 47.5 39 11 TA328C02P AL493113 T. brucei  
140 11.4 47.5 43 1 AA059057 AA059057 zf63b10.s  
141 11.4 47.5 43 2 BG915507 BG915507 602815734  
142 11.4 47.5 43 2 BG915507 BG915507 602815734  
143 11.4 47.5 44 10 CL301852 CL301852 P001C09 G  
144 11.4 47.5 45 9 A2656960 A2656960 1M0532015  
145 11.4 47.5 45 9 BH855197 BH855197 SALK\_0864  
146 11.4 47.5 46 9 CC325236 CC325236 XM09T Bay  
147 11.4 47.5 47 10 CG804917 CG804917 1118054G1  
148 11.4 47.5 47 10 CL640880 CL640880 M033F06 G  
149 11.4 47.5 48 8 N68498 N68498 za30a10.s1  
150 11.4 47.5 48 2 BG656805 BG656805 602589152  
151 11.4 47.5 49 2 AA082362 AA082362 Drosophil  
152 11.4 47.5 49 10 AB587732 AB587732 Arabidops  
153 11.4 47.5 50 1 AU104319 AU104319  
154 11.4 47.5 50 1 AU105201 AU105201  
155 11.4 47.5 50 1 AU106877 AU106877  
156 11.4 47.5 50 1 AU107938 AU107938  
157 11.4 47.5 50 1 AU107939 AU107939  
158 11.4 47.5 50 1 AU107940 AU107940  
159 11.4 47.5 50 1 AU107950 AU107950  
160 11.4 47.5 50 1 AU107952 AU107952  
161 11.4 47.5 50 1 A2862767 A2862767 2M0170A09  
162 11.2 46.7 22 9 AA916047 AA916047 oq30d01.s  
163 11.2 46.7 29 6 CF295257 CF295257 30DG5--05  
164 11.2 46.7 29 9 A2961088 A2961088  
165 11.2 46.7 30 1 AJ746842 AJ746842  
166 11.2 46.7 31 1 AA865336 AA865336 og88d08.s  
167 11.2 46.7 32 10 CG783947 CG783947 0180720-0  
168 11.2 46.7 32 10 CG783947 CG783947 0180720-0  
169 11.2 46.7 34 1 AI355502 AI355502  
170 11.2 46.7 34 1 AI634365 AI634365  
171 11.2 46.7 36 10 CZ318895 CZ318895  
172 11.2 46.7 37 1 AA862514 AA862514 ml67501.r  
173 11.2 46.7 37 1 AA869693 AA869693 tq54c02.r  
174 11.2 46.7 37 1 AI446533 AI446533 tq5b05.x  
175 11.2 46.7 37 9 AZ586716 AZ586716 1M0392B19  
176 11.2 46.7 38 10 AG218131 AG218131 Drosophil  
177 11.2 46.7 38 10 AJ587439 AJ587439 Arabidops  
178 11.2 46.7 40 1 AA886208 AA886208 of86c10.s  
179 11.2 46.7 40 1 AA894396 AA894396 of85g05.s  
180 11.2 46.7 40 8 DN954852 DN954852 ic78g03.g  
181 11.2 46.7 40 9 BH618694 BH618694 SALK\_0395  
182 11.2 46.7 40 10 AG218131 AG218131 Drosophil  
183 11.2 46.7 40 10 AG218131 AG218131 Drosophil  
184 11.2 46.7 42 10 AJ594706 AJ594706 Arabidops  
185 11.2 46.7 43 1 AA861070 AA861070 uc32e03.s  
186 11.2 46.7 43 1 AA987068 AA987068 uc74h06.x  
187 11.2 46.7 43 1 AI446161 AI446161 tj07g03.x  
188 11.2 46.7 43 1 AI799404 AI799404 tw56a07.x  
189 11.2 46.7 44 1 AL663346 AL663346  
190 11.2 46.7 44 9 BH619149 BH619149 SALK\_0402  
191 11.2 46.7 45 10 CL301892 CL301892 Po17F01 G  
192 11.2 46.7 45 10 CL301892 CL301892 Po17F01 G  
193 11.2 46.7 45 10 CL658678 CL658678 PR10132a  
194 11.2 46.7 45 10 CL658678 CL658678 PR10132a  
195 11.2 46.7 46 1 AI440092 AI440092 ti56f07.x  
196 11.2 46.7 46 1 AI581136 AI581136 ti56f07.x  
197 11.2 46.7 46 9 BH753392 BH753392 SALK\_0287  
198 11.2 46.7 46 10 CL517566 CL517566 Yx82d01.s1  
199 11.2 46.7 47 8 N29994 N29994  
200 11.2 46.7 47 9 CC178014 CC178014 XC898 Bay  
201 11.2 46.7 47 10 AJ587894 AJ587894 Arabidops  
202 11.2 46.7 49 1 AA687445 AA687445 ns58g06.s  
203 11.2 46.7 49 1 AA101215 AA101215 zn37f07.s  
204 11.2 46.7 49 1 AA478678 AA478678 zv19g04.r  
205 11.2 46.7 49 5 BW963171 BW963171  
206 11.2 46.7 49 5 A2839676 A2839676 2M0135123  
207 11.2 46.7 49 9 BH171096 BH171096 SALK\_0037  
208 11.2 46.7 49 9 BH610503 BH610503 SALK\_0175  
209 11.2 46.7 49 11 TA235H07Q AL481912 T. brucei  
210 11.2 46.7 50 1 AU102452 AU102452  
211 11.2 46.7 50 1 AU103724 AU103724  
212 11.2 46.7 50 1 AU103964 AU103964  
213 11.2 46.7 50 1 AU103965 AU103965  
214 11.2 46.7 50 1 AU103985 AU103985  
215 11.2 46.7 50 1 AU104813 AU104813  
216 11.2 46.7 50 1 AU104814 AU104814  
217 11.2 46.7 50 1 AU104815 AU104815  
218 11.2 46.7 50 1 AU105636 AU105636  
219 11.2 46.7 50 1 AU105846 AU105846  
220 11.2 46.7 50 1 AU105966 AU105966  
221 11.2 46.7 50 1 AU106765 AU106765  
222 11.2 46.7 50 1 AU106766 AU106766  
223 11.2 46.7 50 1 AK212863 AK212863 Mus muscu  
224 11.2 46.7 50 4 AK212863 AK212863 Mus muscu  
225 11.2 46.7 50 10 CZ488116 CZ488116 f05526-3p  
226 11.2 46.7 50 9 AZ461315 AZ461315 1M0267F09  
227 11.2 46.7 23 9 A1682835 A1682835 wc66h10.x  
228 11.2 46.7 25 1 CD746276 CD746276 S6\_E09\_S6  
229 11.2 46.7 30 10 BX662165 BX662165 Arabidops  
230 11.2 46.7 31 1 AI459772 AI459772 ao93c06.x  
231 11.2 46.7 32 2 BF529719 BF529719 602043970  
232 11.2 46.7 32 2 B6819845 B6819845 602781913  
233 11.2 46.7 33 1 AV834163 AV834163  
234 11.2 46.7 34 9 A2492829 A2492829 1M0327J11  
235 11.2 46.7 35 9 AZ767704 AZ767704 1M0567B11  
236 11.2 46.7 35 10 CZ551699 CZ551699 CB1\_4902  
237 11.2 46.7 37 1 AI683527 AI683527 tx67e09.x  
238 11.2 46.7 38 9 A2513025 A2513025 1M0358P20  
239 11.2 46.7 38 1 AI002051 AI002051 ov19h03.s  
240 11.2 46.7 39 1 BH629306 BH629306 1007070B0  
241 11.2 46.7 40 9 BH629306 BH629306 1007070B0

```
242 11 45.8 43 9 A2473927
243 11 45.8 44 8 H92936
c 244 11 45.8 44 10 CL520163
c 245 11 45.8 45 7 CN757501
c 246 11 45.8 45 7 CN733354
c 247 11 45.8 45 9 AQ025518
c 248 11 45.8 46 1 A2802142
c 249 11 45.8 46 1 AA630952
c 250 11 45.8 46 1 AA828900
c 251 11 45.8 47 1 AJ728273
c 252 11 45.8 47 3 BM046304
c 253 11 45.8 47 3 BM047185
c 254 11 45.8 47 6 CD530897
c 255 11 45.8 47 7 CN973499
c 256 11 45.8 47 10 BX121223
c 257 11 45.8 47 10 CL213837
c 258 11 45.8 49 5 C30871
c 259 11 45.8 49 5 A2812913
c 260 11 45.8 50 1 AU103440
c 261 11 45.8 50 1 AU103444
c 262 11 45.8 50 1 AU103445
c 263 11 45.8 50 1 AU106643
c 264 11 45.8 50 1 AU106655
c 265 11 45.8 50 1 AU107016
c 266 10.8 45.0 19 9 A232931
c 267 10.8 45.0 25 1 AA909237
c 268 10.8 45.0 25 10 CZ474839
c 269 10.8 45.0 28 1 A1287864
c 270 10.8 45.0 28 1 A1357706
c 271 10.8 45.0 29 10 CG718745
c 272 10.8 45.0 31 1 AA868659
c 273 10.8 45.0 31 1 A1262512
c 274 10.8 45.0 33 10 AB082692
c 275 10.8 45.0 33 11 TA82C04P
c 276 10.8 45.0 35 9 A2784718
c 277 10.8 45.0 35 10 AL938116
c 278 10.8 45.0 36 7 CV064406
c 279 10.8 45.0 36 8 DN652373
c 280 10.8 45.0 38 1 AU256510
c 281 10.8 45.0 38 2 BG292849
c 282 10.8 45.0 38 10 AJ599761
c 283 10.8 45.0 38 10 AL760976
c 284 10.8 45.0 38 10 AL940456
c 285 10.8 45.0 40 2 BE296536
c 286 10.8 45.0 40 1 A3680963
c 287 10.8 45.0 41 1 AA509356
c 288 10.8 45.0 41 9 BH639962
c 289 10.8 45.0 42 9 BH626517
c 290 10.8 45.0 43 1 A1423979
c 291 10.8 45.0 43 2 BG866682
c 292 10.8 45.0 44 5 BX620428
c 293 10.8 45.0 44 8 N47451
c 294 10.8 45.0 44 10 CZ194596
c 295 10.8 45.0 44 11 TA131E01P
c 296 10.8 45.0 45 9 BH810609
c 297 10.8 45.0 46 1 AA847140
c 298 10.8 45.0 46 1 AA867748
c 299 10.8 45.0 46 1 A1793579
c 300 10.8 45.0 46 1 A1793579
```

## ALIGNMENTS

```
RESULT 1
AUI07435
LOCUS AUI07435 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION AUI07435 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AUI07435.1 GI:13556956
VERSION AUI07435.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
```

```
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EXBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LNG15924"
/clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match 62.5%; Score 15; DB 1; Length 50;
Best Local Similarity 78.3%; Pred. No. 7.3e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 GGGTCGACGCGCGCCATGGGG 24
||| ||||| ||||| ||||| |||||
Db 5 GGGGCCAGCGCTCGGCATGCGCG 27
||| ||||| ||||| ||||| |||||
RESULT 2
AUI07436
LOCUS AUI07436 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION AUI07436 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION AUI07436
VERSION AUI07436.1 GI:13556957
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
REFERENCE
AUTHORS Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EXBO Rep. 2 (5), 388-393 (2001)
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
```

```

/db_xref="taxon:9606"
/clone="ADSE00456"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      62.5%; Score 15; DB 1; Length 50;
Best Local Similarity 78.3%; Pred. No. 7.3e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGGTCACGCGTCGCCATGGGG 24
    ||| ||||| || ||||| ||
Db 5 GGGCCACGCGCTCGCATGGCG 27

RESULT 3
AJ796516
LOCUS      AJ796516 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
DEFINITION 018_3_11_d04, mRNA sequence.
ACCESSION  AJ796516.1 GI:51111844
VERSION     AJ796516.1
KEYWORDS    Antirrhinum majus (snapdragon)
SOURCE      Antirrhinum majus
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Plantaginales; Antirrhineae;
Antirrhinum.
REFERENCE   1 (bases 1 to 49)
AUTHORS     Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H.,
Saedler, H. and Zachgo, S.
TITLE       Characterization of Antirrhinum Petal Development and
            Identification of Target Genes of the Class B MADS Box Gene
            DEFICIENS
JOURNAL     Plant Cell 16 (12), 3197-3215 (2004)
PUBMED     15539471
COMMENT     Contact: Schwarz-Sommer Z
            Molekulare Pflanzen-genetik
            MPI fuer Zuechtungs-forschung
            Carl-von-Linne Weg 10, D-50829, Germany.
            Location/Qualifiers
FEATURES             source
    mol_type="mRNA"
    /db_xref="taxon:4151"
    /clone="018_3_11_d04"
    /tissue_type="whole plant"
    /clone_lib="Antirrhinum majus whole plant"

ORIGIN
Query Match      61.7%; Score 14.8; DB 1; Length 49;
Best Local Similarity 88.9%; Pred. No. 8.9e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TCCACGCGTCGCATGGG 22
    ||| ||||| ||||| ||
Db 26 TCCACGCGCGCCAAAG 43

RESULT 4
AA878878/c
LOCUS      AA878878/c
DEFINITION of88h03.s1 NCI CGAP L15 Homo sapiens cDNA clone IMAGE:1437461.3,
similar to WP:F59E12.9 Cell1534 ; contains PTR5.t3 MSRI repetitive
element ;, mRNA sequence.
ACCESSION  AA878878
VERSION     AA878878.1 GI:2987843
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

```

```

REFERENCE   1 (bases 1 to 46)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgaps-r@mail.nih.gov
            unknown library type
            Trace considered overall poor quality
            Insert Length: 315 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
            Location/Qualifiers
FEATURES             source
    mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:1437461"
    /tissue_type="hepatic adenoma"
    /lab_host="DH10B"
    /clone_lib="NCI CGAP L15"
    /note="Organ: Liver; Vector: pCMV-SPORT4; Site 1: SalI;
            Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 0.8 kb."

ORIGIN
Query Match      60.0%; Score 14.4; DB 1; Length 46;
Best Local Similarity 75.0%; Pred. No. 1.3e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTCGCCATGGGG 24
    ||| ||| || ||||| |||||
Db 45 GGGGCCCTCCATCGCCAGGGGG 22

RESULT 5
CF661152/c
LOCUS      CF661152
DEFINITION CcLM09a34a07f1 Carp muscle library 1 Cyprinus carpio cDNA clone
34a07_5', mRNA sequence.
ACCESSION  CF661152
VERSION     CF661152.2 GI:50743359
KEYWORDS    EST.
SOURCE      Cyprinus carpio (common carp)
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprinus.
REFERENCE   1 (bases 1 to 47)
AUTHORS     Gracey, A.Y., Fraser, E.J., Li, W., Fang, Y., Taylor, R.R., Rogers, J.,
            Brass, A. and Cossins, A.R.
TITLE       Coping with cold: An integrative, multitissue analysis of the
            transcriptome of a poikilothermic vertebrate
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 101 (48), 16970-16975 (2004)
PUBMED     15550548
COMMENT     On Oct 7, 2003 this sequence version replaced gi:37558281.
            Contact: Andrew R. Cossins
            Laboratory for Environmental Gene Regulation
            University of Liverpool
            School of Biological Sciences, The Biosciences Building, Crown
            Street, Liverpool, United Kingdom, L69 7ZB
            Tel: +44(0)151-795-4510
            Fax: +44(0)151-795-4431
            Email: cossins@liv.ac.uk
            Vector has been trimmed from this EST.
            Plate: 34 row: a column: 07
            Seq primer: Triplex 5' LD (5'-CTCGGAGCGCCCATGTGTGGT-3')
            High quality sequence stop: 47
            POLYA=No.
            Location/Qualifiers
FEATURES             source
    mol_type="mRNA"

```

/db\_xref="taxon:7962"  
/clone="34a07"  
/sex="Male & female"  
/tissue type="Muscle"  
/dev stage="Adult"  
/lab host="E.coli Electromax DH10B"  
/clone lib="Carp muscle library 1"  
/note="Vector: pTriplex2; Site 1: sf11 GCCATTAGGGCC;  
Site 2: sf11 GCCCGCTCGGCC; Serially subcloned cDNA  
library prepared from muscle of warm, cold and hypoxia  
challenged animals"

## ORIGIN

Query Match 59.2%; Score 14.2; DB 6; Length 47;  
Best Local Similarity 84.2%; Pred. No. 1.6e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GTCCAGCTGCGCCATGGG 22  
|||||  
Db 47 GTCCAGAGAGTGGCCATGGG 29

## RESULT 6

AA993146/c

LOCUS

DEFINITION ot77a10.81 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone  
IMAGE:1622778 3' similar to SW:FBRL\_HUMAN P22087 FIBRILLARIN ;  
mRNA sequence.

ACCESSION AA993146

VERSION AA993146.1 GI:3179691

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (infoimage.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

1. 49  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1622778"  
/dev stage="8-9 weeks"  
/lab host="DH10B"  
/clone lib="Soares total fetus Nb2HF8 9w"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from pooled 8-9 week  
(total) fetus material with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 59.2%; Score 14.2; DB 1; Length 49;  
Best Local Similarity 84.2%; Pred. No. 1.6e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCATGGGG 24  
|||||  
Db 33 CCTTCTGGCCATGGGG 15

## RESULT 7

AI098584/c

LOCUS

DEFINITION ue29h07.x1 Sugano mouse liver mlia Mus musculus cDNA clone  
IMAGE:1481821 3' similar to SW:A2HS MOUSE P29699  
ALPHA-2-HS-GLYCOPROTEIN PRECURSOR ; mRNA sequence.

ACCESSION AI098584

VERSION AI098584.1 GI:3448109

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 49)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

TITLE

JOURNAL

COMMENT

The WashU-HMI Mouse EST Project  
Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (infoimage.llnl.gov) for further information.

MGI:930177

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: custom primer used

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

1. 49  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1481821"  
/sex="female"  
/dev stage="adult"  
/lab host="DH10B"  
/clone lib="Sugano mouse liver mlia"  
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII  
(CACTGTGTG); Site 2: DraIII (CAACATGTG); 1st strand cDNA  
was primed with an oligo(dT) primer  
[ATGTGGCTTTTTTTTTTTT]; double-stranded cDNA was  
ligated to a DraIII adaptor [TGTGGCTACTGG], digested  
and cloned into distinct DraIII sites of the pME18S-FL3  
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should  
be used to isolate the cDNA insert. Size selection was  
performed to exclude fragments <1.5kb. Library  
constructed by Dr. Sumio Sugano (University of Tokyo  
Institute of Medical Science). Custom primers for  
sequencing: 5' end primer CTTCTGCTCTAAAGCTCG and 3' end  
primer CGACCTGCAGCTCGACACA."

## ORIGIN

Query Match 56.7%; Score 13.6; DB 1; Length 49;  
Best Local Similarity 80.0%; Pred. No. 2.9e+05;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGTCACGCTGGCCATGGG 22

|||||



```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2219127"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Ov23"
/notes="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"

ORIGIN
Query Match      55.8%; Score 13.4; DB 1; Length 40;
Best Local Similarity 73.9%; Pred. No. 3.5e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2 GGGTCCAGCGTCGCCATGGGG 24
      ||||| ||| | | | | | |
Db   35 GGGTCCCGGGCGGCCGGGGGG 13

RESULT 11
AA863355
LOCUS
DEFINITION
oh04e09.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1456840 3'
similar to SW:PRPB_HUMAN P02814 PROLINE-RICH PEPTIDE P-B.; mRNA
sequence.
AA863355
VERSION
AA863355.1 GI:2955834
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 43)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 606 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1456840"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid3"
/notes="Organ: kidney; Vector: p7T73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p7T73 vector. mRNA
source: 2 pooled kidneys. Library went through one round

of normalization. Library constructed by Bento Soares and
M. Fatima Bonaldo. "

ORIGIN
Query Match      55.8%; Score 13.4; DB 1; Length 43;
Best Local Similarity 73.9%; Pred. No. 3.5e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 GGGGTCCAGCGTCGCCATGGGG 23
      ||||| ||||| | | | | |
Db   17 GGGGGCCAGCGGTCCCGAGGGGG 39

RESULT 12
AA2434579
LOCUS
DEFINITION
LM022111OF Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0221110 F, genomic survey sequence.
AA2434579
ACCESSION
AA2434579.1 GI:10558592
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 33)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0221 row: I column: 10
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1. .33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0221110"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to

```

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 54.2%; Score 13; DB 9; Length 33;  
 Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCATGG 21  
 ||||| ||||| ||||| |||||  
 Db 7 GGGGTCAAGCGTGGGTGGTG 27

RESULT 13  
 BI548958  
 LOCUS  
 DEFINITION 603188912F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5260442 5',  
 mRNA sequence.

ACCESSION BI548958  
 VERSION BI548958.1 GI:15436270  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 38)  
 NTH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM11656 row: g column: 03  
 High quality sequence stop: 38.

## FEATURES

Location/Qualifiers  
 1..38  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5260442"  
 /tissue\_type="hippocampus"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_95"  
 /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 54.2%; Score 13; DB 3; Length 38;  
 Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GTCCAGCGTGGCCATGGGG 24  
 ||||| ||||| ||||| |||||  
 Db 11 GTCAGCGCGGGGCCAGGGGG 31

## RESULT 14

LOCUS AU104320  
 DEFINITION AU104320 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 HEP06849, mRNA sequence.

ACCESSION AU104320  
 VERSION AU104320.1 GI:13553841  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 TITLE Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 PUBMED 11375929  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).

## FEATURES

Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="HEP06849"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 50;  
 Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCATGG 21  
 ||||| ||||| ||||| |||||  
 Db 10 GGTGCCATCGTGGCATGG 30

## RESULT 15

LOCUS AU105443  
 DEFINITION AU105443 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 KAT00863, mRNA sequence.

ACCESSION AU105443  
 VERSION AU105443.1 GI:13554964  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 TITLE Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 PUBMED 11375929  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan



Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).

FEATURES  
 source  
 Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="KAT00863"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 50;  
 Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 GTCCAGCGTGGCCCATGGGG 24  
 ||||| ||||| ||||| |||||  
 Db 26 GCCCAGCGCGCCCATGGGTG 46

## RESULT 16

AU107884  
 LOCUS AU107884 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 DEFINITION CAS03672, mRNA sequence.

ACCESSION AU107884

VERSION AU107884.1 GI:13557406

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

PUBMED 11375929

COMMENT

Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).

FEATURES  
 source  
 Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CAS03672"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 50;  
 Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCCATGG 21  
 ||||| ||||| ||||| |||||  
 Db 18 GCGAGCGCGCGCCCATGG 38

## RESULT 17

AU107885

LOCUS AU107885  
 DEFINITION AU107885 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 HSI05714, mRNA sequence.

ACCESSION AU107885

VERSION AU107885.1 GI:13557407

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

PUBMED 11375929

COMMENT Contact: Yutaka Suzuki

Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).

FEATURES

source

Location/Qualifiers  
 1..50  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="HSI05714"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 50;  
 Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCCATGG 21

||||| ||||| ||||| |||||

Db 20 GCGAGCGCGCGCCCATGG 40

## RESULT 18

AU107886

LOCUS AU107886  
 DEFINITION AU107886 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 HSI05735, mRNA sequence.

ACCESSION AU107886

VERSION AU107886.1 GI:13557408

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
 Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale  
 mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

PUBMED 11375929

COMMENT Contact: Yutaka Suzuki

Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

## FEATURES

source  
1.50  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="HS105735"  
/clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 54.2%; Score 13; DB 1; Length 50;  
Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCATGG 21

Db 20 GGGAGCGCGGAGGCCATGG 40

## RESULT 19

R85071/c

## LOCUS

DEFINITION R85071 50 bp mRNA linear EST 14-AUG-1995  
Y042d10.r1 Soares adult brain N2b4HB55V Homo sapiens cDNA clone  
IMAGE:180595 5' similar to gb:J05096\_rna1  
SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN (HUMAN); mRNA  
sequence.

## ACCESSION

VERSION R85071.1 GI:943477

## KEYWORDS

SOURCE EST.

## ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

AUTHORS

1 (bases 1 to 50)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Mafr, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.

The WashU-Merck EST Project

## TITLE

JOURNAL

COMMENT

Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 2244

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 2244 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

Location/Qualifiers

## FEATURES

source

1.50  
/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3827242"

/db\_xref="taxon:9606"

/clone="IMAGE:180595"

/sex="Male"

/dev\_stage="55-year old"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares adult brain N2b4HB55y"

/note="Organ: brain; Vector: pT7T3D (Pharmacia) with a

modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; 1st

## ORIGIN

Query Match 54.2%; Score 13; DB 8; Length 50;  
Best Local Similarity 76.2%; Pred. No. 5.1e+05;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGTCCAGCGTGGCCATGGG 23

Db 34 GGTCCAGGATGGCGTCGGGG 14

## RESULT 20

BF384787

## LOCUS

DEFINITION 602046279F1 NCI\_CGAP\_Li9 Mus musculus cDNA clone IMAGE:4195795 5',  
mRNA sequence.

## ACCESSION

VERSION BF384787.1 GI:11366092

## KEYWORDS

SOURCE EST.

## ORGANISM

Mus musculus (house mouse)  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 34)  
NTH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: csapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LIAM9531 row: n column: 20

High quality sequence stop: 34.

Location/Qualifiers

## FEATURES

source

1.34  
/organism="Mus musculus"

/mol\_type="mRNA"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clones="IMAGE:4195795"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NCI CGAP Li9"

/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.9 kb. Constructed by Life

Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Query Match 53.3%; Score 12.8; DB 2; Length 34;  
Best Local Similarity 70.8%; Pred. No. 6.2e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

QY 1 GGGGTCACGCGGCCCATGGGG 24
    ||||| ||||| ||||| |||||
Db 8 GGGGCCACGCTGGGGCCACTCGG 31

RESULT 21
AI755616
LOCUS      37 bp      mRNA      linear      EST 18-JAN-2000
DEFINITION Eimeria S5-2 Sporozoite stage Eimeria tenella cDNA
            5' similar to TR:Q28583 Q28583 KAP5.4 KERATIN PROTEIN. ;, mRNA
            sequence.
ACCESSION  AI755616
VERSION     AI755616.1  GI:5149339
KEYWORDS    Eimeria tenella
SOURCE      Eimeria tenella
ORGANISM    Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
            Eimeria.
REFERENCE   1 (bases 1 to 37)
AUTHORS    Liberator,P., Diaz,C., Tang,K., Marra,M., Hillier,L., Kucaba,T.,
            Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B.,
            Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D.,
            Harvey,N., Schurk,R., Ritter,E., Kohn,S., Florence,N., Shin,T.,
            Jackson,Y., Cardenas,M., McCann,R., Waterston,R., Wilson,R. and
            Sibley,D.
TITLE      WashU-Merck Eimeria tenella project
JOURNAL    Unpublished (1999)
COMMENT    Contact: David Sibley, Ph.D.
            WashU-Merck Eimeria tenella project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@wustl.wustl.edu
            Contact David Sibley (toxest@borcim.wustl.edu) for further
            information relating to organism, libraries, or clone availability.
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40RP from Gibco
            High quality sequence stop: 1.
FEATURES   Location/Qualifiers
            1..37
            /organism="Eimeria tenella"
            /mol_type="mRNA"
            /strain="LS18"
            /db_xref="taxon:5802"
            /dev_stage="Sporozoite"
            /lab_host="SOLR E. coli"
            /clone_lib="Eimeria S5-2 Sporozoite stage"
            /note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
            XhoI; Sporozoites were obtained from in vitro sporulated
            and excysted oocysts of E. tenella grown in chickens.
            cDNA was synthesized from poly mRNA using an oligo-dT
            primer containing a XhoI site. Following second strand
            synthesis, EcoRI adapters were ligated to the cDNA and
            products were size-selected on Sephacryl S500. cDNAs were
            digested with EcoRI/XhoI and cloned into lambda Zap II
            (Stratagene). Clones were converted to phagemids by mass
            excision using ExAssist helper phage and SOLR cells
            (Stratagene). Insert sizes range from 1.2-2.9 kb."
ORIGIN
Query Match      53.3%; Score 12.8; DB 1; Length 37;
Best Local Similarity 70.8%; Pred. No. 6.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGTCACGCGGCCCATGGGG 24
    ||||| ||||| ||||| |||||
Db 5 GGGGCCACGCGGCCCATGGGG 28

RESULT 22
BI597957
LOCUS      39 bp      mRNA      linear      EST 29-JUN-2004
DEFINITION AJ683869 CSEORAN04 Sus scrofa cDNA clone C0001803_F11, mRNA
            sequence.
ACCESSION  AJ683869
VERSION     AJ683869.1  GI:49416459
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1 (bases 1 to 39)
AUTHORS    Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE      Development of cDNA and EST resources for studying reproduction and

```

```

LOCUS      38 bp      mRNA      linear      EST 07-SEP-2001
DEFINITION 603249661F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5301590 5',
            mRNA sequence.
ACCESSION  BI597957
VERSION     BI597957.1  GI:15490896
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 38)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
JOURNAL
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: L2AM11763 row: i column: 15
            High quality sequence stop: 38.
FEATURES   Location/Qualifiers
            1..38
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5301590"
            /tissue_type="hypothalamus"
            /lab_host="DH10B"
            /clone_lib="NIH_MGC_96"
            /note="Organ: brain; Vector: pBluescriptR (modified
            pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
            (gtcgag); Oligo-dT primed using primer
            5'-TTTTTTTTTTTTTTVN-3', size-selected for average
            insert size 2.3 kb and normalized to 200 ng. This is a
            primary library enriched for full-length clones and
            constructed using the cap-trapper method (Carninci, in
            preparation). Library constructed by M. Brownstein
            (NIH/NHGRI, National Institutes of Health). Note: this is
            a NIH_MGC Library."
ORIGIN
Query Match      53.3%; Score 12.8; DB 3; Length 38;
Best Local Similarity 70.8%; Pred. No. 6.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGTCACGCGGCCCATGGGG 24
    ||||| ||||| ||||| |||||
Db 6 GAGGCCCTGCGAGCCCATGAGG 29

RESULT 23
AJ683869/c
LOCUS      39 bp      mRNA      linear      EST 29-JUN-2004
DEFINITION AJ683869 CSEORAN04 Sus scrofa cDNA clone C0001803_F11, mRNA
            sequence.
ACCESSION  AJ683869
VERSION     AJ683869.1  GI:49416459
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1 (bases 1 to 39)
AUTHORS    Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE      Development of cDNA and EST resources for studying reproduction and

```

```
JOURNAL
COMMENT
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with the phred
v0.020425.c. vector identified by cross_match with the _minscore 20
and _mismatch 12 options. Vector:pBluescriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1. .39
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001803_F11"
/tissue_type="uterus"
/clone_lib="CSEQUAN04"
/notes="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."

ORIGIN
Query Match 53.3%; Score 12.8; DB 1; Length 39;
Best Local Similarity 70.8%; Pred. No. 6.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTCGCCATGGGG 24
|||||
Db 26 GGGTCCAAACAGGCTCCAGGAGG 3

RESULT 24
AZ998247/c
LOCUS
DEFINITION
40 bp DNA linear GSS 27-APR-2001
2M0285P03F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0285P03 F, genomic survey sequence.
AZ998247
ACCESSION
AZ998247.1 GI:13869474
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0285 row: P column: 03
Seg primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers
1. .40
/organism="Mus musculus"
/mol_type="genomic DNA"

FEATURES
source
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0285P03"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 53.3%; Score 12.8; DB 9; Length 40;
Best Local Similarity 70.8%; Pred. No. 6.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTCGCCATGGGG 24
|||||
Db 29 GGCCTCCAGCGGTGAGCGCGGGG 6

RESULT 25
BI561395
LOCUS
DEFINITION
41 bp mRNA linear EST 05-SEP-2001
603255161F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5297390 5',
mRNA sequence.
BI561395
ACCESSION
BI561395.1 GI:15448709
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 41)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
CDNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11752 row: j column: 15
High quality sequence stop: 41.
Location/Qualifiers
1. .41
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5297390"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"

FEATURES
source
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0285P03"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [G14732141g1b1AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

```
Query Match      53.3%; Score 12.8; DB 9; Length 44;
Best Local Similarity 70.8%; Pred. No. 6.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

Qy 1 GGGTCCAGCGTGCCTCGGG 24  
||| | | | | | | |  
Db 12 GGGCGGGCGGGGCCATCGGG 35

RESULT 27					
AZ510921					
LOCUS					
DEFINITION	AZ510921	48 bp	DNA	linear	GSS 05-OCT-2000
	1M0355P08R	Mouse 10kb	plasmid	UUGCIM library	Mus musculus genomic
	clone UUGCIM0355P08 R,	genomic survey	sequence.		

```

VERSION  AZ510921.1  GI:10692237
KEYWORDS GSS.

```

**Mus musculus**  
ORGANISM

REFERENCE 1 (bases 1 to 48)

**AUTHORS**

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niedermauern, A. and Wright, D., Weiss, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT  
84112, USA

**Tel: 801 585 5606**  
**Fax: 801 585 7177**

Insert Length: 10000 Std Error: 0.00

Plate: 0355 row: P column: 08  
Seq primer: CACACAGGAAACAGCTATGACC

**FEATURES**

High quality sequence stop: 48.  
Location/Qualifiers

source

```
/organism="Mus musculus"  
/mol_type="genomic DNA"
```

```
/db_xref="taxon:10090"  
/clone="UUGC1M0355P08"
```

```

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, p-
/crone_lib="Mouse 10kb plasmid UUGC1M library"

```

**musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource**

was hydrodynamically sheared by repeated passage through a

was blunt end-repaired with T4 DNA polymerase and 14

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [gi14732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 53.3%; Score 12.8; DB 9; Length 48;  
Best Local Similarity 70.8%; Pred. No. 6.2e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCATGGGG 24  
23 GTGTCTCTGGTGGCCCTCTGGG 46

## RESULT 28

AA903627 49 bp mRNA linear EST 09-JUN-1998  
LOCUS ok59902.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1518290 3'  
DEFINITION similar to SW:ICLN HUMAN P54105 CHLORIDE CONDUCTANCE REGULATORY  
PROTEIN ICLN ;, mRNA sequence.

ACCESSION AA903627.1 GI:3038750

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 49)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.  
Cloning by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)

Insert Length: 555 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

## FEATURES

Location/Qualifiers  
1..49  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1518290"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP\_GC4"

/note="Vector: pRT3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pRT3  
vector. Library is normalized. Library was constructed by  
Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 53.3%; Score 12.8; DB 1; Length 49;  
Best Local Similarity 70.8%; Pred. No. 6.2e+05;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCATGGGG 24  
2 GGGCCCTTCGTGGGCCAGGGG 25

## RESULT 29

AU106561 50 bp mRNA linear EST 28-JAN-2004  
LOCUS AU106561 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION KAT03341, mRNA sequence.

ACCESSION AU106561

VERSION AU106561.1 GI:13556082

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL PUBMED

COMMENT 11375929

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: [yu Suzuki@ims.u-tokyo.ac.jp](mailto:yu Suzuki@ims.u-tokyo.ac.jp)

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full

length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),

149-156 (1997).

FEATURES Location/Qualifiers

1..50

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="KAT03341"

/clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 53.3%; Score 12.8; DB 1; Length 50;  
Best Local Similarity 87.5%; Pred. No. 6.2e+05;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGGCC 17  
35 GGGTCCGCGCTGGCC 50

## RESULT 30

BB616279

LOCUS

DEFINITION BB616279 RIKEN full-length enriched, adult male testis Mus musculus  
cDNA clone 4931436G19 5', mRNA sequence.

ACCESSION BB616279

VERSION BB616279.1 GI:16456400

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 50)

Akakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,



```

Qy 1 GGGTCCAGCGTGCCTCATGGGG 24
    |||||
Db 32 GGGTCCAGCGTTCGAGAGGGGG 9

RESULT 32
CL521622/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) genomic, genomic survey
sequence.
ACCESSION
CL521622
VERSION
CL521622.1 GI:46148422
KEYWORDS
GSS.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 50)
Sallaud,C., Gay,C., Larmande,P., Bes,M., Piffanelli,P., Plegu,B.,
Droc,G., Regad,F., Bourgeois,E., Meynard,D., Perin,C.,
Ghesquiere,A., Delsevy,M., Glaszmann,J.C. and Guiderdoni,E.
High throughput T-DNA insertion mutagenesis in rice: A first step
towards in silico reverse genetics
JOURNAL
Plant J. (2004) In press
COMMENT
Contact: Guiderdoni
UMR PIA Biotrop program
CIRAD
TA 40/03 ave Agropolis 34398 Montpellier cedex 5 FRANCE
Tel: 33467615629
Fax: 33467615605
Email: emmanuel.guiderdoni@cirad.fr
Class: TDNA tagged.
FEATURES
    source
        location/Qualifiers
            1..50
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="genomic DNA"
                /cultivar="Nipponbare"
                /db_xref="taxon:39947"
                /clone_lib="Flanking Sequence Tag of Oryza sativa T-DNA
                insertion lines"
                /note="PCR was performed on DNA of primary transformants
                of Oryza sativa plants. The DNA fragment(s) resulting of
                PCR were directly sequenced from the left border to
                determine the genomic sequence flanking the insertion.
                T-DNA derived sequences were removed. Information to order
                the corresponding mutant line and a link to a database
                providing a graphical display is available from June 2004
                at http://genoplante-info.infobiogen.fr/oryzatagline/.
                This sequence has been generated in the framework of the
                French plant genomics program Genoplante
                (http://www.genoplante.org and
                http://genoplante-info.infobiogen.fr)."
ORIGIN
Query Match 53.3%; Score 12.8; DB 10; Length 50;
Best Local Similarity 70.8%; Pred. NO. 6.2e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGCCTCATGGGG 24
    |||||
Db 46 GGGCTGAGCGCGCTCCATAGGAG 23

RESULT 33
AZ829200/c
LOCUS
DEFINITION
2M0106N11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0106N11 R, genomic survey sequence.
ACCESSION
AZ829200
VERSION
AZ829200.1 GI:12999108

```

```

KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0106 row: N column: 11
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
FEATURES
    source
        location/Qualifiers
            1..28
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0106N11"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
ORIGIN
Query Match 52.5%; Score 12.6; DB 9; Length 28;
Best Local Similarity 78.9%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGTCCAGCGTGCCTCATGG 21
    |||||
Db 21 GGTCTCCGTGGGCCATCG 3

RESULT 34
AK216071
LOCUS
DEFINITION
Mus musculus cDNA, clone:Y2G0137B14, strand:plus,
reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST0000040729, based
on BLAT search.

```







**SOURCE**  
**ORGANISM** Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 49)  
**REFERENCE**  
**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Life technologies catalog #: 11547-015  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
 Insert Length: 1030 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..49  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2133436"  
 /tissue\_type="lymphoma, follicular mixed small and large cell"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP\_Lym12"  
 /note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

**FEATURES**  
 source  
 1..49  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2133436"  
 /tissue\_type="lymphoma, follicular mixed small and large cell"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP\_Lym12"  
 /note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

**ORIGIN**  
 Query Match 52.5%; Score 12.6; DB 1; Length 49;  
 Best Local Similarity 78.9%; Pred. No. 7.5e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 GGGGTCCAGCGTGGCCAT 19  
 ||||| |||||  
 Db 9 GGGGCCCGCCGGGCCAT 27

**RESULT 40**  
**AA594397**  
**LOCUS** n193g10.81 NCI CGAP Col0 Homo sapiens cDNA clone IMAGE:1058274 3'  
**DEFINITION** similar to gb:J03905 GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30  
**PRECUSOR** (HUMAN); mRNA sequence.  
**AA594397**  
**VERSION** AA594397.1 GI:2409747  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 49)  
**REFERENCE**  
**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
 Insert Length: 1930 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..49  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1058274"  
 /tissue\_type="colon tumor RER+"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Col0"  
 /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4)."

**ORIGIN**  
 Query Match 52.5%; Score 12.6; DB 1; Length 49;  
 Best Local Similarity 78.9%; Pred. No. 7.5e+05;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 4 GTCCAGCGTGGCCATGGG 22  
 ||||| |||||  
 Db 24 GTCCAGCATTCACATGGG 42

**RESULT 41**  
**CZ295110**  
**LOCUS** P070E01 GGTC Gene Trap Library GV18C05 Mus musculus cDNA clone  
**DEFINITION** P070E01, mRNA sequence.  
**ACCESSION** CZ295110  
**VERSION** CZ295110.1 GI:61682860  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 49)  
**REFERENCE**  
**AUTHORS** Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F., Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.  
**TITLE** A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
**PUBMED** 12904583  
**COMMENT** Contact: GGTC  
 German Genetrap Consortium (GGTC)  
 Email: [info@genetrap.de](mailto:info@genetrap.de)  
 FlipRAGeoC2 gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at: [http://genetrap.gsf.de/project/web\\_new/database/result\\_clone.html?clone\\_id=P070E01](http://genetrap.gsf.de/project/web_new/database/result_clone.html?clone_id=P070E01). ES cell line harboring insertion mutation of target gene is available at: [http://genetrap.gsf.de/project/web\\_new/order\\_clones/howtoorder.htm](http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm)  
 1' Inhouse Sequence Identifier: 25645  
 Class: Gene Trap.  
 Location/Qualifiers  
 1..49  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129 Sv"  
 /db\_xref="taxon:10090"

**FEATURES**  
 source  
 1..49  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129 Sv"  
 /db\_xref="taxon:10090"

```

/clone="P070E01"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells [C57BL/6J x 129S6/SvEvTac] F1"
/clone_lib="GTC Gene Trap Library GV18C05"
/note="Vector: FlpROSAceoc+2"

ORIGIN
Query Match          52.5%; Score 12.6; DB 10; Length 49;
Best Local Similarity 78.9%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 CCACGCGTGGCCATGGGG 24
    ||||| ||||| ||||| |||||
Db 8 CAAGCGCGCCGACGGGG 26

RESULT 42
CR900779/c
LOCUS CR900779 49 bp DNA linear GSS 23-NOV-2004
DEFINITION Sus scrofa BES, genomic survey sequence.
ACCESSION CR900779
VERSION CR900779.1 GI:56225276
KEYWORDS GSS; Bac-end sequence BES; Genome Survey Sequence.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
          Sus.
REFERENCE 1 (bases 1 to 49)
AUTHORS Rogel-Gallard,C., Bourgeaux,N., Billault,A., Vaiman,M. and
          Chardon,P.
TITLE Construction of a swine BAC library: application to the
JOURNAL characterization and mapping of porcine type C endoviral elements
PUBMED Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
1049899
REFERENCE 2 (bases 1 to 49)
AUTHORS Chardon,P., Iannuccelli,N., Roig,A., Dossat,C., Demars,J.,
          Rogel-Gallard,C., Roy,A., Schibler,L. and Milan,D.
TITLE A physical map of the swine genome
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 49)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secre@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
FEATURES
source
Location/Qualifiers
1..49
/organism="Sus scrofa"
/mol_type="genomic DNA"
/strain="Large White"
/db_xref="taxon:9823"
/clone="bi0280E04"
/sex="male"
/cell_type="fibroblast"
/clone_lib="SBAB"
/note="Genoscope sequence ID : IH0AAA28BF12FM1"

ORIGIN
Query Match          52.5%; Score 12.6; DB 11; Length 49;
Best Local Similarity 78.9%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGGCCATGGGG 23
    ||||| ||||| ||||| |||||
Db 49 TCCAGTGTGCCCAACGGG 31

RESULT 43
CR221472
LOCUS CR221472 50 bp mRNA linear EST 10-FEB-2003
DEFINITION lDuo13A09 Bos taurus Duodenum #1 library Bos taurus cDNA, mRNA

```

```

sequence.
ACCESSION CB221472
VERSION CR221472.1 GI:28291986
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
          Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 50)
AUTHORS Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Sensen,C.W.,
          Gordon,P.M.K. and Moore,S.S.
TITLE Gene Expression Profiling of the Bovine Gastrointestinal Tract
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Stephen Moore
          Beef Genomics Laboratory
          Dept of AFNS, University of Alberta
          410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
          Tel: 780 492 0169
          Fax: 780 492 4265
          Email: stephen.moore@ualberta.ca
          POLYA-No.
FEATURES
source
Location/Qualifiers
1..50
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Smooth muscle"
/cell_type="Simple columnar epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'strain"
/clone_lib="Bos taurus Duodenum #1 library"
/note="Organ: Intestine/duodenum; Vector: Uni-ZAPXR;
          Site_1: EcoRI; Site_2: Xho I"

ORIGIN
Query Match          52.5%; Score 12.6; DB 6; Length 50;
Best Local Similarity 78.9%; Pred. No. 7.5e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGTCCAGCGTGGCCATGG 21
    ||||| ||||| |||||
Db 2 GGGCCGCGTGTGCGGTGG 20

RESULT 44
AZ619403
LOCUS AZ619403 23 bp DNA linear GSS 13-DEC-2000
DEFINITION lM0451E09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0451E09 R, genomic survey sequence.
ACCESSION AZ619403
VERSION AZ619403.1 GI:11741593
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausen,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL plasmid inserts
COMMENT Unpublished (2000)
          Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606

```

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0451 row: E column: 09  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 23.  
 Location/Qualifiers  
 1. .23

#### FEATURES

source  
 1. .23  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0451E09"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4731114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

#### ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 23;  
 Best Local Similarity 72.7%; Pred. No. 9.1e+05;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTCCAGGTCGCGCATGGGG 24  
 ||||| ||||| |||||  
 Db 1 GGTCCAGGTCGCGCATGGGG 22

#### RESULT 45

A1619702/c  
 LOCUS  
 DEFINITION ty52a05.x1 NCI CGAP Ut2 Homo sapiens cDNA clone IMAGE:2282672 3',  
 similar to TR:O00599 O00599 CON1.; contains element MSR1 repetitive  
 element ; mRNA sequence.

ACCESSION A1619702.1 GI:4628828

VERSION A1619702.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

1 (bases 1 to 37)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Insert Length: 2109 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1

POLYA=No.

#### FEATURES

source  
 1. .37  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2282672"  
 /tissue\_type="moderately-differentiated endometrial  
 adenocarcinoma, 3 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP\_Ut2"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.85 kb. Life Technologies catalog #:  
 11539-012"

#### ORIGIN

Query Match 51.7%; Score 12.4; DB 1; Length 37;  
 Best Local Similarity 72.7%; Pred. No. 9.1e+05;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGTCCAGGTCGCGCATGGG 22  
 ||||| ||||| |||||  
 Db 22 GGGCCCCCGGGCGCCCTGGG 1

#### RESULT 46

AZ434030  
 LOCUS  
 DEFINITION 1M0220B14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0220B14 F, genomic survey sequence.

ACCESSION AZ434030

VERSION AZ434030.1 GI:10558043

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

#### REFERENCE

AUTHORS  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

#### JOURNAL

COMMENT Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0220 row: B column: 14

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 45.

#### FEATURES

source  
 1. .45  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"

/db\_xref="taxon:10090"  
 /clone="UUGC1M0220B14"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GII4732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 45;  
 Best Local Similarity 72.7%; Pred. No. 9.1e+05;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGGG 22  
 |||||  
 Db 20 GAGTCTCGGTGTGCTAGGGG 41  
 |||||

## RESULT 47

CL210842/c  
 LOCUS 46 bp mRNA linear GSS 22-MAR-2005  
 DEFINITION W126F07 GGTC Gene Trap Library GV03C04 Mus musculus cDNA clone  
 W126F07, mRNA sequence.

ACCESSION CL210842  
 VERSION CL210842.2 GI:61684034  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 46)

AUTHORS Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F.,

Arnold, H.H., Schnug, F., Wurst, W., Von Melchner, H. and Ruiz, P.  
 A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)

## PUBMED

12904583

COMMENT On Mar 22, 2005 this sequence version replaced gi:40727743.

Contact: GGTC

German Genetrap Consortium (GGTC)

Email: info@genetrap.de

pribetago gene trap. Sequence tag generated by 5'RACE. Additional

sequence information can be found at:

'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=W126F07', RS cell line harboring insertion mutation of target gene is available at:

'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm'

1' Inhouse Sequence Identifier: 08571

Class: Gene Trap.

## FEATURES

source

1..46

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129 Sv"

/db\_xref="taxon:10090"

/clone="W126F07"  
 /sex="Male"  
 /cell\_type="Embryonic stem cell"  
 /cell\_line="ES cells 129S2 (formerly 129/SvPas)"  
 /clone\_lib="GGTC Gene Trap Library GV03C04"  
 /notes="Vector: pTlbetago"

## ORIGIN

Query Match 51.7%; Score 12.4; DB 10; Length 46;  
 Best Local Similarity 72.7%; Pred. No. 9.1e+05;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGGG 22  
 |||||  
 Db 36 GGGTCCCGTGGCCACGGG 15  
 |||||

## RESULT 48

BZ585242  
 LOCUS 47 bp DNA linear GSS 17-DEC-2002  
 DEFINITION 3590.1\_30.1\_H08.2EL.x.1.3590 - RescueMu Grid M Zea mays genomic, genomic survey sequence.

ACCESSION BZ585242

VERSION BZ585242.1 GI:27220303

KEYWORDS GSS.

SOURCE Zea mays

## ORGANISM

Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 47)

AUTHORS Walbot, V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished (2001)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 3590.1\_30.1 column: 14

Class: transposon-tagged.

## FEATURES

source

1..47

/organism="Zea mays"

/mol\_type="genomic DNA"

/culturivar="mixed background W23/A188/B73/K55"

/db\_xref="taxon:4577"

/tissue\_type="leaf"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="3590 - RescueMu Grid M"

/notes="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'www.zmdb.iastate.edu' and follow the links for

'RescueMu,' Grid M was grown at University of Arizona in

2001. DNA was extracted from leaf punches, double digested

using BamHI and BglII, and ligated to form circular

plasmids. DH10B cells were transformed and then screened

on LB plates with ampicillin."

## ORIGIN

Query Match 51.7%; Score 12.4; DB 9; Length 47;  
 Best Local Similarity 72.7%; Pred. No. 9.1e+05;  
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

Qy 2 GGGTCCAGCGTGGCCATGGGG 23
   | | | | | | | | | | | | | |
Db 16 GCGGCCAGCGGGCGCCATGGG 37

RESULT 49
BWS90752
LOCUS      48 bp      mRNA      linear      EST 01-SEP-2004
DEFINITION BWS90752 Yutaka Satou unpublished cDNA library (csef2) Ciona
            savignyi cDNA clone csef029n10 5', mRNA sequence.
ACCESSION  BWS90752
VERSION     BWS90752.1 GI:51841552
KEYWORDS   EST.
SOURCE     Ciona savignyi
            Ciona savignyi
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
            1 (bases 1 to 48)
REFERENCE  Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
            Expressed genes in Ciona savignyi (Satou, Shin-i, Kohara, Satoh)
            Unpublished (2004)
JOURNAL    Contact: Yutaka Satou
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4095
            Fax: 81-75-705-1113
            Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
FEATURES   Location/Qualifiers
            source          1..48
                           /organism="Ciona savignyi"
                           /mol_type="mRNA"
                           /db_xref="taxon:51511"
                           /clone="csef029n10"
                           /dev_stage="egg"
                           /clone_lib="Yutaka Satou unpublished cDNA library (csef2)"

ORIGIN
Query Match      51.7%; Score 12.4; DB 5; Length 48;
Best Local Similarity 66.7%; Pred. No. 9.2e+05;
Matches 16; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCATGGGG 24
   | | | | | | | | | | | | | |
Db 6 GGGCTGCAGNATCGGCACGNGG 29

RESULT 50
AA906151/c
LOCUS      49 bp      mRNA      linear      EST 09-JUN-1998
DEFINITION OJ82h01.s1 Soares NPL T GBC S1 Homo sapiens cDNA clone
            IMAGE:1504849 3', similar to TR:P94909 P94909 HYPOTHETICAL 58.7 KD
            PROTEIN ;, mRNA sequence.
ACCESSION  AA906151
VERSION     AA906151.1 GI:3041274
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
            1 (bases 1 to 49)
REFERENCE  NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
AUTHORS    Contact: Robert Strausberg, Ph.D.
            Email: cgapsb@mail.nih.gov
TITLE      This clone is available royalty-free through LNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Trace considered overall poor quality
            Insert Length: 1605 Std Error: 0.00
            Seq primer: -40ml3 fwd. ET from Amersham

```

```

FEATURES   High quality sequence stop: 1.
            Location/Qualifiers
            source          1..49
                           /organism="Homo sapiens"
                           /mol_type="mRNA"
                           /db_xref="taxon:9606"
                           /db_xref="IMAGE:1504849"
                           /lab_host="DH10B"
                           /clone_lib="Soares NPL T GBC S1"
                           /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                           a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
                           Equal amounts of plasmid DNA from three normalized
                           libraries (fetal lung NBHL19W, testis NHT, and B-cell
                           NCI CGAP GCBI) were mixed, and ss circles were made in
                           vitro. Following HAP purification, this DNA was used as
                           tracer in a subtractive hybridization reaction. The driver
                           was PCR-amplified cDNAs from pools of 5,000 clones made
                           from the same 3 libraries. The pools consisted of
                           I.M.A.G.E. Clones 297480-302087, 682632-687239,
                           726408-728711, and 729096-731399. Subtraction by Bento
                           Soares and M. Fatima Bonaldo. "
ORIGIN
Query Match      51.7%; Score 12.4; DB 1; Length 49;
Best Local Similarity 72.7%; Pred. No. 9.2e+05;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 GGTCCAGCGTGGCCATGGGG 24
   | | | | | | | | | | | | | |
Db 24 GATCCCGCTGGCGCTGGCGGG 3

Search completed: February 15, 2006, 21:10:23
Job time : 1612.3 secs

```

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:56:18 ; Search time 53.9504 Seconds  
(without alignments)  
790.754 Million cell updates/sec

Title: US-09-669-187A-81

Perfect score: 24

Sequence: 1 ggggtccagcgtgcgcattggggg 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Issued Patents NA.\*

1: /cgn2\_6/ptodata/1/ina/1-COMB.seq.\*

2: /cgn2\_6/ptodata/1/ina/5-COMB.seq.\*

3: /cgn2\_6/ptodata/1/ina/6A-COMB.seq.\*

4: /cgn2\_6/ptodata/1/ina/6B-COMB.seq.\*

5: /cgn2\_6/ptodata/1/ina/H-COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/PCTUS-COMB.seq.\*

7: /cgn2\_6/ptodata/1/ina/PP-COMB.seq.\*

8: /cgn2\_6/ptodata/1/ina/RE-COMB.seq.\*

9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.2	67.5	25	3	US-08-617-874-1
2	16	66.7	33	3	US-09-249-585A-11
3	15.8	65.8	33	3	US-08-650-726-1
4	15.2	63.3	25	3	US-09-396-196G-107962
5	15.2	63.3	35	3	US-09-875-453B-69
6	15	62.5	27	2	US-08-410-804-13
7	15	62.5	27	2	US-08-607-269-8
8	15	62.5	27	2	US-08-259-514-13
9	15	62.5	27	2	US-08-858-311-13
10	15	62.5	27	6	PCT-US95-04600-8
11	14.6	60.8	47	3	US-09-258-689-5
12	14.6	60.8	47	3	US-09-866-073A-5
13	14.4	60.0	29	3	US-09-830-433A-127
14	14.2	59.2	19	3	US-09-109-858-14
15	14	58.3	17	2	US-08-217-082A-9
16	14	58.3	17	2	US-08-217-082A-10
17	14	58.3	18	2	US-08-217-082A-17
18	14	58.3	18	2	US-08-465-485A-17
19	14	58.3	18	2	US-08-465-485A-24
20	14	58.3	18	3	US-09-080-285-17
21	14	58.3	18	3	US-09-080-285-24
22	14	58.3	18	3	US-09-080-285-24
23	14	58.3	18	3	US-09-249-730-218
24	14	58.3	18	3	US-09-118-220-1
					Sequence 55, Appl

18	3	US-09-030-701-27	Sequence 27, Appl
18	3	US-09-286-098-59	Sequence 59, Appl
18	3	US-09-286-098-104	Sequence 104, Appl
18	3	US-08-960-774-45	Sequence 45, Appl
18	3	US-08-978-954-14	Sequence 14, Appl
18	3	US-03-325-193A-51	Sequence 51, Appl
18	3	US-09-724-426-17	Sequence 17, Appl
18	3	US-09-724-426-24	Sequence 24, Appl
18	3	US-09-191-170-53	Sequence 53, Appl
18	3	US-09-136-080E-45	Sequence 45, Appl
18	3	US-09-690-921-2	Sequence 2, Appl
18	3	US-09-301-829A-2	Sequence 2, Appl
18	3	US-09-249-247-218	Sequence 218, Appl
18	3	US-09-337-619-45	Sequence 45, Appl
18	3	US-09-835-370-21	Sequence 21, Appl
18	3	US-09-634-320-7	Sequence 7, Appl
18	3	US-09-654-373-14	Sequence 14, Appl
18	3	US-09-724-425-17	Sequence 17, Appl
18	3	US-09-724-425-24	Sequence 24, Appl
18	3	US-09-895-480A-14	Sequence 14, Appl
18	3	US-10-002-884A-6	Sequence 6, Appl
18	3	US-09-108-673A-34	Sequence 34, Appl
18	3	US-09-835-371-21	Sequence 21, Appl
18	3	US-09-954-987B-115	Sequence 115, Appl
18	3	US-09-672-126B-110	Sequence 110, Appl
19	3	US-09-634-320-8	Sequence 8, Appl
19	3	US-09-634-320-9	Sequence 9, Appl
19	3	US-09-632-748-7	Sequence 7, Appl
19	3	US-09-082-649B-60	Sequence 60, Appl
20	3	US-09-965-101-60	Sequence 60, Appl
23	3	US-09-634-320-1	Sequence 1, Appl
23	3	US-09-634-320-2	Sequence 2, Appl
25	3	US-09-396-196G-16637	Sequence 16637, A
30	3	US-09-349-884-12	Sequence 12, Appl
35	2	US-08-217-082A-2	Sequence 2, Appl
35	2	US-08-465-485A-2	Sequence 2, Appl
35	3	US-09-080-285-2	Sequence 2, Appl
35	3	US-09-724-426-2	Sequence 2, Appl
35	3	US-09-724-425-2	Sequence 2, Appl
40	2	US-08-301-722A-6	Sequence 6, Appl
50	3	US-10-131-827-4669	Sequence 4669, Ap
25	3	US-09-396-196G-55452	Sequence 55452, A
30	3	US-09-720-655B-4	Sequence 4, Appl
45	3	US-08-979-608A-40	Sequence 40, Appl
45	3	US-09-517-849-40	Sequence 40, Appl
45	3	US-09-616-289-40	Sequence 40, Appl
45	3	US-09-976-740-40	Sequence 40, Appl
45	3	US-09-971-773-40	Sequence 40, Appl
47	3	US-09-422-978-3636	Sequence 3636, Ap
21	2	US-08-461-030C-3	Sequence 3, Appl
21	6	PCT-US95-07135-3	Sequence 3, Appl
27	3	US-09-877-243A-21	Sequence 21, Appl
27	3	US-09-877-243A-22	Sequence 22, Appl
27	3	US-09-877-705A-21	Sequence 21, Appl
27	3	US-09-877-705A-22	Sequence 22, Appl
27	3	US-09-877-738C-21	Sequence 21, Appl
27	3	US-09-877-738C-22	Sequence 22, Appl
33	3	US-09-816-697-4	Sequence 4, Appl
38	2	US-08-671-947-30	Sequence 30, Appl
38	2	US-08-671-947-31	Sequence 31, Appl
43	2	US-08-467-568-4	Sequence 4, Appl
43	2	US-08-467-568-8	Sequence 8, Appl
43	2	US-09-030-582-4	Sequence 4, Appl
43	2	US-09-030-582-8	Sequence 8, Appl
25	3	US-09-396-196G-109443	Sequence 109443, A
25	3	US-09-396-196G-109444	Sequence 109444, A
25	3	US-09-396-196G-109445	Sequence 109445, A
29	3	US-09-635-705-22	Sequence 22, Appl
29	3	US-09-635-705-22	Sequence 22, Appl
29	3	US-09-634-858A-22	Sequence 22, Appl
29	3	US-08-869-927C-22	Sequence 22, Appl
20	2	US-08-217-082A-1	Sequence 1, Appl
20	2	US-08-217-082A-7	Sequence 7, Appl
13			
54.2			

c 98	13	54.2	13	20	2	US-08-465-485A-1	Sequence 1, Appli	c 171	12.4	51.7	21	3	US-09-657-472-2332	Sequence 2332, Ap
c 99	13	54.2	20	2	2	US-08-480-485A-7	Sequence 7, Appli	c 172	12.4	51.7	23	3	US-09-756-283A-12	Sequence 12, Appl
c 100	13	54.2	20	2	3	US-09-080-285-1	Sequence 1, Appli	c 173	12.4	51.7	24	3	US-08-281-082A-18	Sequence 18, Appl
c 101	13	54.2	20	3	3	US-09-080-285-7	Sequence 7, Appli	c 174	12.4	51.7	25	3	US-09-396-196G-41595	Sequence 41595, A
c 102	13	54.2	20	3	3	US-09-379-718-1	Sequence 1, Appli	c 175	12.4	51.7	25	3	US-09-396-196G-61432	Sequence 61432, A
c 103	13	54.2	20	3	3	US-09-379-718-2	Sequence 2, Appli	c 176	12.4	51.7	25	3	US-09-396-196G-61443	Sequence 61443, A
c 104	13	54.2	20	3	3	US-09-724-426-1	Sequence 1, Appli	c 177	12.4	51.7	25	3	US-09-396-196G-61444	Sequence 61444, A
c 105	13	54.2	20	3	3	US-09-724-426-7	Sequence 7, Appli	c 178	12.4	51.7	27	3	US-09-612-852A-9	Sequence 9, Appli
c 106	13	54.2	20	3	3	US-09-724-425-1	Sequence 1, Appli	c 179	12.4	51.7	30	2	US-09-988-194A-45	Sequence 45, Appl
c 107	13	54.2	20	3	3	US-09-724-425-7	Sequence 7, Appli	c 180	12.4	51.7	30	2	US-07-860-925-15	Sequence 15, Appl
c 108	13	54.2	25	3	3	US-09-396-196G-26931	Sequence 26931, A	c 181	12.4	51.7	30	2	US-08-334-215-15	Sequence 15, Appl
c 109	13	54.2	35	3	3	US-09-396-196G-101993	Sequence 101993,	c 182	12.4	51.7	30	3	US-08-479-732-47	Sequence 47, Appl
c 110	13	54.2	35	3	3	US-09-215-252-41	Sequence 41, Appl	c 183	12.4	51.7	30	3	US-08-475-442A-47	Sequence 47, Appl
c 111	13	54.2	35	3	3	US-09-043-230B-6	Sequence 6, Appli	c 184	12.4	51.7	32	3	US-09-128-354-7	Sequence 7, Appli
c 112	13	54.2	35	3	3	US-09-970-989A-41	Sequence 41, Appl	c 185	12.4	51.7	32	3	US-09-250-580-3	Sequence 3, Appli
c 113	13	54.2	46	3	3	US-09-486-241-26	Sequence 26, Appl	c 186	12.4	51.7	45	2	US-07-795-859B-36	Sequence 36, Appl
c 114	13	54.2	48	3	3	US-09-203-623-31	Sequence 31, Appl	c 187	12.4	51.7	45	2	US-08-457-616-36	Sequence 36, Appl
c 115	13	54.2	48	3	3	US-09-523-462-31	Sequence 31, Appl	c 188	12.4	51.7	47	2	US-08-307-682B-20	Sequence 20, Appl
c 116	13	54.2	48	3	3	US-09-522-980-31	Sequence 31, Appl	c 189	12.4	51.7	50	3	US-09-270-767-28633	Sequence 28633, A
c 117	12.8	53.3	23	2	2	US-08-281-082A-32	Sequence 32, Appl	c 190	12.2	50.8	17	3	US-09-474-432B-572	Sequence 572, App
c 118	12.8	53.3	24	2	2	US-08-281-082A-17	Sequence 17, Appl	c 191	12.2	50.8	17	3	US-09-476-387-571	Sequence 571, App
c 119	12.8	53.3	25	3	3	US-09-396-196G-107963	Sequence 107963,	c 192	12.2	50.8	19	2	US-08-512-681-11	Sequence 11, Appl
c 120	12.8	53.3	25	3	3	US-09-396-196G-109446	Sequence 109446,	c 193	12.2	50.8	20	3	US-09-344-519-13	Sequence 13, Appl
c 121	12.8	53.3	26	3	3	US-08-832-488-3	Sequence 3, Appli	c 194	12.2	50.8	20	3	US-09-344-519-14	Sequence 14, Appl
c 122	12.8	53.3	29	3	3	US-09-195-666A-19	Sequence 19, Appl	c 195	12.2	50.8	21	6	PCT-US94-07091-5	Sequence 5, Appli
c 123	12.8	53.3	29	3	3	US-09-635-705-19	Sequence 19, Appl	c 196	12.2	50.8	22	2	US-08-410-804-7	Sequence 7, Appli
c 124	12.8	53.3	29	3	3	US-09-634-958A-19	Sequence 19, Appl	c 197	12.2	50.8	22	2	US-08-410-804-8	Sequence 8, Appli
c 125	12.8	53.3	29	3	3	US-08-869-327C-19	Sequence 19, Appl	c 198	12.2	50.8	22	2	US-08-607-269-6	Sequence 6, Appli
c 126	12.8	53.3	31	2	2	US-08-225-757B-4	Sequence 4, Appli	c 199	12.2	50.8	22	2	US-08-607-269-7	Sequence 7, Appli
c 127	12.8	53.3	32	3	3	US-10-083-246A-29	Sequence 29, Appl	c 200	12.2	50.8	22	2	US-08-259-514-7	Sequence 7, Appli
c 128	12.8	53.3	39	3	3	US-09-752-110A-11	Sequence 11, Appl	c 201	12.2	50.8	22	2	US-08-259-514-8	Sequence 8, Appli
c 129	12.8	53.3	39	3	3	US-10-131-827-7883	Sequence 7883, Ap	c 202	12.2	50.8	22	2	US-08-858-311-7	Sequence 7, Appli
c 130	12.6	52.5	20	3	3	US-09-166-448-19	Sequence 19, Appl	c 203	12.2	50.8	22	2	US-08-858-311-8	Sequence 8, Appli
c 131	12.6	52.5	20	3	3	US-09-697-884-19	Sequence 19, Appl	c 204	12.2	50.8	22	3	US-10-038-835-53	Sequence 53, Appl
c 132	12.6	52.5	20	3	3	US-09-806-254-29	Sequence 29, Appl	c 205	12.2	50.8	22	6	PCT-US95-04600-6	Sequence 6, Appli
c 133	12.6	52.5	20	3	3	US-09-018-125-6	Sequence 6, Appli	c 206	12.2	50.8	22	6	PCT-US95-04600-7	Sequence 7, Appli
c 134	12.6	52.5	20	3	3	US-09-579-791-4	Sequence 4, Appli	c 207	12.2	50.8	25	2	US-08-614-686A-8	Sequence 8, Appli
c 135	12.6	52.5	20	3	3	US-09-396-196G-103531	Sequence 19, Appl	c 208	12.2	50.8	25	3	US-09-527-972-26	Sequence 26, Appl
c 136	12.6	52.5	21	2	2	US-08-860-299-1	Sequence 1, Appli	c 209	12.2	50.8	25	3	US-09-396-196G-16675	Sequence 16675, A
c 137	12.6	52.5	21	3	3	US-09-287-623-1	Sequence 1, Appli	c 210	12.2	50.8	25	3	US-09-396-196G-19903	Sequence 19903, A
c 138	12.6	52.5	24	2	2	US-08-241-372-7	Sequence 7, Appli	c 211	12.2	50.8	25	3	US-09-396-196G-19904	Sequence 19904, A
c 139	12.6	52.5	24	2	2	US-08-110-294A-1	Sequence 1, Appli	c 212	12.2	50.8	25	3	US-09-396-196G-26932	Sequence 26932, A
c 140	12.6	52.5	24	2	2	US-08-389-926-1	Sequence 1, Appli	c 213	12.2	50.8	25	3	US-09-396-196G-97216	Sequence 97216, A
c 141	12.6	52.5	24	6	6	PCT-US95-05420-7	Sequence 7, Appli	c 214	12.2	50.8	26	3	US-09-108-020-29	Sequence 29, Appl
c 142	12.6	52.5	25	3	3	US-09-396-196G-103529	Sequence 103529,	c 215	12.2	50.8	26	3	US-09-685-296-29	Sequence 29, Appl
c 143	12.6	52.5	25	3	3	US-09-396-196G-103530	Sequence 103530,	c 216	12.2	50.8	27	3	US-09-253-396A-14	Sequence 14, Appl
c 144	12.6	52.5	25	3	3	US-09-396-196G-103531	Sequence 103531,	c 217	12.2	50.8	28	3	US-08-434-099A-31	Sequence 31, Appl
c 145	12.6	52.5	25	3	3	US-09-396-196G-103832	Sequence 103832,	c 218	12.2	50.8	36	2	US-08-435-350-3	Sequence 3, Appli
c 146	12.6	52.5	26	3	3	US-09-009-156-10	Sequence 10, Appl	c 219	12.2	50.8	36	3	US-08-508-436-10	Sequence 10, Appl
c 147	12.6	52.5	26	3	3	US-09-372-154-10	Sequence 10, Appl	c 220	12.2	50.8	40	3	US-09-546-483-1	Sequence 1, Appli
c 148	12.6	52.5	26	3	3	US-09-950-688-10	Sequence 10, Appl	c 221	12.2	50.8	40	3	US-09-823-177-1	Sequence 1, Appli
c 149	12.6	52.5	36	3	3	US-09-189-129-7	Sequence 7, Appli	c 222	12.2	50.8	40	3	US-09-752-110A-12	Sequence 12, Appl
c 150	12.6	52.5	36	3	3	US-09-824-286-7	Sequence 7, Appli	c 223	12.2	50.8	47	3	US-09-422-978-3553	Sequence 3553, Ap
c 151	12.6	52.5	36	3	3	US-09-269-332-9	Sequence 9, Appli	c 224	12.2	50.8	49	2	US-08-384-708A-121	Sequence 121, App
c 152	12.6	52.5	38	2	2	US-08-611-757-52	Sequence 52, Appl	c 225	12.2	50.8	49	3	US-08-687-421-121	Sequence 121, App
c 153	12.6	52.5	38	6	6	PCT-US95-05980-52	Sequence 52, Appl	c 226	12.2	50.8	49	3	US-08-442-423-121	Sequence 121, App
c 154	12.6	52.5	38	9	9	5182260-16	Patent No. 5182260	c 227	12.2	50.8	50	3	US-09-513-999C-15423	Sequence 15423, A
c 155	12.6	52.5	41	2	2	US-08-761-277A-56	Sequence 56, Appl	c 228	12	50.0	15	3	US-09-162-484-1	Sequence 1, Appli
c 156	12.6	52.5	41	2	2	US-08-761-277A-67	Sequence 67, Appl	c 229	12	50.0	16	2	US-08-241-372-32	Sequence 32, Appl
c 157	12.6	52.5	43	2	2	US-08-911-774-4	Sequence 4, Appli	c 230	12	50.0	16	2	US-08-241-372-33	Sequence 33, Appl
c 158	12.6	52.5	43	3	3	US-09-228-243-4	Sequence 4, Appli	c 231	12	50.0	16	6	PCT-US95-05420-32	Sequence 32, Appl
c 159	12.6	52.5	50	3	3	US-09-538-709-996	Sequence 996, App	c 232	12	50.0	16	6	PCT-US95-05420-33	Sequence 33, Appl
c 160	12.4	51.7	18	3	3	US-09-030-701-41	Sequence 41, Appl	c 233	12	50.0	20	3	US-09-433-694-31	Sequence 31, Appl
c 161	12.4	51.7	18	3	3	US-09-030-701-60	Sequence 60, Appl	c 234	12	50.0	20	3	US-09-371-674-9	Sequence 9, Appli
c 162	12.4	51.7	18	3	3	US-09-286-098-72	Sequence 72, Appl	c 235	12	50.0	20	3	US-10-160-792-37	Sequence 37, Appl
c 163	12.4	51.7	18	3	3	US-09-960-774-72	Sequence 72, Appl	c 236	12	50.0	20	3	US-10-160-792-104	Sequence 104, App
c 164	12.4	51.7	18	3	3	US-09-191-170-66	Sequence 66, Appl	c 237	12	50.0	21	2	US-08-379-078-584	Sequence 584, App
c 165	12.4	51.7	18	3	3	US-09-337-619-72	Sequence 72, Appl	c 238	12	50.0	21	3	US-07-974-409C-207	Sequence 207, App
c 166	12.4	51.7	18	3	3	US-09-954-987B-113	Sequence 113, App	c 239	12	50.0	21	6	PCT-US93-00977-207	Sequence 207, App
c 167	12.4	51.7	20	3	3	US-09-286-098-16	Sequence 16, Appl	c 240	12	50.0	23	3	US-08-815-469-7	Sequence 7, Appli
c 168	12.4	51.7	20	3	3	US-09-109-663-72	Sequence 72, Appl	c 241	12	50.0	23	3	US-09-557-908-7	Sequence 7, Appli
c 169	12.4	51.7	21	2	2	US-08-837-190C-1	Sequence 1, Appli	c 242	12	50.0	23	3	US-09-333-366-7	Sequence 7, Appli
c 170	12.4	51.7	21	2	2	US-08-837-190C-11	Sequence 11, Appl	c 243	12	50.0	23	3	US-09-314-889-7	Sequence 7, Appli

```
244 12 50.0 25 3 US-09-396-196G-379 Sequence 379, Appl
245 12 50.0 25 3 US-09-396-196G-36030 Sequence 36030, A
246 12 50.0 25 3 US-09-396-196G-36031 Sequence 36031, A
247 12 50.0 25 3 US-09-396-196G-36042 Sequence 36042, A
248 12 50.0 25 3 US-09-396-196G-61431 Sequence 61431, A
249 12 50.0 25 3 US-09-396-196G-69257 Sequence 69257, A
250 12 50.0 25 3 US-09-396-196G-69265 Sequence 69265, A
251 12 50.0 25 3 US-09-396-196G-72550 Sequence 72550, A
252 12 50.0 25 3 US-09-396-196G-72550 Sequence 72550, A
253 12 50.0 25 3 US-09-396-196G-86851 Sequence 86851, A
254 12 50.0 25 3 US-09-396-196G-95621 Sequence 95621, A
255 12 50.0 25 3 US-09-396-196G-96812 Sequence 96812, A
256 12 50.0 25 3 US-09-396-196G-101992 Sequence 101992,
257 12 50.0 25 3 US-09-396-196G-105225 Sequence 105225,
258 12 50.0 25 3 US-09-396-196G-120382 Sequence 120382,
259 12 50.0 25 3 US-09-396-196G-120383 Sequence 120383,
260 12 50.0 26 3 US-08-722-719-36 Sequence 36, Appl
261 12 50.0 26 3 US-09-513-729B-6 Sequence 6, Appl
262 12 50.0 26 3 US-09-334-951-36 Sequence 36, Appl
263 12 50.0 26 3 US-09-334-923A-36 Sequence 36, Appl
264 12 50.0 26 3 US-09-334-954A-36 Sequence 36, Appl
265 12 50.0 26 3 US-09-571-013-38 Sequence 38, Appl
266 12 50.0 27 3 US-09-741-171-1 Sequence 1, Appl
267 12 50.0 30 2 US-08-117-952-510 Sequence 510, Appl
268 12 50.0 30 3 US-09-282-147-5 Sequence 5, Appl
269 12 50.0 30 3 US-09-282-147-19 Sequence 19, Appl
270 12 50.0 30 3 US-10-216-981A-13 Sequence 13, Appl
271 12 50.0 31 3 US-09-040-025-2 Sequence 2, Appl
272 12 50.0 31 3 US-09-040-025-2 Sequence 2, Appl
273 12 50.0 32 3 US-09-972-800A-33 Sequence 33, Appl
274 12 50.0 33 2 US-08-049-284C-37 Sequence 37, Appl
275 12 50.0 33 2 US-08-476-562-37 Sequence 37, Appl
276 12 50.0 33 2 US-08-479-723A-37 Sequence 37, Appl
277 12 50.0 33 6 PCT-US94-04310-37 Sequence 37, Appl
278 12 50.0 34 3 US-09-040-025-8 Sequence 8, Appl
279 12 50.0 34 3 US-09-481-288-29 Sequence 29, Appl
280 12 50.0 34 3 US-09-040-025-8 Sequence 8, Appl
281 12 50.0 34 3 US-09-646-561-53 Sequence 53, Appl
282 12 50.0 37 3 US-09-025-769B-318 Sequence 318, Appl
283 12 50.0 37 3 US-09-490-070A-318 Sequence 318, Appl
284 12 50.0 37 3 US-09-490-153-318 Sequence 318, Appl
285 12 50.0 37 3 US-09-490-324-318 Sequence 318, Appl
286 12 50.0 38 3 US-08-983-397-10 Sequence 10, Appl
287 12 50.0 43 2 US-08-549-757A-3 Sequence 3, Appl
288 12 50.0 47 3 US-09-641-638-1196 Sequence 1196, Ap
289 12 50.0 47 3 US-09-422-978-1833 Sequence 1833, Ap
290 12 50.0 47 3 US-08-422-978-1833 Sequence 2794, Ap
291 12 50.0 47 3 US-10-170-097-1196 Sequence 1196, Ap
292 12 50.0 50 2 US-08-171-389-481 Sequence 481, App
293 12 50.0 50 2 US-08-123-936-481 Sequence 481, App
294 12 50.0 50 2 US-08-475-228A-481 Sequence 481, App
295 12 50.0 50 3 US-08-482-080A-481 Sequence 481, App
296 12 50.0 50 3 US-09-354-947-481 Sequence 481, App
297 12 50.0 50 3 US-09-993-346-481 Sequence 481, App
298 11.8 50.0 50 6 PCT-US93-12388-481 Sequence 481, App
299 49.2 18 3 US-09-260-629-12 Sequence 12, Appl
300 49.2 18 3 US-10-146-221-12 Sequence 12, Appl
```

## ALIGNMENTS

```
RESULT 1
US-08-617-874-1
; Sequence 1, Application US/08617874
; Patent No. 633850
; GENERAL INFORMATION:
; APPLICANT: Jevnikar, Anthony M.
; APPLICANT: Ma, Shengwu
; APPLICANT: Sciller, Calvin R.
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING
; TITLE OF INVENTION: IMMUNE RESPONSES IN MAMMALS
; NUMBER OF SEQUENCES: 10
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.
; STREET: George Mason Building, 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/617,874
; FILING DATE: 21-MAY-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 024916-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA - primer"
US-08-617-874-1

Query Match 67.5%; Score 16.2; DB 3; Length 25;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGTCCAGCGTGGCCCATGGG 22
||| ||| ||| ||| ||| |||
Db 2 GGATCCGCGCGCGCCCATGGG 22

RESULT 2
US-09-249-585A-11/c
; Sequence 11, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentn version 3.0
; SEQ ID NO 11
; LENGTH: 33
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(33)
; OTHER INFORMATION: oligonucleotide used for RT-PCR amplification of Bcl2
US-09-249-585A-11

Query Match 66.7%; Score 16; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCCCATGG 21
||||| ||| ||| ||| |||
Db 27 CCAGCGTGGCCCATGG 12
```

```
RESULT 3
US-08-650-726-1/c
; Sequence 1, Application US/08650726
; Patent No. 6027721
; GENERAL INFORMATION:
; APPLICANT: Hamhang, Joseph P
; APPLICANT: Aebischer, Patrick
; TITLE OF INVENTION: DEVICE AND METHOD FOR ENCAPSULATED GENE
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Ave. of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650,726
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Eirifi, Ivor R
; REGISTRATION NUMBER: 39,529
; REFERENCE/DOCKET NUMBER: CFI-35
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 596 9000
; TELEFAX: 212 596 9030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-650-726-1

Query Match 65.8%; Score 15.8; DB 3; Length 33;
Best Local Similarity 89.5%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCGCCATGGGGG 24
| | | | | | | | | | | | | | |
Db 30 CCAGCGTGGCGCATGGTGG 12

RESULT 4
US-09-396-196G-107962
; Sequence 107962, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107962
; LENGTH: 25
; TYPE: DNA
```

```
; ORGANISM: mus musculus
US-09-396-196G-107962

Query Match 63.3%; Score 15.2; DB 3; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GGTCCAGCGTGGCCATGGG 22
| | | | | | | | | | | | | | |
Db 1 GTTCCAGCCTGCGCCATGGG 20

RESULT 5
US-09-875-453B-69/c
; Sequence 69, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-875-453B-69

Query Match 63.3%; Score 15.2; DB 3; Length 35;
Best Local Similarity 85.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGTCCAGCGTGGCCATGG 21
| | | | | | | | | | | | | | |
Db 28 GGTCCAGCGCGAGCCATGG 9

RESULT 6
US-08-410-804-13/c
; Sequence 13, Application US/08410804
; Patent No. 5632994
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: PAS ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cathryn Campbell
; STREET: 4370 La Jolla Village Drive. Ste 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/410,804  
FILING DATE: 27-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/259,514  
FILING DATE: 14-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 1389  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-410-804-13

Query Match 62.5%; Score 15; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCATG 20  
Db 21 CCAGCGTGGCCATG 7

## RESULT 7

US-08-607-269-8/c  
Sequence 8, Application US/08607269  
Patent No. 5702897  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Sato, Takaaki  
TITLE OF INVENTION: Interaction of Proteins Involved in a  
TITLE OF INVENTION: Cell Death Pathway  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/607,269  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/226,876  
FILING DATE: 13-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9882  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-607-269-8

Query Match 62.5%; Score 15; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCATG 20  
Db 21 CCAGCGTGGCCATG 7

## RESULT 8

US-08-259-514-13/c  
Sequence 13, Application US/08259514  
Patent No. 5747245  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Sato, Takaaki  
TITLE OF INVENTION: FAS ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cathryn Campbell  
STREET: 4370 La Jolla Village Drive, Ste 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/259,514  
FILING DATE: 14-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9954  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-259-514-13

Query Match 62.5%; Score 15; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCATG 20  
Db 21 CCAGCGTGGCCATG 7

## RESULT 9

US-08-858-311-13/c  
Sequence 13, Application US/08858311  
Patent No. 5876939  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Sato, Takaaki  
TITLE OF INVENTION: FAS ASSOCIATED PROTEINS  
NUMBER OF SEQUENCES: 22

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Cathryn Campbell  
;; STREET: 4370 La Jolla Village Drive, Ste 700  
;; CITY: San Diego  
;; STATE: California  
;; COUNTRY: United States  
;; ZIP: 92122  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/858,311  
;; FILING DATE: 14-JUN-1994  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/410,804  
;; FILING DATE: 27-MAR-1995  
;; APPLICATION NUMBER: US 08/259,514  
;; FILING DATE: 14-JUN-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Campbell, Cathryn  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-LJ 1389  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 27 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cdna  
US-08-858-311-13

Query Match 62.5%; Score 15; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCACGGTGGCCCATG 20  
Db 21 CCACGGTGGCCCATG 7

RESULT 10  
PCT-US95-04600-8/c  
Sequence 8, Application PC/TUS9504600  
GENERAL INFORMATION:  
APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION  
TITLE OF INVENTION: Interaction of Proteins Involved in  
TITLE OF INVENTION: a Cell Death Pathway  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04600  
FILING DATE: 12-APR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Imbra, Richard J.  
REGISTRATION NUMBER: 37,643

;; REFERENCE/DOCKET NUMBER: FP-LJ 1361  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 27 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
PCT-US95-04600-8

Query Match 62.5%; Score 15; DB 6; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCACGGTGGCCCATG 20  
Db 21 CCACGGTGGCCCATG 7

RESULT 11  
US-09-258-689-5  
Sequence 5, Application US/09258689  
Patent No. 6451527  
GENERAL INFORMATION:  
APPLICANT: Larocca, David  
APPLICANT: Baird, Andrew  
APPLICANT: Kassner, Paul  
TITLE OF INVENTION: METHODS USING GENETIC PACKAGE DISPLAY FOR  
TITLE OF INVENTION: SELECTING INTERNALIZING LIGANDS FOR GENE DELIVERY  
FILE REFERENCE: 760100.430C3  
CURRENT APPLICATION NUMBER: US/09/258,689  
CURRENT FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR Primer  
US-09-258-689-5

Query Match 60.8%; Score 14.6; DB 3; Length 47;  
Best Local Similarity 81.0%; Pred. No. 3.2e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCCATGG 21  
Db 10 GGGTTCGCGGTGGCGCATGG 30

RESULT 12  
US-09-866-073A-5  
Sequence 5, Application US/09866073A  
Patent No. 6723512  
GENERAL INFORMATION:  
APPLICANT: Larocca, David  
APPLICANT: Baird, Andrew  
APPLICANT: Kassner, Paul  
TITLE OF INVENTION: METHODS USING GENETIC PACKAGE DISPLAY FOR  
TITLE OF INVENTION: DETECTING AND IDENTIFYING PROTEIN-PROTEIN  
TITLE OF INVENTION: INTERACTIONS THAT FACILITATE INTERNALIZATION  
TITLE OF INVENTION: AND TRANSGENE EXPRESSION AND CELLS OR TISSUE  
TITLE OF INVENTION: COMPETENT FOR THE SAME AND METHODS FOR EVOLVING  
TITLE OF INVENTION: GENE DELIVERY VECTORS  
FILE REFERENCE: 760100.430C4  
CURRENT APPLICATION NUMBER: US/09/866,073A  
CURRENT FILING DATE: 2001-05-24  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5

```
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-866-073A-5

Query Match          60.8%; Score 14.6; DB 3; Length 47;
Best Local Similarity 81.0%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGCGCCATGG 21
    |||||
Db 10 GGGTCCAGCGTGCGCCATGG 30
    |||||

RESULT 13
US-09-830-433A-127
; Sequence 127, Application US/09830433A
; Patent No. 6835384
; GENERAL INFORMATION:
; APPLICANT: AUJAME et al.
; TITLE OF INVENTION: Nucleic acids and polypeptides specific for pathogenic
; FILE REFERENCE: P07180US00/BAS
; CURRENT APPLICATION NUMBER: US/09/830,433A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: FR 98 13 693
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 127
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-830-433A-127

Query Match          60.0%; Score 14.4; DB 3; Length 29;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGCGCCATGGGG 24
    |||||
Db 2 GGGATCCAACTGCTTCATGGTG 25
    |||||

RESULT 14
US-09-109-858-14
; Sequence 14, Application US/09109858
; Patent No. 6787353
; GENERAL INFORMATION:
; APPLICANT: Rao, Mahendra S.
; APPLICANT: Kalyani, Anjali J.
; TITLE OF INVENTION: Lineage-Restricted Neuronal Precursors
; FILE REFERENCE: T5530.CIP
; CURRENT APPLICATION NUMBER: US/09/109,858
; CURRENT FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 08/909,435
; EARLIER FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: WordPerfect 8.0
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-109-858-14

Query Match          59.2%; Score 14.2; DB 3; Length 19;
Best Local Similarity 84.2%; Pred. No. 4.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-866-073A-5

Query Match          60.8%; Score 14.6; DB 3; Length 47;
Best Local Similarity 81.0%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGCGCCATGG 21
    |||||
Db 10 GGGTCCAGCGTGCGCCATGG 30
    |||||

RESULT 15
US-08-217-082A-9
; Sequence 9, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: P.C.
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: Synthetic DNA
; ANTI-SENSE: YES
US-08-217-082A-9

Query Match          58.3%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGCGCCAT 19
    |||||
Db 4 CCAGCGTGCGCCAT 17
    |||||

RESULT 16
US-08-217-082A-10
; Sequence 10, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; NUMBER OF SEQUENCES: 17
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; NAME: Fortney, Andrew D.
; REGISTRATION/DOCKET NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: Synthetic DNA
; ANTI-SENSE: YES
; US-08-217-082A-10
;
; Query Match 58.3%; Score 14; DB 2; Length 17;
; Best Local Similarity 100.0%; Pred. No. 5.8e+03;
; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 6 CCAGCGTGGCCCAT 19
; DB 1 CCAGCGTGGCCCAT 14
;
; RESULT 17
; US-08-217-082A-17
; Sequence 17, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; NAME: Fortney, Andrew D.
; REGISTRATION/DOCKET NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: Synthetic DNA
; US-08-217-082A-17
;
; Query Match 58.3%; Score 14; DB 2; Length 18;
; Best Local Similarity 100.0%; Pred. No. 5.8e+03;
; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 6 CCAGCGTGGCCCAT 19
; DB 5 CCAGCGTGGCCCAT 18
;
; RESULT 18
; US-08-465-485A-17
; Sequence 17, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; NAME: Fortney, Andrew D.
; REGISTRATION/DOCKET NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
```



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-465-485A-17

Query Match 58.3%; Score 14; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

RESULT 19  
US-08-465-485A-24  
Sequence 24, Application US/08465485A  
Patent No. 5831066  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465.485A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid;  
DESCRIPTION: Synthetic DNA  
ANTI-SENSE: YES  
FEATURE:  
NAME/KEY: Modified\_base  
LOCATION: 16..17

OTHER INFORMATION: Last two internucleoside linkages are  
OTHER INFORMATION: phosphorothioates  
US-08-465-485A-24

Query Match 58.3%; Score 14; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

RESULT 20  
US-09-080-285-17  
Sequence 17, Application US/09080285  
Patent No. 6040181  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/080,285  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,485  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-080-285-17

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

RESULT 21  
US-09-080-285-24  
; Sequence 24, Application US/09080285  
; Patent No. 6040181  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John  
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/080,285  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/465,485  
; FILING DATE: 05-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/124,256  
; FILING DATE: 20-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/840,716  
; FILING DATE: 21-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/288,692  
; FILING DATE: 22-DEC-1988  
; NAME: Fortney, Andrew D.  
; ATTORNEY/AGENT INFORMATION:  
; REGISTRATION NUMBER: 34,600  
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (408) 435-2070  
; TELEFAX: (408) 436-2075  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid;  
; DESCRIPTION: Synthetic DNA  
; ANTI-SENSE: YES  
; FEATURE:  
; NAME/KEY: Modified\_base  
; LOCATION: 16..17  
; OTHER INFORMATION: Last two internucleoside linkages are  
; OTHER INFORMATION: phosphorothioates  
US-09-080-285-24

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

RESULT 22  
US-09-249-730-218  
; Sequence 218, Application US/09249730

; Patent No. 6121000  
; GENERAL INFORMATION:  
; APPLICANT: WRIGHT, Jim A.  
; APPLICANT: YOUNG, Alping H.  
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and  
; TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase  
; FILE REFERENCE: 032396-040  
; CURRENT APPLICATION NUMBER: US/09/249,730  
; CURRENT FILING DATE: 1999-02-11  
; NUMBER OF SEQ ID NOS: 220  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 218  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-249-730-218

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

RESULT 23  
US-09-118-220-1  
; Sequence 1, Application US/09118220  
; Patent No. 6140051  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Lauren R.  
; APPLICANT: Xu, Cheng  
; TITLE OF INVENTION: FLUORESCENT DIBENZAZOLE DERIVATIVES  
; TITLE OF INVENTION: AND METHODS RELATED THERETO  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive, 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/118,220  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bartfeld, Neil S  
; REGISTRATION NUMBER: 39,901  
; REFERENCE/DOCKET NUMBER: GENTA.050A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-09-118-220-1

Query Match 58.3%; Score 14; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.8e+03; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19  
Db 5 CCAGCGTGGCCCAT 18

## RESULT 24

US-08-738-652-55  
; Sequence 55, Application US/08738652B  
; Patent No. 6207646  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules  
; FILE REFERENCE: C1039/7004 HCL  
; CURRENT APPLICATION NUMBER: US/08/738,652B  
; CURRENT FILING DATE: 1996-10-30  
; EARLIER APPLICATION NUMBER: US 08/276,358  
; EARLIER FILING DATE: 1994-07-15  
; EARLIER APPLICATION NUMBER: US 08/386,063  
; EARLIER FILING DATE: 1995-02-07  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 55  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-08-738-652-55

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19  
Db 5 CCAGCGTGGCCCAT 18

## RESULT 25

US-09-030-701-27  
; Sequence 27, Application US/09030701B  
; Patent No. 6214806  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schwartz, David A.  
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF LPS-ASSOCIATED DISORDERS  
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS  
; FILE REFERENCE: C1039/7011  
; CURRENT APPLICATION NUMBER: US/09/030,701B  
; CURRENT FILING DATE: 1998-02-25  
; PRIOR FILING DATE: 1997-02-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
US-09-030-701-27

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19  
Db 5 CCAGCGTGGCCCAT 18

## RESULT 26

US-09-286-098-59  
; Sequence 59, Application US/09286098  
; Patent No. 6218371  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Weiner, George  
; TITLE OF INVENTION: Methods and Products for Stimulating the Immune System Using Immunotherapeutic Oligonucleotides and Cytokines  
; TITLE OF INVENTION: Cytokines  
; FILE REFERENCE: C1039/7026/HCL  
; CURRENT APPLICATION NUMBER: US/09/286,098  
; CURRENT FILING DATE: 1999-04-02  
; EARLIER APPLICATION NUMBER: US 60/080,729  
; EARLIER FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 105  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 59  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-286-098-59

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19  
Db 5 CCAGCGTGGCCCAT 18

## RESULT 27

US-09-286-098-104  
; Sequence 104, Application US/09286098  
; Patent No. 6218371  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Weiner, George  
; TITLE OF INVENTION: Methods and Products for Stimulating the Immune System Using Immunotherapeutic Oligonucleotides and Cytokines  
; TITLE OF INVENTION: Cytokines  
; FILE REFERENCE: C1039/7026/HCL  
; CURRENT APPLICATION NUMBER: US/09/286,098  
; CURRENT FILING DATE: 1999-04-02  
; EARLIER APPLICATION NUMBER: US 60/080,729  
; EARLIER FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 105  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 104  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-286-098-104

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCCAT 19  
Db 5 CCAGCGTGGCCCAT 18

## RESULT 28

US-08-960-774-45  
; Sequence 45, Application US/08960774

; Patent No. 6239116  
; GENERAL INFORMATION:  
; APPLICANT: Krieg et al.,  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES  
; NUMBER OF SEQUENCES: 111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/960,774  
; FILING DATE: 30-October-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652  
; FILING DATE: October 30, 1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 08918/012001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-960-774-45

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCGCCAT 19  
|||||  
DB 5 CCAGCGTGGCGCCAT 18

RESULT 29  
US-09-078-954-14  
; Sequence 14, Application US/09078954  
; Patent No. 6287591  
; GENERAL INFORMATION:  
; APPLICANT: SEMPLE, Sean C.  
; APPLICANT: Klimuk, Sandra K.  
; APPLICANT: Harasym, Troy  
; APPLICANT: Hope, Michael J.  
; APPLICANT: Ansell, Steven M.  
; APPLICANT: Cullis, Pieter  
; APPLICANT: Scherrer, Peter  
; APPLICANT: Geiser, Timothy  
; APPLICANT: Zon, Gerald  
; APPLICANT: Debever, Dan  
; TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic Agents in  
; TITLE OF INVENTION: Lipid Vesicles  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Oppedahl & Larson  
; STREET: PO Box 5270  
; CITY: Frisco  
; STATE: CO

; COUNTRY: USA  
; ZIP: 80443-5270  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/078,954  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/856,374  
; FILING DATE: 14-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marina T. Larson  
; REGISTRATION NUMBER: 32,038  
; REFERENCE/DOCKET NUMBER: INEX.P-003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (970) 668-2050  
; TELEFAX: (970) 668-2082  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: no  
; ANTI-SENSE: yes  
US-09-078-954-14

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCAGCGTGGCGCCAT 19  
|||||  
DB 5 CCAGCGTGGCGCCAT 18

RESULT 30  
US-09-325-193A-51  
; Sequence 51, Application US/09325193A  
; Patent No. 6406705  
; GENERAL INFORMATION:  
; APPLICANT: Davis, Heather L.  
; APPLICANT: Schorr, Joachim  
; APPLICANT: Krieg, Arthur M.  
; TITLE OF INVENTION: Use of Nucleic Acids Containing  
; TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant  
; FILE REFERENCE: C1039/7025/HCL  
; CURRENT APPLICATION NUMBER: US/09/325,193A  
; CURRENT FILING DATE: 1999-06-03  
; PRIOR APPLICATION NUMBER: US 09/154,614  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: PCT/US98/04703  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: US 60/040,376  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 51  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-325-193A-51

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

## RESULT 31

US-09-724-426-17  
; Sequence 17, Application US/09724426

; Patent No. 6414134

; GENERAL INFORMATION:

; APPLICANT: Reed, John

; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression

; FILE REFERENCE: 10412-024

; CURRENT APPLICATION NUMBER: US/09/724,426

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 17

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-426-17

Query Match 58.3%; Score 14; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

## RESULT 32

US-09-724-426-24

; Sequence 24, Application US/09724426

; Patent No. 6414134

; GENERAL INFORMATION:

; APPLICANT: Reed, John

; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression

; FILE REFERENCE: 10412-024

; CURRENT APPLICATION NUMBER: US/09/724,426

; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 24

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-724-426-24

Query Match 58.3%; Score 14; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

## RESULT 33

US-09-191-170-53

; Sequence 53, Application US/09191170

; Patent No. 6429199

; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.

; APPLICANT: Hartmann, Gunther

; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules

; TITLE OF INVENTION: for Activating Dendritic Cells

; FILE REFERENCE: C1039/7017

; CURRENT APPLICATION NUMBER: US/09/191,170

; CURRENT FILING DATE: 1998-11-13

; EARLIER APPLICATION NUMBER: US 08/960,774  
; EARLIER FILING DATE: 1997-10-30  
; EARLIER APPLICATION NUMBER: US 08/738,652  
; EARLIER FILING DATE: 1996-10-30  
; EARLIER APPLICATION NUMBER: US 08/386,063  
; EARLIER FILING DATE: 1995-02-07  
; EARLIER APPLICATION NUMBER: US 08/276,358  
; EARLIER FILING DATE: 1994-07-15  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 53  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide

US-09-191-170-53

Query Match 58.3%; Score 14; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

## RESULT 34

US-09-136-080E-45

; Sequence 45, Application US/09136080E

; Patent No. 6518017

; GENERAL INFORMATION:

; APPLICANT: Riley, Timothy A.

; APPLICANT: Brown, Bob D.

; APPLICANT: Arnold, Lyle J.

; TITLE OF INVENTION: COMBINATORIAL ANTISENSE LIBRARY

; FILE REFERENCE: OASBIO.003A

; CURRENT APPLICATION NUMBER: US/09/136,080E

; CURRENT FILING DATE: 1998-08-18

; NUMBER OF SEQ ID NOS: 54

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 45

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic oligonucleotide

US-09-136-080E-45

Query Match 58.3%; Score 14; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

## RESULT 35

US-09-690-921-2

; Sequence 2, Application US/09690921

; Patent No. 6544518

; GENERAL INFORMATION:

; APPLICANT: Friede, Martin

; APPLICANT: Gerard, Catherine

; APPLICANT: Hermand, Philippe

; TITLE OF INVENTION: Vaccines

; FILE REFERENCE: B45181-1

; CURRENT APPLICATION NUMBER: US/09/690,921

; CURRENT FILING DATE: 2000-10-18

; PRIOR APPLICATION NUMBER: PCT/EP00/02920

; PRIOR FILING DATE: 2000-04-04

; PRIOR APPLICATION NUMBER: 09/301,829

```
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 9908885.8
; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human
; US-09-690-921-2

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 36
US-09-301-829A-2
; Sequence 2, Application US/09301829A
; Patent No. 6558670
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Hermand, Philippe
; TITLE OF INVENTION: VACCINES
; FILE REFERENCE: B45181
; CURRENT APPLICATION NUMBER: US/09/301,829A
; CURRENT FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: GB9908885.8
; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunostimulatory oligonucleotide sequence comprising
; OTHER INFORMATION: one or more CpG motifs
US-09-301-829A-2

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 37
US-09-249-247-218
; Sequence 218, Application US/09249247
; Patent No. 6593305
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; FILE REFERENCE: 032396-023
; CURRENT APPLICATION NUMBER: US/09/249,247
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: US 60/023,040
; EARLIER FILING DATE: 1996-08-02
; EARLIER APPLICATION NUMBER: US 60/039,959
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: US 08/904,901
; EARLIER FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
;

; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 9908885.8
; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human
; US-09-690-921-2

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 38
US-09-337-619-45
; Sequence 45, Application US/09337619
; Patent No. 6653292
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Methods of Treating Cancer Using
; FILE REFERENCE: C1039/7021/HCL
; CURRENT APPLICATION NUMBER: US/09/337,619
; CURRENT FILING DATE: 1999-06-21
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-337-619-45

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 39
US-09-835-370-21
; Sequence 21, Application US/09835370
; Patent No. 6777544
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; APPLICANT: WILL, DAVID W
; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
; FILE REFERENCE: 02481.1742 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/09/835,370
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: Description of Artificial Sequence: nucleotide  
; OTHER INFORMATION: base sequence of PNA derivatives that bind to  
; OTHER INFORMATION: viral and cellular targets  
US-09-835-370-21

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
|||||  
Db 5 CCAGCGTGGCCAT 18

## RESULT 40

US-09-634-320-7/c  
; Sequence 7, Application US/09634320  
; Patent No. 6822086  
; GENERAL INFORMATION:  
; APPLICANT: Papisov, Mikhail, I.  
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF  
; FILE REFERENCE: 0838.1003-001  
; CURRENT APPLICATION NUMBER: US/09/634,320  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-634-320-7

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
|||||  
Db 14 CCAGCGTGGCCAT 1

## RESULT 41

US-09-654-373-14  
; Sequence 14, Application US/09654373  
; Patent No. 6835395  
; GENERAL INFORMATION:

; APPLICANT: SEMPLE, Sean C.  
; Klimuk, Sandra K.  
; Harasym, Troy O.  
; Dos Santos, Nancy  
; Ansell, Steven M.  
; Cullis, Pieter R.  
; Hope, Michael J.  
; Scherrer, Peter  
; McIntosh, Deirdre  
; Wong, Kim F.  
; TITLE OF INVENTION: Small Multilamellar Oligodeoxynucleotide-Containing Lipid Vesicles and Method of Making Same

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:  
ADDRESS: Oppedahl & Larson LLP  
STREET: PO Box 5068  
CITY: Dillon  
STATE: CO  
COUNTRY: USA  
ZIP: 80435-5068  
COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS 5.0  
; SOFTWARE: Word Perfect  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/654,373  
; FILING DATE: 01-Sep-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/152,179  
; FILING DATE: SEPTEMBER 2, 1999  
; APPLICATION NUMBER: 09/078,954  
; FILING DATE: MAY 14, 1998  
; APPLICATION NUMBER: 08/856,374  
; FILING DATE: MAY 14, 1997

; ATTORNEY/AGENT INFORMATION:  
; NAME: Marina T. Larson  
; REGISTRATION NUMBER: 32,038  
; REFERENCE/DOCKET NUMBER: INEX.P-007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (970) 468-6600  
; TELEFAX: (970) 468-0104  
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: no  
; ANTI-SENSE: Yes  
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-654-373-14

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
|||||  
Db 5 CCAGCGTGGCCAT 18

## RESULT 42

US-09-724-425-17  
; Sequence 17, Application US/09724425  
; Patent No. 6841541  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION  
; FILE REFERENCE: 04040/1200990-US7  
; CURRENT APPLICATION NUMBER: US/09/724,425  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: US 09/080,285  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: US 08/465,485  
; PRIOR FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: US 08/124,256  
; PRIOR FILING DATE: 1993-09-20  
; PRIOR APPLICATION NUMBER: US 07/840,716  
; PRIOR FILING DATE: 1992-02-21  
; PRIOR APPLICATION NUMBER: US 07/288,692  
; PRIOR FILING DATE: 1988-12-22  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-724-425-17

```
Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 43
US-09-724-425-24
; Sequence 24, Application US/09724425
; Patent No. 6841541
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
; FILE REFERENCE: 04040/1200930-US7
; CURRENT APPLICATION NUMBER: US/09/724,425
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 09/080,285
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: US 08/465,485
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/124,256
; PRIOR FILING DATE: 1993-09-20
; PRIOR APPLICATION NUMBER: US 07/840,716
; PRIOR FILING DATE: 1992-02-21
; PRIOR APPLICATION NUMBER: US 07/288,692
; PRIOR FILING DATE: 1988-12-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-724-425-24

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 44
US-09-895-480A-14
; Sequence 14, Application US/09895480A
; Patent No. 6858225
; GENERAL INFORMATION:
; APPLICANT: Inex Pharmaceuticals Inc.
; TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic
; Agents in Lipid Vesicles
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson LLP
; STREET: PO Box 5068
; CITY: Dillon
; STATE: CO
; COUNTRY: US
; ZIP: 80435
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,480A
```

```
; FILING DATE: 29-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: <Unknown>
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: <Unknown>
; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHEICAL: no
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-895-480A-14

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 45
US-10-002-884A-6
; Sequence 6, Application US/10002884A
; Patent No. 6867043
; GENERAL INFORMATION:
; APPLICANT: Stein, Cy A
; APPLICANT: Benimetskaya, Lyuba
; APPLICANT: Guzzo-Pernell, Nancy
; TITLE OF INVENTION: PEPTIDES THAT COMPLEX WITH ANTISENSE OLIGONUCLEOTIDES WHICH DOWNR
; TITLE OF INVENTION: PKC-PROTEIN EXPRESSION IN CELLS
; FILE REFERENCE: 0575/63293
; CURRENT APPLICATION NUMBER: US/10/002,884A
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: ANTISENSE OLIGONUCLEOTIDE
; US-10-002-884A-6

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCAT 19
Db      5 CCAGCGTGGCCCAT 18

RESULT 46
US-09-108-673A-34
; Sequence 34, Application US/09108673A
; Patent No. 6887306
; GENERAL INFORMATION:
; APPLICANT: Ching-Leou Teng and Greg Hardee
; TITLE OF INVENTION: Compositions and Methods for the Delivery of
```



;; TITLE OF INVENTION: Oligonucleotides Via the Alimentary Canal  
;; NUMBER OF SEQUENCES: 132  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6887906ris LLP  
;; STREET: One Liberty Place, 46th Floor  
;; CITY: Philadelphia  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19103  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
;; COMPUTER: IBM PS/2  
;; OPERATING SYSTEM: PC-DOS  
;; SOFTWARE: WORDPERFECT 6.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/108,673A  
;; FILING DATE: July 1, 1998  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/886,829  
;; FILING DATE: 01-JUL-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Paul K. Legaard  
;; REGISTRATION NUMBER: 38,534  
;; REFERENCE/DOCKET NUMBER: ISIS-3105  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (215) 568-3100  
;; TELEFAX: (215) 568 3439  
;; INFORMATION FOR SEQ ID NO: 34:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 base pairs  
;; TYPE: Nucleic Acid  
;; STRANDEDNESS: Single  
;; TOPOLOGY: Linear  
;; ANTI-SENSE: Yes  
;; FEATURE:  
;; OTHER INFORMATION: Antisense to bcl-2 mRNA; a.k.a. "BCL-2"  
;; PUBLICATION INFORMATION:  
;; DOCUMENT NUMBER: WO 95/08350 (SEQ ID NO:17)  
;; FILING DATE: 20-SEP-1994  
;; PUBLICATION DATE: 30-MAR-1995  
;; US-09-108-673A-34

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

RESULT 47  
US-09-835-371-21  
; Sequence 21, Application US/09835371  
; Patent No. 6905820  
; GENERAL INFORMATION:  
; APPLICANT: UHLMANN, Eugen  
; APPLICANT: BREIPOHL, Gerhard  
; APPLICANT: WILLL, David W  
; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES, AND AGENTS AND  
; TITLE OF INVENTION: PROCESSES FOR PREPARING THEM  
; FILE REFERENCE: 02481.1743 SEQUENCE LISTING  
; CURRENT APPLICATION NUMBER: US/09/835,371  
; CURRENT FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: base sequence

;; OTHER INFORMATION: of PNA targeting CMV  
US-09-835-371-21

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

RESULT 48  
US-09-954-987B-115  
; Sequence 115, Application US/09954987B  
; Patent No. 6943240  
; GENERAL INFORMATION:  
; APPLICANT: Stefan Bauer  
; APPLICANT: Grayson B. Lipford  
; APPLICANT: Hermann Wagner  
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF  
; TITLE OF INVENTION: CDG-BASED IMMUNO-AGONIST/ANTAGONIST  
; FILE REFERENCE: C1041/7016 (AWS)  
; CURRENT APPLICATION NUMBER: US/09/954,987B  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: US 60/233,035  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: US 60/263,657  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: US 60/291,726  
; PRIOR FILING DATE: 2001-05-17  
; PRIOR APPLICATION NUMBER: US 60/300,210  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 230  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 115  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
; US-09-954-987B-115

Query Match 58.3%; Score 14; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

RESULT 49  
US-09-672-126B-110  
; Sequence 110, Application US/09672126B  
; Patent No. 6949520  
; GENERAL INFORMATION:  
; APPLICANT: Hartmann, Gunther  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Krieg, Arthur  
; TITLE OF INVENTION: Methods Related to Immunostimulatory  
; TITLE OF INVENTION: Nucleic Acid-Induced Interferon  
; FILE REFERENCE: C1039/7044  
; CURRENT APPLICATION NUMBER: US/09/672,126B  
; CURRENT FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/156,147  
; PRIOR FILING DATE: 1999-09-29  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 110  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-672-126B-110

Query Match      58.3%; Score 14; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CCACGCGTGC GCCAT 19
      |||||
Db      5 CCACGCGTGC GCCAT 18

RESULT 50
US-09-634-320-8
; Sequence 8, Application US/09634320
; Patent No. 6822086
; GENERAL INFORMATION:
; APPLICANT: Papisov, Mikhail, I.
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 0838.1003-0D1
; CURRENT APPLICATION NUMBER: US/09/634,320
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/147,919
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; OTHER INFORMATION: c indicates an RNA base
US-09-634-320-8

Query Match      58.3%; Score 14; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CCACGCGTGC GCCAT 19
      |||||
Db      5 CCACGCGTGC GCCAT 18

Search completed: February 15, 2006, 21:14:18
Job time : 57.9504 secs

```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 01:43:22 ; Search time 348.298 Seconds  
(without alignments)  
569.815 Million cell updates/sec

Title: US-09-669-187A-81

Perfect score: 24

Sequence: 1 ggggtccagcgtgcgcattggggg 24

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications NA Main:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	3	US-09-888-326-440
2	24	100.0	24	3	US-09-776-479-81
3	24	100.0	24	3	US-09-776-479-81
4	24	100.0	24	5	US-10-112-653-75
5	24	100.0	24	5	US-10-017-995-81
6	24	100.0	24	6	US-10-314-578-81
7	24	100.0	24	8	US-10-831-778-81
8	16.2	67.5	25	5	US-10-005-073-1
9	15.4	64.2	25	7	US-10-719-956-368311
10	15.2	63.3	25	9	US-10-809-189-107962
11	15.2	63.3	25	9	US-10-956-157-200607
12	15.2	63.3	25	10	US-11-036-317-240612
13	15.2	63.3	25	10	US-11-036-317-827644
14	15.2	63.3	35	3	US-09-875-453-69
15	15	62.5	16	3	US-09-888-326-533
16	15	62.5	16	3	US-09-776-479-90
17	15	62.5	16	3	US-09-776-479-90
18	15	62.5	16	5	US-10-112-653-84
19	15	62.5	16	5	US-10-017-995-90
20	15	62.5	16	6	US-10-314-578-90
21	15	62.5	16	8	US-10-831-778-90
22	15	62.5	25	5	US-10-098-263B-96172
23	15	62.5	29	3	US-10-817-387-12
					Sequence 440, App
					Sequence 81, Appl
					Sequence 81, Appl
					Sequence 75, Appl
					Sequence 81, Appl
					Sequence 81, Appl
					Sequence 81, Appl
					Sequence 1, Appl
					Sequence 1, Appl
					Sequence 368311,
					Sequence 107962,
					Sequence 200607,
					Sequence 240612,
					Sequence 827644,
					Sequence 69, Appl
					Sequence 533, App
					Sequence 90, Appl
					Sequence 84, Appl
					Sequence 90, Appl
					Sequence 90, Appl
					Sequence 90, Appl
					Sequence 90, Appl
					Sequence 90, Appl
					Sequence 96172, A
					Sequence 12, Appl

Sequence 91312, A  
Sequence 35445, A  
Sequence 55179, A  
Sequence 87293, A  
Sequence 87909, A  
Sequence 765784,  
Sequence 765785,  
Sequence 773179,  
Sequence 5, Appli  
Sequence 52, Appl  
Sequence 53, Appl  
Sequence 217604,  
Sequence 195172,  
Sequence 228536,  
Sequence 304181,  
Sequence 313397,  
Sequence 531172,  
Sequence 874107,  
Sequence 937038,  
Sequence 942273,  
Sequence 127, App  
Sequence 3, Appli  
Sequence 35, Appl  
Sequence 33, Appl  
Sequence 41, Appl  
Sequence 14, Appl  
Sequence 94301, A  
Sequence 94319, A  
Sequence 91361, A  
Sequence 91541, A  
Sequence 345118,  
Sequence 345119,  
Sequence 879335,  
Sequence 879336,  
Sequence 231532,  
Sequence 540895,  
Sequence 682056,  
Sequence 9, Appli  
Sequence 50, Appl  
Sequence 51, Appl  
Sequence 52, Appl  
Sequence 41, Appl  
Sequence 42, Appl  
Sequence 43, Appl  
Sequence 2, Appli  
Sequence 59, Appl  
Sequence 104, App  
Sequence 77, Appl  
Sequence 98, Appl  
Sequence 99, Appl  
Sequence 51, Appl  
Sequence 51, Appl  
Sequence 51, Appl  
Sequence 21, Appl  
Sequence 21, Appl  
Sequence 21, Appl  
Sequence 755, App  
Sequence 756, App  
Sequence 20, Appl  
Sequence 55, Appl  
Sequence 1, Appli  
Sequence 54, Appl  
Sequence 55, Appl  
Sequence 91, Appl  
Sequence 115, App  
Sequence 14, Appl  
Sequence 14, Appl  
Sequence 1, Appli  
Sequence 54, Appl  
Sequence 55, Appl  
Sequence 91, Appl  
Sequence 51, Appl



243	14	58.3	32	9	US-10-878-175B-19	Sequence 19, Appl
c 244	14	58.3	35	6	US-10-053-645A-2	Sequence 2, Appl
c 245	14	58.3	35	8	US-10-822-205-7	Sequence 7, Appl
c 246	14	58.3	35	9	US-10-961-458-2	Sequence 2, Appl
c 247	14	58.3	36	7	US-10-148-953A-20	Sequence 20, Appl
c 248	14	58.3	40	7	US-10-714-310-19	Sequence 19, Appl
c 249	14	58.3	40	7	US-10-714-310-36	Sequence 36, Appl
c 250	14	58.3	50	6	US-10-131-827-4669	Sequence 4669, Ap
c 251	13.8	57.5	25	7	US-10-719-956-368310	Sequence 368310,
c 252	13.8	57.5	25	7	US-10-719-956-654807	Sequence 654807,
c 253	13.8	57.5	25	8	US-10-719-900-499977	Sequence 499977,
c 254	13.8	57.5	25	9	US-10-809-189-55452	Sequence 55452, A
c 255	13.8	57.5	25	10	US-11-036-317-230523	Sequence 230523,
c 256	13.8	57.5	25	10	US-11-036-317-304711	Sequence 304711,
c 257	13.8	57.5	25	10	US-11-036-317-341671	Sequence 341671,
c 258	13.8	57.5	25	10	US-11-036-317-341671	Sequence 341671,
c 259	13.8	57.5	25	10	US-11-036-317-344131	Sequence 344131,
c 260	13.8	57.5	25	10	US-11-036-317-374577	Sequence 374577,
c 261	13.8	57.5	25	10	US-11-036-317-385736	Sequence 385736,
c 262	13.8	57.5	45	3	US-09-962-055-40	Sequence 40, Appl
c 263	13.8	57.5	45	3	US-09-976-740-40	Sequence 40, Appl
c 264	13.8	57.5	45	3	US-09-971-773-40	Sequence 40, Appl
c 265	13.8	57.5	45	5	US-10-023-529-40	Sequence 40, Appl
c 266	13.8	57.5	45	5	US-10-023-523-40	Sequence 40, Appl
c 267	13.8	57.5	45	7	US-10-616-187-40	Sequence 40, Appl
c 268	13.8	57.5	45	7	US-10-242-40	Sequence 10, Appl
c 269	13.8	57.5	45	7	US-10-409-616-10	Sequence 10, Appl
c 270	13.8	57.5	45	8	US-10-409-611-40	Sequence 40, Appl
c 271	13.6	56.7	47	6	US-10-349-143-3636	Sequence 3636, Ap
c 272	13.6	56.7	25	7	US-10-719-956-150730	Sequence 150730,
c 273	13.6	56.7	25	7	US-10-719-956-258393	Sequence 258393,
c 274	13.6	56.7	25	8	US-10-719-900-362207	Sequence 362207,
c 275	13.6	56.7	25	8	US-10-719-900-693873	Sequence 693873,
c 276	13.6	56.7	25	8	US-10-719-900-909790	Sequence 909790,
c 277	13.6	56.7	25	10	US-11-036-317-96232	Sequence 96232, A
c 278	13.6	56.7	25	10	US-11-036-317-169884	Sequence 169884,
c 279	13.6	56.7	25	10	US-11-036-317-210932	Sequence 210932,
c 280	13.6	56.7	25	10	US-11-036-317-261969	Sequence 261969,
c 281	13.6	56.7	25	10	US-11-036-317-280319	Sequence 280319,
c 282	13.6	56.7	25	10	US-11-036-317-296876	Sequence 296876,
c 283	13.6	56.7	25	10	US-11-036-317-318406	Sequence 318406,
c 284	13.6	56.7	25	10	US-11-036-317-348286	Sequence 348286,
c 285	13.6	56.7	25	10	US-11-036-317-364480	Sequence 364480,
c 286	13.6	56.7	25	10	US-11-036-317-372473	Sequence 372473,
c 287	13.6	56.7	25	10	US-11-036-317-391771	Sequence 391771,
c 288	13.6	56.7	25	10	US-11-036-317-406309	Sequence 406309,
c 289	13.6	56.7	25	10	US-11-036-317-534861	Sequence 534861,
c 290	13.6	56.7	25	10	US-11-036-317-544751	Sequence 544751,
c 291	13.6	56.7	25	10	US-11-036-317-644731	Sequence 644731,
c 292	13.6	56.7	25	10	US-11-036-317-827645	Sequence 827645,
c 293	13.6	56.7	25	10	US-11-036-317-841463	Sequence 841463,
c 294	13.6	56.7	25	10	US-11-036-317-932297	Sequence 932297,
c 295	13.6	56.7	25	10	US-11-036-317-953383	Sequence 953383,
c 296	13.6	56.7	31	6	US-11-060-756-251519	Sequence 251519,
c 297	13.6	56.7	34	8	US-10-349-858-19	Sequence 19, Appl
c 298	13.6	56.7	34	5	US-10-482-926-10	Sequence 10, Appl
c 299	13.4	55.8	25	7	US-10-098-263B-96171	Sequence 96171, A
c 300	13.4	55.8	25	7	US-10-719-956-82043	Sequence 82043, A
			25	7	US-10-719-956-470890	Sequence 470890,

Query Match 100.0%; Score 24; DB 3; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCATGGGG 24  
Db 1 GGGTCCAGCGTGGCCATGGGG 24

RESULT 2  
US-09-776-479-81  
; Sequence 81, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 81  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-81

Query Match 100.0%; Score 24; DB 3; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCATGGGG 24  
Db 1 GGGTCCAGCGTGGCCATGGGG 24

RESULT 3  
US-09-776-479-81  
; Sequence 81, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479

ALIGNMENTS

RESULT 1  
US-09-888-326-440  
; Sequence 440, Application US/09888326  
; Publication No. US20030026801A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Hartmann, Gunther  
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced  
; TITLE OF INVENTION: Cell Lysis and Treating Cancer  
; FILE REFERENCE: C1039/7052 (AWS)

```
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-81

Query Match      100.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCCATGGGG 24
Db 1 GGGTCCAGCGTGGCCCATGGGG 24

RESULT 4
US-10-112-653-75
; Sequence 75, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060 (AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-75

Query Match      100.0%; Score 24; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCCATGGGG 24
Db 1 GGGTCCAGCGTGGCCCATGGGG 24

RESULT 5
US-10-017-995-81
; Sequence 81, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-81

Query Match      100.0%; Score 24; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCCATGGGG 24
Db 1 GGGTCCAGCGTGGCCCATGGGG 24

RESULT 6
US-10-314-578-81
; Sequence 81, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-81

Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCCATGGGG 24
Db 1 GGGTCCAGCGTGGCCCATGGGG 24

RESULT 7
US-10-831-778-81
; Sequence 81, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
```

US-10-831-778-81

Query Match 100.0%; Score 24; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.7; Indels 0; Gaps 0;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTCCAGCGTGCCTATGGGG 24  
Db 1 GGGTCCAGCGTGCCTATGGGG 24

RESULT 8

US-10-005-073-1  
; Sequence 1, Application US/10005073  
; Publication No. US2002090371A1  
; GENERAL INFORMATION:  
; APPLICANT: Jevnikar, Anthony M.  
; Ma, Shengwu  
; Stiller, Calvin R.  
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR CONTROLLING  
; IMMUNE RESPONSES IN MAMMALS  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis, L.L.P.  
; STREET: George Mason Building, 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22314-3187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/005,073  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/617,874  
; FILING DATE: 21-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rea, Teresa Stanek  
; REGISTRATION NUMBER: 30,427  
; REFERENCE/DOCKET NUMBER: 024916-002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA - primer"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-005-073-1

Query Match 67.5%; Score 16.2; DB 5; Length 25;  
Best Local Similarity 85.7%; Pred. No. 3.4e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGCCTATGGG 22  
Db 2 GGATCCGCGCGCCATGGG 22

RESULT 9

US-10-719-956-368311/c  
; Sequence 368311, Application US/10719956  
; Publication No. US20040146910A1  
; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat  
; FILE REFERENCE: 3527.1  
; CURRENT APPLICATION NUMBER: US/10/719,956  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,836  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 699466  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 368311  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-10-719-956-368311

Query Match 64.2%; Score 15.4; DB 7; Length 25;  
Best Local Similarity 94.1%; Pred. No. 7.4e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 GGTCCAGCGTGCCTATGG 19  
Db 18 GTTCCAGCGTGCCTATGG 2

RESULT 10

US-10-809-189-107962  
; Sequence 107962, Application US/10809189  
; Publication No. US20050048531A1  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/10/809,189  
; CURRENT FILING DATE: 2004-03-25  
; PRIOR APPLICATION NUMBER: US/09/396,196  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 107962  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-10-809-189-107962

Query Match 63.3%; Score 15.2; DB 9; Length 25;  
Best Local Similarity 85.0%; Pred. No. 9e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 3 GGTCCAGCGTGCCTATGGG 22  
Db 1 GTTCCAGCGTGCCTATGGG 20

RESULT 11

US-10-956-157-200607/c  
; Sequence 200607, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 200607

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-200607

Query Match      63.3%; Score 15.2; DB 9; Length 25;
Best Local Similarity 85.0%; Pred. No. 9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGCCTGG 21
Db 20 GGGTCCAGCATTTGCCATGG 1

RESULT 12
US-11-036-317-240612/c
; Sequence 240612, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 240612
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-240612

Query Match      63.3%; Score 15.2; DB 10; Length 25;
Best Local Similarity 85.0%; Pred. No. 9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGCCTGG 21
Db 20 GGGTCCGCGTGCCTGG 1

RESULT 13
US-11-036-317-827644/c
; Sequence 827644, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 827644
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-827644

Query Match      63.3%; Score 15.2; DB 10; Length 25;
Best Local Similarity 85.0%; Pred. No. 9e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGCCTGG 21
Db 23 GGGGCTCGTTCGCTGG 4
```

```
RESULT 14
US-09-875-453-69/c
; Sequence 69, Application US/09875453
; Publication No. US20030027320A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lam, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 4600-0135.30
; CURRENT APPLICATION NUMBER: US/09/875,453
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-875-453-69

Query Match      63.3%; Score 15.2; DB 3; Length 35;
Best Local Similarity 85.0%; Pred. No. 8.3e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGCCTGG 21
Db 28 GGGTCCAGCGGAGCCATGG 9

RESULT 15
US-09-888-326-533
; Sequence 533, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 533
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-533

Query Match      62.5%; Score 15; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
```



Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
Db 1 TCCAGCGTGC GCCAT 15

## RESULT 16

US-09-776-479-90  
; Sequence 90, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 90  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-90

Query Match 62.5%; Score 15; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
Db 1 TCCAGCGTGC GCCAT 15

## RESULT 17

US-09-776-479-90  
; Sequence 90, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 90  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-90

Query Match 62.5%; Score 15; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
Db 1 TCCAGCGTGC GCCAT 15

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 18  
US-10-112-653-84  
; Sequence 84, Application US/10112653  
; Publication No. US20030050268A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR  
; FILE REFERENCE: C01039/70060(AWS)  
; CURRENT APPLICATION NUMBER: US/10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 84  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-112-653-84

Query Match 62.5%; Score 15; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
Db 1 TCCAGCGTGC GCCAT 15

## RESULT 19

US-10-017-995-90  
; Sequence 90, Application US/10017995  
; Publication No. US20030055014A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
; FILE REFERENCE: C1037/7025 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/017,995  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,534  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 90  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-017-995-90

Query Match 62.5%; Score 15; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGC GCCAT 19  
Db 1 TCCAGCGTGC GCCAT 15

## RESULT 20

US-10-314-578-90  
; Sequence 90, Application US/10314578  
; Publication No. US20030212026A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schetter, Christian

```
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-10-314-578-90

Query Match      62.5%; Score 15; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5  TCCAGCGTGCGCCCAT 19
Db      1  TCCAGCGTGCGCCCAT 15

RESULT 21
US-10-831-778-90
; Sequence 90, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-10-831-778-90

Query Match      62.5%; Score 15; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5  TCCAGCGTGCGCCCAT 19
Db      1  TCCAGCGTGCGCCCAT 15

RESULT 22
US-10-098-263B-96172/c
; Sequence 96172, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mitzman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B

; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-10-314-578-90

Query Match      62.5%; Score 15; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5  TCCAGCGTGCGCCCAT 19
Db      1  TCCAGCGTGCGCCCAT 15

RESULT 23
US-09-817-387-12
; Sequence 12, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotides, linkages between positions 1
; OTHER INFORMATION: to 18 are phosphorothioates, linkages between
; OTHER INFORMATION: positions 18 to 26 are phosphodiester
; OTHER INFORMATION: positions 19 to 29 carry 2'-OCH3 modified ribosyl
; OTHER INFORMATION: residues
; OTHER INFORMATION: linkages between positions 26 to 29 are
; OTHER INFORMATION: phosphorothioates
; US-09-817-387-12

Query Match      62.5%; Score 15; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  CCAGCGTGCGCCCATG 20
Db      5  CCAGCGTGCGCCCATG 19

RESULT 24
US-10-719-900-91312
; Sequence 91312, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
```

```
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 91312
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-91312

Query Match      61.7%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      7 CAGCGTGCCTCCATGGGG 24
        ||||| ||||| ||||| |||||
Db      7 CAGCGTGCCTCCATGGG 24

RESULT 25
US-10-098-263B-35445
; Sequence 35445, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 35445
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-35445

Query Match      60.8%; Score 14.6; DB 5; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GTCCAGCGTGCCTCCATGGGG 24
        ||||| ||||| ||||| |||||
Db      1 GTCCACTGTGCTCCATGGGT 21

RESULT 26
US-10-098-263B-55179
; Sequence 55179, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 55179
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-55179

Query Match      60.8%; Score 14.6; DB 5; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GTCCAGCGTGCCTCCATGGGG 24
        ||||| ||||| ||||| |||||
Db      1 GTCCACTGTGCTCCATGGGT 24
```

```
RESULT 27
US-10-098-263B-87293
; Sequence 87293, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87293
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87293

Query Match      60.8%; Score 14.6; DB 5; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GTCCAGCGTGCCTCCATGGGG 24
        ||||| ||||| ||||| |||||
Db      3 GTCCACTGTGCTCCATGGGT 23

RESULT 28
US-10-098-263B-87909
; Sequence 87909, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87909
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-87909

Query Match      60.8%; Score 14.6; DB 5; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4 GTCCAGCGTGCCTCCATGGGG 24
        ||||| ||||| ||||| |||||
Db      3 GTCCACTGTGCTCCATGGGT 23

RESULT 29
US-10-719-900-765784
; Sequence 765784, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 765784
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-765784

Query Match      60.8%; Score 14.6; DB 8; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGG 21
Db 4 GTGGACCAGAGTGTGCCATGG 24

RESULT 30
US-10-719-900-765785
; Sequence 765785, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 765785
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-765785

Query Match      60.8%; Score 14.6; DB 8; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGG 21
Db 4 GTGGACCAGAGTGTGCCATGG 24

RESULT 31
US-11-036-317-773179/c
; Sequence 773179, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 773179
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-773179

Query Match      60.8%; Score 14.6; DB 10; Length 25;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGG 21
Db 22 GGGCTCCAGCATAGCCATGG 2

RESULT 32
US-09-866-073-5
; Sequence 5, Application US/09866073
; Patent No. US20020068272A1
; GENERAL INFORMATION:
; APPLICANT: Larocca, David
; APPLICANT: Baird, Andrew
; APPLICANT: Kassner, Paul
; TITLE OF INVENTION: METHODS USING GENETIC PACKAGE DISPLAY FOR
; TITLE OF INVENTION: DETECTING AND IDENTIFYING PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTIONS THAT FACILITATE INTERNALIZATION
; TITLE OF INVENTION: AND TRANSGENE EXPRESSION AND CELLS OR TISSUE
; TITLE OF INVENTION: COMPETENT FOR THE SAME AND METHODS FOR EVOLVING
; TITLE OF INVENTION: GENE DELIVERY VECTORS
; FILE REFERENCE: 760100.430C4
; CURRENT APPLICATION NUMBER: US/09/866,073
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-866-073-5

Query Match      60.8%; Score 14.6; DB 3; Length 47;
Best Local Similarity 81.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGG 21
Db 10 GGGTTCCTCCGCGTGGCGCATGG 30

RESULT 33
US-10-151-204-5
; Sequence 5, Application US/10151204
; Publication No. US20030148263A1
; GENERAL INFORMATION:
; APPLICANT: Larocca, David
; APPLICANT: Kassner, Paul
; APPLICANT: Baird, Andrew
; APPLICANT: Burg, Michael
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USING
; TITLE OF INVENTION: GENETIC PACKAGE DISPLAY
; FILE REFERENCE: 760100.430CS
; CURRENT APPLICATION NUMBER: US/10/151,204
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-151-204-5

Query Match      60.8%; Score 14.6; DB 6; Length 47;
Best Local Similarity 81.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGGGTCCAGCGTGGCCATGG 21
Db 10 GGGTTCCTCCGCGTGGCGCATGG 30

RESULT 34
US-10-735-592-52
; Sequence 52, Application US/10735592
```

```

; Publication No. US20040017157A1
;
; GENERAL INFORMATION:
; APPLICANT: Art, Krieg
; APPLICANT: Joerg, Vollmer
; TITLE OF INVENTION: 5' CPG Nuc
; FILE REFERENCE: C1037.70038US0
; CURRENT APPLICATION NUMBER: US
; CURRENT FILING DATE: 2003-12-
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent version 3.2
; SEQ ID NO 52
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
;
; FEATURES:
;
; US-10-735-592-52
; US-10-735-592-52

```

Query Match 60.0%; Score 14.4; DB 7; Length 18;  
Best Local Similarity 93.8%; Pred. No. 2.1e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels

Qy 4 GTCCAGCGTGC GCCAT 19  
Dp 3 GTCGAGCGTGC GCCAT 18

```

RESULT 35
US-10-735-592-53
; Sequence 53, Application US/10735592
; Publication No. US20040171571A1
; GENERAL INFORMATION:
; APPLICANT: Art, Krieg
; APPLICANT: Joerg, Vollmer
; TITLE OF INVENTION: 5' CPG Nucleic
; FILE REFERENCE: C1037.70038US01
; CURRENT APPLICATION NUMBER: US/10/7
; CURRENT FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic oligo
US-10-735-592-53

```

```
Query Match          60.0%; Score 14.4; DB 7; Length 18;
Best Local Similarity 93.8%; Pred. No. 2.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 4 GTCCAGCGTGC GCCAT 19  
Db 3 GCCAGCGTGC GCCAT 18

```

RESULT 36
US-10-719-900-217604
; Sequence 217604, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 217604
; LENGTH: 25

```

; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-217604

```

Query Match      50.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 75.0%; Pred.NO. 2e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0
Qy 1 GGGGTCCAGCGTGCCTATGGGG 24
    | | | | | | | | | |
Db 2 GTGGTCCAGTGTCTCCATCAGG 25
    | | | | | | | | | |

```

```

RESULT 37
US-11-036-317-195172
; Sequence 195172, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blum, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 195172
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-195172

```

```
Query Match      60.0%;   Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%;
Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

RESULT 38
US-11-036-317-228536
; Sequence 228536, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 228536
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-228536

```

```
Query Match      60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

RESULT 39
US-11-036-317-304181
; Sequence 304181, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 304181
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-304181

Query Match          60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGC GCC 17
| | | | | | | | | |
Db 4 GCGTCCAGCGTGC GCC 19

RESULT 40
US-11-036-317-313397
; Sequence 313397, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 313397
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-313397

Query Match          60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGC GCC 17
| | | | | | | | | |
Db 1 GCGTCCAGCGTGC GCC 16

RESULT 41
US-11-036-317-531172/c
; Sequence 531172, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13

```

```

; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 531172
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-531172

Query Match          60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGC GCC 16
| | | | | | | | | |
Db 23 GCGTCCAGCGTGC GCC 8

RESULT 42
US-11-036-317-874107
; Sequence 874107, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 874107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-874107

Query Match          60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGC GCC 17
| | | | | | | | | |
Db 2 GCGTCCAGCGTGC GCC 17

RESULT 43
US-11-036-317-937038
; Sequence 937038, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 937038
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-937038

Query Match          60.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGC GCC 17

```



```
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
; FILE REFERENCE: 10412-022-999
; CURRENT APPLICATION NUMBER: US/10/053,645A
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,244
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
; OTHER INFORMATION: Oligonucleotide
US-10-053-645A-35

Query Match          60.0%; Score 14.4; DB 6; Length 34;
Best Local Similarity 93.8%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCATGG 21
Db      13 CCAGCGTGGCCCATGG 28

RESULT 49
US-10-053-645A-41
; Sequence 41, Application US/10053645A
; Publication No. US20030176376A1
; GENERAL INFORMATION:
; APPLICANT: Robert E. Klem
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
; TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
; FILE REFERENCE: 10412-022-999
; CURRENT APPLICATION NUMBER: US/10/053,645A
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,244
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
; OTHER INFORMATION: Oligonucleotide
US-10-053-645A-41

Query Match          60.0%; Score 14.4; DB 6; Length 34;
Best Local Similarity 93.8%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 CCAGCGTGGCCCATGG 21
Db      13 CCAGCGTGGCCCATGG 28

RESULT 50
US-10-911-374-14
; Sequence 14, Application US/10911374
; Publication No. US20050003531A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Mahendra S
; APPLICANT: Mayer-Proschel, Margot
; APPLICANT: Kalyani, Anjali J
; TITLE OF INVENTION: Lineage-Restricted Neuronal Precursors
; FILE REFERENCE: T5530.CIP
; CURRENT APPLICATION NUMBER: US/10/911,374
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US/09/109,858
```

```
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 08/909,435
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-911-374-14

Query Match          59.2%; Score 14.2; DB 8; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.6e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 GGTCCAGCGTGGCCCATGG 21
Db      1 GGTCCAGCATTTGCCATGG 19

Search completed: February 16, 2006, 02:34:08
Job time : 352.298 secs
```



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 02:03:53 ; Search time 223.736 Seconds  
(without alignments)  
98.157 Million cell updates/sec

Title: US-09-669-187a-81

Perfect score: 24

Sequence: 1 ggggtccagctgcgcattggggg 24

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6247088 seqs, 457523669 residues

Total number of hits satisfying chosen parameters: 11812030

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications NA New.\*

1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*

2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*

3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*

4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*

5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*

6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*

7: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*

8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

12: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	11	US-11-127-654-75
2	16.2	67.5	25	11	US-11-127-654-75
3	16	66.7	25	7	US-10-310-914A-402269
4	16	66.7	30	11	US-11-201-322-2
5	15.8	65.8	22	7	US-10-310-914A-1185838
6	15.8	65.8	25	11	US-11-121-849-235244
7	15.2	63.3	24	7	US-10-310-914A-34498
8	15	62.5	16	11	US-11-127-654-84
9	15	62.5	23	7	US-10-310-914A-94891
10	15	62.5	25	11	US-11-121-849-23997
11	15	62.5	25	11	US-11-121-849-46868
12	15	62.5	25	11	US-11-121-849-46869
13	14.6	60.8	21	7	US-10-310-914A-45418
14	14.6	60.8	21	7	US-10-310-914A-402274
15	14.6	60.8	24	7	US-10-310-914A-38276
16	14.6	60.8	26	7	US-10-310-914A-895311
17	14.4	60.0	21	7	US-10-310-914A-650086
18	14.2	59.2	24	7	US-10-310-914A-721320
19	14	58.3	18	6	US-10-994-213-7
20	14	58.3	18	7	US-10-918-638-24
21	14	58.3	18	7	US-10-658-947-14

18	7	US-10-469-561-6	58.3	14	22
18	7	US-10-619-279-45	58.3	14	23
18	7	US-10-435-656-55	58.3	14	24
18	11	US-11-127-654-1	58.3	14	25
18	11	US-11-127-654-85	58.3	14	26
18	11	US-11-081-140-6	58.3	14	27
18	11	US-11-134-918-55	58.3	14	28
18	11	US-11-031-460-55	58.3	14	29
18	11	US-11-067-587-55	58.3	14	30
18	11	US-11-099-683-131	58.3	14	31
18	11	US-11-099-683-132	58.3	14	32
18	11	US-11-099-683-132	58.3	14	33
18	11	US-11-099-683-132	58.3	14	34
18	11	US-11-099-683-132	58.3	14	35
18	11	US-11-099-683-132	58.3	14	36
18	11	US-11-099-683-132	58.3	14	37
18	11	US-11-099-683-132	58.3	14	38
18	11	US-11-099-683-132	58.3	14	39
18	11	US-11-099-683-132	58.3	14	40
18	11	US-11-099-683-132	58.3	14	41
18	11	US-11-099-683-132	58.3	14	42
18	11	US-11-099-683-132	58.3	14	43
18	11	US-11-099-683-132	58.3	14	44
18	11	US-11-099-683-132	58.3	14	45
18	11	US-11-099-683-132	58.3	14	46
18	11	US-11-099-683-132	58.3	14	47
18	11	US-11-099-683-132	58.3	14	48
18	11	US-11-099-683-132	58.3	14	49
18	11	US-11-099-683-132	58.3	14	50
18	11	US-11-099-683-132	58.3	14	51
18	11	US-11-099-683-132	58.3	14	52
18	11	US-11-099-683-132	58.3	14	53
18	11	US-11-099-683-132	58.3	14	54
18	11	US-11-099-683-132	58.3	14	55
18	11	US-11-099-683-132	58.3	14	56
18	11	US-11-099-683-132	58.3	14	57
18	11	US-11-099-683-132	58.3	14	58
18	11	US-11-099-683-132	58.3	14	59
18	11	US-11-099-683-132	58.3	14	60
18	11	US-11-099-683-132	58.3	14	61
18	11	US-11-099-683-132	58.3	14	62
18	11	US-11-099-683-132	58.3	14	63
18	11	US-11-099-683-132	58.3	14	64
18	11	US-11-099-683-132	58.3	14	65
18	11	US-11-099-683-132	58.3	14	66
18	11	US-11-099-683-132	58.3	14	67
18	11	US-11-099-683-132	58.3	14	68
18	11	US-11-099-683-132	58.3	14	69
18	11	US-11-099-683-132	58.3	14	70
18	11	US-11-099-683-132	58.3	14	71
18	11	US-11-099-683-132	58.3	14	72
18	11	US-11-099-683-132	58.3	14	73
18	11	US-11-099-683-132	58.3	14	74
18	11	US-11-099-683-132	58.3	14	75
18	11	US-11-099-683-132	58.3	14	76
18	11	US-11-099-683-132	58.3	14	77
18	11	US-11-099-683-132	58.3	14	78
18	11	US-11-099-683-132	58.3	14	79
18	11	US-11-099-683-132	58.3	14	80
18	11	US-11-099-683-132	58.3	14	81
18	11	US-11-099-683-132	58.3	14	82
18	11	US-11-099-683-132	58.3	14	83
18	11	US-11-099-683-132	58.3	14	84
18	11	US-11-099-683-132	58.3	14	85
18	11	US-11-099-683-132	58.3	14	86
18	11	US-11-099-683-132	58.3	14	87
18	11	US-11-099-683-132	58.3	14	88
18	11	US-11-099-683-132	58.3	14	89
18	11	US-11-099-683-132	58.3	14	90
18	11	US-11-099-683-132	58.3	14	91
18	11	US-11-099-683-132	58.3	14	92
18	11	US-11-099-683-132	58.3	14	93
18	11	US-11-099-683-132	58.3	14	94

95	13.2	55.0	23	7	US-10-310-914A-1287448	Sequence 1287448,	168	12.8	53.3	24	7	US-10-310-914A-1322959	Sequence 1322959,
c 96	13.2	55.0	25	7	US-10-310-914A-952672	Sequence 952672,	c 169	12.8	53.3	25	7	US-10-310-914A-124102	Sequence 124102,
97	13.2	55.0	25	11	US-11-121-849-46863	Sequence 46863, A	c 170	12.8	53.3	25	7	US-10-310-914A-654008	Sequence 654008,
c 98	13.2	55.0	25	11	US-11-121-849-46864	Sequence 46864, A	c 171	12.8	53.3	25	7	US-10-310-914A-888056	Sequence 888056,
c 99	13.2	55.0	25	11	US-11-121-849-161691	Sequence 161691,	c 172	12.8	53.3	25	7	US-10-310-914A-937024	Sequence 937024,
c 100	13.2	55.0	25	11	US-11-121-849-218741	Sequence 218741,	c 173	12.8	53.3	25	7	US-10-310-914A-1108583	Sequence 1108583,
c 101	13.2	55.0	25	11	US-11-121-849-485732	Sequence 485732,	c 174	12.8	53.3	25	11	US-11-121-849-4918	Sequence 4918, Ap
c 102	13.2	55.0	25	11	US-11-121-849-530933	Sequence 530933,	c 175	12.8	53.3	25	11	US-11-121-849-115647	Sequence 115647,
c 103	13.2	55.0	25	11	US-11-121-849-510833	Sequence 510833,	c 176	12.8	53.3	25	11	US-11-121-849-119305	Sequence 119305,
c 104	13.2	55.0	25	11	US-11-136-527-322812	Sequence 322812,	c 177	12.8	53.3	25	11	US-11-121-849-152114	Sequence 152114,
c 105	13.2	55.0	25	11	US-11-136-527-322827	Sequence 322827,	c 178	12.8	53.3	25	11	US-11-121-849-277491	Sequence 277491,
c 106	13.2	55.0	32	7	US-10-939-294A-17085	Sequence 17085, A	c 179	12.8	53.3	25	11	US-11-121-849-477615	Sequence 477615,
c 107	13.2	55.0	32	7	US-10-939-294A-19184	Sequence 19184, A	c 180	12.8	53.3	25	11	US-11-121-849-495760	Sequence 495760,
c 108	13.2	55.0	32	7	US-10-939-294A-19322	Sequence 19322, A	c 181	12.8	53.3	25	11	US-11-121-849-531561	Sequence 531561,
c 109	13.2	55.0	32	7	US-10-939-294A-19614	Sequence 19614, A	c 182	12.8	53.3	25	11	US-11-121-849-561885	Sequence 561885,
c 110	13	54.2	18	7	US-10-310-914A-1145446	Sequence 1145446,	c 183	12.8	53.3	25	11	US-11-136-527-202901	Sequence 202901,
c 111	13	54.2	21	7	US-10-310-914A-650092	Sequence 650092,	c 184	12.8	53.3	25	11	US-11-136-527-202912	Sequence 202912,
c 112	13	54.2	21	7	US-10-310-914A-999814	Sequence 999814,	c 185	12.8	53.3	25	11	US-11-136-527-213830	Sequence 213830,
c 113	13	54.2	21	7	US-10-310-914A-1326696	Sequence 1326696,	c 186	12.8	53.3	25	11	US-10-310-914A-456437	Sequence 456437,
c 114	13	54.2	21	7	US-10-310-914A-1349496	Sequence 1349496,	c 187	12.8	53.3	26	7	US-10-310-914A-584159	Sequence 584159,
c 115	13	54.2	21	7	US-10-310-914A-1353255	Sequence 1353255,	c 188	12.8	53.3	27	7	US-10-310-914A-16826	Sequence 16826, A
c 116	13	54.2	22	7	US-10-310-914A-247384	Sequence 247384,	c 189	12.8	53.3	32	7	US-10-939-294A-19144	Sequence 19144, A
c 117	13	54.2	22	7	US-10-310-914A-419193	Sequence 419193,	c 190	12.8	53.3	32	7	US-10-310-914A-143463	Sequence 143463,
c 118	13	54.2	22	7	US-10-310-914A-43799	Sequence 43799,	c 191	12.6	52.5	19	7	US-10-310-914A-329734	Sequence 329734,
c 119	13	54.2	22	7	US-10-310-914A-919447	Sequence 919447,	c 192	12.6	52.5	19	7	US-10-310-914A-45398	Sequence 45398, A
c 120	13	54.2	23	7	US-10-310-914A-192445	Sequence 192445,	c 193	12.6	52.5	20	7	US-10-310-914A-362430	Sequence 362430,
c 121	13	54.2	23	7	US-10-310-914A-373241	Sequence 373241,	c 194	12.6	52.5	20	7	US-10-310-914A-949114	Sequence 949114,
c 122	13	54.2	23	7	US-10-310-914A-779267	Sequence 779267,	c 195	12.6	52.5	20	7	US-10-310-914A-996597	Sequence 996597,
c 123	13	54.2	23	7	US-10-310-914A-779288	Sequence 779288,	c 196	12.6	52.5	20	7	US-10-310-914A-965524	Sequence 965524,
c 124	13	54.2	23	7	US-10-310-914A-854057	Sequence 854057,	c 197	12.6	52.5	21	7	US-10-310-914A-313024	Sequence 313024,
c 125	13	54.2	24	7	US-10-310-914A-543153	Sequence 543153,	c 198	12.6	52.5	21	11	US-11-099-683-106	Sequence 106, App
c 126	13	54.2	25	7	US-10-310-914A-1120422	Sequence 1120422,	c 199	12.6	52.5	22	7	US-10-310-914A-227730	Sequence 227730,
c 127	13	54.2	25	7	US-10-310-914A-1145447	Sequence 1145447,	c 200	12.6	52.5	22	7	US-10-310-914A-313230	Sequence 313230,
c 128	13	54.2	25	11	US-11-121-849-46871	Sequence 46871, A	c 201	12.6	52.5	22	7	US-10-310-914A-313230	Sequence 313230,
c 129	13	54.2	25	11	US-11-121-849-58477	Sequence 58477, A	c 202	12.6	52.5	22	7	US-10-310-914A-338152	Sequence 338152,
c 130	13	54.2	25	11	US-11-121-849-111933	Sequence 111933,	c 203	12.6	52.5	22	7	US-10-310-914A-553929	Sequence 553929,
c 131	13	54.2	25	11	US-11-121-849-151665	Sequence 151665,	c 204	12.6	52.5	22	7	US-10-310-914A-919628	Sequence 919628,
c 132	13	54.2	25	11	US-11-121-849-274533	Sequence 274533,	c 205	12.6	52.5	22	7	US-10-310-914A-1059406	Sequence 1059406,
c 133	13	54.2	25	11	US-11-121-849-428663	Sequence 428663,	c 206	12.6	52.5	22	7	US-10-310-914A-1353243	Sequence 1353243,
c 134	13	54.2	25	11	US-11-136-527-272460	Sequence 272460,	c 207	12.6	52.5	23	7	US-10-310-914A-63757	Sequence 63757, A
c 135	13	54.2	26	7	US-10-310-914A-252968	Sequence 252968,	c 208	12.6	52.5	23	7	US-10-310-914A-81055	Sequence 81055, A
c 136	13	54.2	26	7	US-10-310-914A-1145495	Sequence 1145495,	c 209	12.6	52.5	23	7	US-10-310-914A-81055	Sequence 81055, A
c 137	13	54.2	32	7	US-10-939-294A-15978	Sequence 15978, A	c 210	12.6	52.5	23	7	US-10-310-914A-313231	Sequence 313231,
c 138	13	54.2	32	7	US-10-939-294A-17843	Sequence 17843, A	c 211	12.6	52.5	23	7	US-10-310-914A-313245	Sequence 313245,
c 139	12.8	53.3	18	7	US-10-310-914A-357751	Sequence 357751,	c 212	12.6	52.5	23	7	US-10-310-914A-751283	Sequence 751283,
c 140	12.8	53.3	18	7	US-10-310-914A-1185928	Sequence 1185928,	c 213	12.6	52.5	23	7	US-10-310-914A-771167	Sequence 771167,
c 141	12.8	53.3	19	7	US-10-310-914A-1223834	Sequence 1223834,	c 214	12.6	52.5	23	7	US-10-310-914A-919581	Sequence 919581,
c 142	12.8	53.3	19	9	US-11-101-244-211677	Sequence 211677,	c 215	12.6	52.5	24	7	US-10-310-914A-30115	Sequence 30115, A
c 143	12.8	53.3	19	9	US-11-101-244-211779	Sequence 211779,	c 216	12.6	52.5	24	7	US-10-310-914A-313025	Sequence 313025,
c 144	12.8	53.3	19	9	US-11-101-244-211877	Sequence 211877,	c 217	12.6	52.5	24	7	US-10-310-914A-313231	Sequence 313231,
c 145	12.8	53.3	19	9	US-11-101-244-1175465	Sequence 1175465,	c 218	12.6	52.5	24	7	US-10-310-914A-313246	Sequence 313246,
c 146	12.8	53.3	19	10	US-11-083-784-211677	Sequence 211677,	c 219	12.6	52.5	24	7	US-10-310-914A-313284	Sequence 313284,
c 147	12.8	53.3	19	10	US-11-083-784-211779	Sequence 211779,	c 220	12.6	52.5	24	7	US-10-310-914A-362492	Sequence 362492,
c 148	12.8	53.3	19	10	US-11-083-784-211877	Sequence 211877,	c 221	12.6	52.5	24	7	US-10-310-914A-362500	Sequence 362500,
c 149	12.8	53.3	19	10	US-11-083-784-1175465	Sequence 1175465,	c 222	12.6	52.5	24	7	US-10-310-914A-412606	Sequence 412606,
c 150	12.8	53.3	20	7	US-10-310-914A-157160	Sequence 157160,	c 223	12.6	52.5	24	7	US-10-310-914A-525261	Sequence 525261,
c 151	12.8	53.3	20	7	US-10-310-914A-283526	Sequence 283526,	c 224	12.6	52.5	24	7	US-10-310-914A-528504	Sequence 528504,
c 152	12.8	53.3	21	7	US-10-310-914A-157161	Sequence 157161,	c 225	12.6	52.5	24	7	US-10-310-914A-528562	Sequence 528562,
c 153	12.8	53.3	21	7	US-10-310-914A-1117009	Sequence 1117009,	c 226	12.6	52.5	24	7	US-10-310-914A-528571	Sequence 528571,
c 154	12.8	53.3	22	7	US-10-310-914A-283540	Sequence 283540,	c 227	12.6	52.5	24	7	US-10-310-914A-865117	Sequence 865117,
c 155	12.8	53.3	22	7	US-10-310-914A-283541	Sequence 283541,	c 228	12.6	52.5	24	7	US-10-310-914A-865135	Sequence 865135,
c 156	12.8	53.3	22	7	US-10-310-914A-309014	Sequence 309014,	c 229	12.6	52.5	24	7	US-10-310-914A-865245	Sequence 865245,
c 157	12.8	53.3	22	7	US-10-310-914A-654321	Sequence 654321,	c 230	12.6	52.5	24	7	US-10-310-914A-865255	Sequence 865255,
c 158	12.8	53.3	23	7	US-10-310-914A-157162	Sequence 157162,	c 231	12.6	52.5	24	7	US-10-310-914A-865278	Sequence 865278,
c 159	12.8	53.3	23	7	US-10-310-914A-1151691	Sequence 1151691,	c 232	12.6	52.5	24	7	US-10-310-914A-919569	Sequence 919569,
c 160	12.8	53.3	23	7	US-10-310-914A-1223835	Sequence 1223835,	c 233	12.6	52.5	24	7	US-10-310-914A-919580	Sequence 919580,
c 161	12.8	53.3	24	7	US-10-310-914A-29969	Sequence 29969, A	c 234	12.6	52.5	24	7	US-10-310-914A-919629	Sequence 919629,
c 162	12.8	53.3	24	7	US-10-310-914A-33594	Sequence 33594, A	c 235	12.6	52.5	24	7	US-10-310-914A-1059297	Sequence 1059297,
c 163	12.8	53.3	24	7	US-10-310-914A-81056	Sequence 81056, A	c 236	12.6	52.5	24	7	US-10-310-914A-1059426	Sequence 1059426,
c 164	12.8	53.3	24	7	US-10-310-914A-206783	Sequence 206783,	c 237	12.6	52.5	24	7	US-10-310-914A-1059466	Sequence 1059466,
c 165	12.8	53.3	24	7	US-10-310-914A-456389	Sequence 456389,	c 238	12.6	52.5	24	7	US-10-310-914A-1138903	Sequence 1138903,
c 166	12.8	53.3	24	7	US-10-310-914A-1144958	Sequence 1144958,	c 239	12.6	52.5	24	7		
c 167	12.8	53.3	24	7	US-10-310-914A-1204871	Sequence 1204871,	c 240	12.6	52.5	24	7		



```
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-402269

Query Match      66.7%; Score 16; DB 7; Length 25;
Best Local Similarity 70.8%; Pred. No. 5.4e+02;
Matches 17; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCAGCGTGGCCATGGGG 24
    |||||
Db 2 GGGGCCAGCGUCCACCGUGGG 25

RESULT 4
US-11-201-322-2/c
; Sequence 2, Application US/11201322
; Publication No. US20050272129A1
; GENERAL INFORMATION:
; APPLICANT: Sharon, Amir
; APPLICANT: Goldstein-Barhoom, Sima
; TITLE OF INVENTION: TRANSGENIC FUNGI EXPRESSING BCL-2 AND METHODS OF USING BCL-2 OR F
; TITLE OF INVENTION: THEREOF FOR IMPROVING BIOMASS PRODUCTION, SURVIVAL, LONGEVITY AN
; TITLE OF INVENTION: RESISTANCE OF FUNGI
; FILE REFERENCE: 30302
; CURRENT APPLICATION NUMBER: US/11/201,322
; CURRENT FILING DATE: 2005-08-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Single strand DNA oligonucleotide
US-11-201-322-2

Query Match      66.7%; Score 16; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCGCATGG 21
    |||||
Db 20 CCAGCGTGGCGCATGG 5

RESULT 5
US-10-310-914A-1185838
; Sequence 1185838, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1185838
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1185838

Query Match      65.8%; Score 15.8; DB 7; Length 22;
Best Local Similarity 84.2%; Pred. No. 6.6e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCGCATGGGG 24
    |||||
Db 1 CCAGCGGGCCCCAUGGGG 19
```

```
RESULT 6
US-11-121-849-235244/c
; Sequence 235244, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S.
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 235244
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-235244

Query Match      65.8%; Score 15.8; DB 11; Length 25;
Best Local Similarity 89.5%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCGCATGGGG 24
    |||||
Db 25 CCAGCGTGGCGCATGGGG 7

RESULT 7
US-10-310-914A-34498/c
; Sequence 34498, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34498
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-34498

Query Match      63.3%; Score 15.2; DB 7; Length 24;
Best Local Similarity 85.0%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGGCGCATGGGG 24
    |||||
Db 24 TCCAGCTTGGCGCATGGGG 5

RESULT 8
US-11-127-654-84
; Sequence 84, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
```

; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 84  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-84

Query Match 62.5%; Score 15; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TCCAGCGTGCCTCAT 19  
|||  
Db 1 TCCAGCGTGCCTCAT 15

RESULT 9  
US-10-310-914A-94891/c  
; Sequence 94891, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 94891  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-94891

Query Match 62.5%; Score 15; DB 7; Length 23;  
Best Local Similarity 78.3%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGCCTCATGGGG 24  
|||  
Db 23 GGGTCTGTGTGCCACAGGG 1

RESULT 10  
US-11-121-849-23997/c  
; Sequence 23997, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Microarrays  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 23997  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-23997

Query Match 62.5%; Score 15; DB 11; Length 25;

Best Local Similarity 78.3%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 GGGTCCAGCGTGCCTCATGGGG 24  
|||  
Db 25 GGGCCACGCTCCACCTGTGTGG 3

RESULT 11  
US-11-121-849-46868  
; Sequence 46868, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 46868  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-46868

Query Match 62.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 78.3%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGCCTCATGGGG 23  
|||  
Db 3 GGGGACCAGTGTGTGCCAGCGG 25

RESULT 12  
US-11-121-849-46869  
; Sequence 46869, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 46869  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-46869

Query Match 62.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 78.3%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGCCTCATGGGG 23  
|||  
Db 2 GGGGACCAGTGTGTGCCAGCGG 24

RESULT 13  
US-10-310-914A-45418/c  
; Sequence 45418, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:

```

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45418
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-45418

Query Match      60.8%; Score 14.6; DB 7; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGTCCAGCGTGGCCCATGG 21
    ||||| ||||| ||||| |||||
Db 21 GGGGCTCAGCGTGGCCCATGG 1

RESULT 14
US-10-310-914A-402274
; Sequence 402274, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 402274
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-402274

Query Match      60.8%; Score 14.6; DB 7; Length 21;
Best Local Similarity 71.4%; Pred. No. 2.1e+03;
Matches 15; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCCATGG 21
    ||||| ||||| ||||| |||||
Db 1 GGGGCCAGCGUCCACCUUGG 21

RESULT 15
US-10-310-914A-38276
; Sequence 38276, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38276
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-38276
```

```

Query Match      60.8%; Score 14.6; DB 7; Length 24;
Best Local Similarity 71.4%; Pred. No. 2.1e+03;
Matches 15; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GTCCAGCGTGGCCCATGGGGG 24
    ||||| ||||| ||||| |||||
Db 1 GUCCAGGCGCGCGCAUGGGCG 21

RESULT 16
US-10-310-914A-895311/c
; Sequence 895311, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 895311
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-895311

Query Match      60.8%; Score 14.6; DB 7; Length 26;
Best Local Similarity 81.0%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GTCCAGCGTGGCCCATGGGGG 24
    ||||| ||||| ||||| |||||
Db 21 GTCTGGGCGCGCATGGGAG 1

RESULT 17
US-10-310-914A-650086/c
; Sequence 650086, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 650086
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-650086

Query Match      60.0%; Score 14.4; DB 7; Length 21;
Best Local Similarity 93.8%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCGC 16
    ||||| ||||| ||||| |||||
Db 20 GGGGTCCAGCGTGGCAC 5

RESULT 18
US-10-310-914A-721320/c
; Sequence 721320, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
```

```
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 721320
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-721320

Query Match      59.2%; Score 14.2; DB 7; Length 24;
Best Local Similarity 84.2%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4 GTCCAGCGTGCGCCATGGG 22
Db      19 GTCCACCCCTGGCGCATGGG 1

RESULT 19
US-10-994-213-7/c
; Sequence 7, Application US/10994213
; Publication No. US20060019911A1
; GENERAL INFORMATION:
; APPLICANT: Papisov, Mikhail. I.
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF
; FILE OF INVENTION: USE THEREOF
; FILE REFERENCE: 0838.1003-001
; CURRENT APPLICATION NUMBER: US/10/994,213
; CURRENT FILING DATE: 2004-11-19
; PRIOR APPLICATION NUMBER: US/09/634,320
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/147,919
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-994-213-7

Query Match      58.3%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGCGCCAT 19
Db      14 CCAGCGTGCGCCAT 1

RESULT 20
US-10-918-638-24
; Sequence 24, Application US/10918638
; Publication No. US20050249663A1
; GENERAL INFORMATION:
; APPLICANT: Copharos
; TITLE OF INVENTION: COBALAMIN MEDIATED DELIVERY OF NUCLEIC ACIDS, ANALOGS
; FILE OF INVENTION: AND
; FILE REFERENCE: COP1010
; CURRENT APPLICATION NUMBER: US/10/918,638
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US/10/246,300
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
```

```
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide-- G3139 Genta
US-10-918-638-24

Query Match      58.3%; Score 14; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGCGCCAT 19
Db      5 CCAGCGTGCGCCAT 18

RESULT 21
US-10-658-947-14
; Sequence 14, Application US/10658947
; Publication No. US20050255153A1
; GENERAL INFORMATION:
; APPLICANT: Inex Pharmaceuticals Inc.
; TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic
; Agents in
; Lipid Vesicles
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson LLP
; STREET: PO Box 5068
; CITY: Dillon
; STATE: CO
; COUNTRY: US
; ZIP: 80435
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/658,947
; FILING DATE: 09-Sep-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,480
; FILING DATE: 29-Jun-2001
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: <Unknown>
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: <Unknown>
; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-658-947-14

Query Match      58.3%; Score 14; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCAGCGTGCGCCAT 19
Db      5 CCAGCGTGCGCCAT 18
```

```
Db          5 CCAGCGTGGCCCAT 18

RESULT 22
US-10-469-561-6
; Sequence 6, Application US/10469561
; Publication No. US20050260216A1
; GENERAL INFORMATION:
; APPLICANT: Claire Ashman
; APPLICANT: James Scott Crowe
; APPLICANT: Jonathan Henry Ellis
; APPLICANT: Alan Peter Lewis
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: PG4355USK
; CURRENT APPLICATION NUMBER: US/10/469,561
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: synthetic immunostimulatory oligonucleotide
US-10-469-561-6

Query Match          58.3%; Score 14; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 CCAGCGTGGCCCAT 19
Db          5 CCAGCGTGGCCCAT 18

RESULT 23
US-10-619-279-45
; Sequence 45, Application US/10619279
; Publication No. US20050267057A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7023/HCL
; CURRENT APPLICATION NUMBER: US/10/619,279
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-619-279-45

Query Match          58.3%; Score 14; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 CCAGCGTGGCCCAT 19
Db          5 CCAGCGTGGCCCAT 18

RESULT 24
US-10-435-656-55
; Sequence 55, Application US/10435656
; Publication No. US20050277604A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/10/435,656
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-435-656-55

Query Match          58.3%; Score 14; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 CCAGCGTGGCCCAT 19
Db          5 CCAGCGTGGCCCAT 18

RESULT 25
US-11-127-654-1
; Sequence 1, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-1

Query Match          58.3%; Score 14; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 CCAGCGTGGCCCAT 19
Db          5 CCAGCGTGGCCCAT 18

RESULT 26
```



```
US-11-127-654-85
; Sequence 85, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-85

Query Match          58.3%; Score 14; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCACGGTGGCCCAT 19
Db      5 CCACGGTGGCCCAT 18
|||||

RESULT 27
US-11-081-140-6
; Sequence 6, Application US/11081140
; Publication No. US20050261225A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Cy A
; APPLICANT: Benimetskaya, Lyuba
; APPLICANT: Guzzo-Pernelli, Nancy
; TITLE OF INVENTION: PEPTIDES THAT COMPLEX WITH ANTISENSE OLIGONUCLEOTIDES WHICH DOWNR
; FILE REFERENCE: 0575/63293
; CURRENT APPLICATION NUMBER: US/11/081,140
; CURRENT FILING DATE: 2005-03-15
; PRIOR APPLICATION NUMBER: US/10/002,884
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: ANTISENSE OLIGONUCLEOTIDE
US-11-081-140-6

Query Match          58.3%; Score 14; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCACGGTGGCCCAT 19
Db      5 CCACGGTGGCCCAT 18
|||||

RESULT 28
US-11-134-918-55
; Sequence 55, Application US/11134918
; Publication No. US20050267064A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/11/134,918
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: US/09/818,918
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-134-918-55

Query Match          58.3%; Score 14; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCACGGTGGCCCAT 19
Db      5 CCACGGTGGCCCAT 18
|||||

RESULT 29
US-11-031-460-55
; Sequence 55, Application US/11031460
; Publication No. US20050277609A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Kline, Joel N.
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred D.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7048 (AWS)
; CURRENT APPLICATION NUMBER: US/11/031,460
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US/09/818,918
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-031-460-55

Query Match          58.3%; Score 14; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCACGGTGGCCCAT 19
Db      5 CCACGGTGGCCCAT 18
|||||
```

RESULT 30  
US-11-067-587-55  
; Sequence 55, Application US/11067587  
; Publication No. US20060003955A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Kline, Joel N.  
; APPLICANT: Klinman, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules  
; FILE REFERENCE: C1039/7048 (AWS)  
; CURRENT APPLICATION NUMBER: US/11/067,587  
; CURRENT FILING DATE: 2005-02-25  
; PRIOR APPLICATION NUMBER: US/09/818,918  
; PRIOR FILING DATE: 2001-03-27  
; PRIOR APPLICATION NUMBER: US 08/276,358  
; PRIOR FILING DATE: 1994-07-15  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; PRIOR APPLICATION NUMBER: US 08/738,652  
; PRIOR FILING DATE: 1996-10-30  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 55  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-067-587-55

Query Match 58.3%; Score 14; DB 11; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
| | | | | | | | | |  
Db 5 CCAGCGTGGCCAT 18

RESULT 31  
US-11-099-683-131  
; Sequence 131, Application US/11099683  
; Publication No. US20060019916A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR INDUCING IL-10 RESPONSES  
; FILE REFERENCE: C1037.70047US01  
; CURRENT APPLICATION NUMBER: US/11/099,683  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 60/558,951  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 131  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-099-683-131

Query Match 58.3%; Score 14; DB 11; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
| | | | | | | | | |  
Db 5 CCAGCGTGGCCAT 18

RESULT 32  
US-11-099-683-132  
; Sequence 132, Application US/11099683  
; Publication No. US20060019916A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR INDUCING IL-10 RESPONSES  
; FILE REFERENCE: C1037.70047US01  
; CURRENT APPLICATION NUMBER: US/11/099,683  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 60/558,951  
; PRIOR FILING DATE: 2004-04-02  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 132  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-099-683-132

Query Match 58.3%; Score 14; DB 11; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
| | | | | | | | | |  
Db 5 CCAGCGTGGCCAT 18

RESULT 33  
US-10-994-213-8  
; Sequence 8, Application US/10994213  
; Publication No. US20060019911A1  
; GENERAL INFORMATION:  
; APPLICANT: Papisov, Mikhail, I.  
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF  
; FILE REFERENCE: 0838.1003-001  
; CURRENT APPLICATION NUMBER: US/10/994,213  
; CURRENT FILING DATE: 2004-11-19  
; PRIOR APPLICATION NUMBER: US/09/634,320  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: US 60/147,919  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
; FEATURE:  
; OTHER INFORMATION: c indicates an RNA base  
US-10-994-213-8

Query Match 58.3%; Score 14; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
| | | | | | | | | |  
Db 5 CCAGCGTGGCCAT 18

RESULT 34  
US-10-994-213-9/c  
; Sequence 9, Application US/10994213  
; Publication No. US20060019911A1

; GENERAL INFORMATION:  
; APPLICANT: Papisov, Mikhail, I.  
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF  
; FILE REFERENCE: 0838.1003-001  
; CURRENT APPLICATION NUMBER: US/10/994,213  
; CURRENT FILING DATE: 2004-11-19  
; PRIOR APPLICATION NUMBER: US/09/634,320  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: US 60/147,919  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
; FEATURE:  
; OTHER INFORMATION: c indicates an RNA base  
US-10-994-213-9

Query Match 58.3%; Score 14; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 14 CCAGCGTGGCCAT 1

RESULT 35  
US-11-127-654-81  
; Sequence 81, Application US/11127654  
; Publication No. US20050250726A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Beig, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC  
; FILE REFERENCE: C1039.70060US01  
; CURRENT APPLICATION NUMBER: US/11/127,654  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 81  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-81

Query Match 58.3%; Score 14; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 5 CCAGCGTGGCCAT 18

RESULT 36  
US-10-310-914A-100840/c  
; Sequence 100840, Application US/10310914A  
; Publication No. US2006000322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac

; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 100840  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-100840

Query Match 58.3%; Score 14; DB 7; Length 22;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGGCCATGGGG 23  
Db 22 GGGGCCAGCGCTCGGCATGGCG 1

RESULT 37  
US-10-994-213-1  
; Sequence 1, Application US/10994213  
; Publication No. US20060019911A1  
; GENERAL INFORMATION:  
; APPLICANT: Papisov, Mikhail, I.  
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF  
; FILE REFERENCE: 0838.1003-001  
; CURRENT APPLICATION NUMBER: US/10/994,213  
; CURRENT FILING DATE: 2004-11-19  
; PRIOR APPLICATION NUMBER: US/09/634,320  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: US 60/147,919  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-994-213-1

Query Match 58.3%; Score 14; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
Db 8 CCAGCGTGGCCAT 21

RESULT 38  
US-10-994-213-2/c  
; Sequence 2, Application US/10994213  
; Publication No. US20060019911A1  
; GENERAL INFORMATION:  
; APPLICANT: Papisov, Mikhail, I.  
; TITLE OF INVENTION: DRUG-CARRIER COMPLEXES AND METHODS OF  
; FILE REFERENCE: 0838.1003-001  
; CURRENT APPLICATION NUMBER: US/10/994,213  
; CURRENT FILING DATE: 2004-11-19  
; PRIOR APPLICATION NUMBER: US/09/634,320  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: US 60/147,919  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
; FEATURE:  
; OTHER INFORMATION: t = amino modified T  
US-10-994-213-2

Query Match 58.3%; Score 14; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCAGCGTGGCCAT 19  
| | | | | | | | | |  
Db 16 CCAGCGTGGCCAT 3

RESULT 39  
US-10-310-914A-903934  
; Sequence 903934, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 903934  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-903934

Query Match 58.3%; Score 14; DB 7; Length 23;  
Best Local Similarity 63.6%; Pred. No. 3.7e+03;  
Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GGTCCAGCGTGGCCATGGGG 24  
| : | | | | : | | | | |  
Db 2 GCUCACGCCUGGGCAUGAGGG 23

RESULT 40  
US-10-310-914A-989919/c  
; Sequence 989919, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310.914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 989919  
; LENGTH: 25  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-989919

Query Match 58.3%; Score 14; DB 7; Length 25;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCATGGG 22  
| | | | | | | | | | | | | |  
Db 22 GGGGTCCAGGTGTGGACATGGG 1

RESULT 41  
US-11-121-849-46867  
; Sequence 46867, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; TITLE OF INVENTION: Microarrays  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 46867  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-46867

Query Match 58.3%; Score 14; DB 11; Length 25;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTGGCCATGGG 22  
| | | | | | | | | | | | | |  
Db 4 GGGGACCAGTGTGTGCCAGGGG 25

RESULT 42  
US-11-121-849-46870  
; Sequence 46870, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; TITLE OF INVENTION: Microarrays  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 46870  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-46870

Query Match 58.3%; Score 14; DB 11; Length 25;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTGGCCATGGGG 23  
| | | | | | | | | | | | | |  
Db 1 GGGACCAAGTGTGTGCCAGGGG 22

RESULT 43  
US-10-310-914A-1042200/c  
; Sequence 1042200, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1042200  
; LENGTH: 26  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1042200

Query Match 58.3%; Score 14; DB 7; Length 26;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTCGCCCATGGG 22  
Db 24 GTGGTCCAGCGTCGCCCGCGGG 3

RESULT 44

US-10-939-294A-19743/c  
; Sequence 19743, Application US/10939294A  
; Publication No. US20050266417A1  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Turner, Daniel  
; APPLICANT: Pingler, Maneesh  
; APPLICANT: Pincas, Hanna  
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules  
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)  
; CURRENT APPLICATION NUMBER: US/10/939,294A  
; CURRENT FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: US 60/502/731  
; PRIOR FILING DATE: 2003-09-12  
; NUMBER OF SEQ ID NOS: 38895  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 19743  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide probe  
US-10-939-294A-19743

Query Match 58.3%; Score 14; DB 7; Length 32;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTCGCCCATGGG 23  
Db 23 GGCTCCGCGTCGCTCCTGAGG 2

RESULT 45

US-10-310-914A-906465/c  
; Sequence 906465, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 906465  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human

Query Match 58.3%; Score 14; DB 7; Length 32;  
Best Local Similarity 77.3%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

US-10-310-914A-906465

Query Match 57.5%; Score 13.8; DB 7; Length 18;  
Best Local Similarity 88.2%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CCAGCGTCGCCCATGGG 22  
Db 18 CCAGCGTCGCCCGCGGG 2

RESULT 46

US-10-310-914A-775551/c  
; Sequence 775551, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 775551  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-775551

Query Match 57.5%; Score 13.8; DB 7; Length 21;  
Best Local Similarity 88.2%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGTCCAGCGTCGCCCA 18  
Db 17 GGGTCCAGACTGCCCA 1

RESULT 47

US-10-310-914A-321695  
; Sequence 321695, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 321695  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-321695

Query Match 57.5%; Score 13.8; DB 7; Length 23;  
Best Local Similarity 76.5%; Pred. No. 4.5e+03;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGTCCAGCGTCGCC 17  
Db 2 GGGGUCCAGGGUGCACC 18

RESULT 48

US-11-121-849-330122  
; Sequence 330122, Application US/11121849  
; Publication No. US20050272080A1

```
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 330122
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-330122

Query Match      57.5%; Score 13.8; DB 11; Length 25;
Best Local Similarity 88.2%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2  GGGTCCAGCGTGCGCCA 18
        |||||
Db      9  GGGTCCAGTGTCCGCCA 25

RESULT 49
US-11-131-212-40/c
; Sequence 40, Application US/11131212
; Publication No. US20050262593A1
; GENERAL INFORMATION:
; APPLICANT: Yutaka KANDA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Kazuyasu NAKAMURA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Naoko YAMANE
; APPLICANT: Motoo YAMASAKI
; APPLICANT: Nobuo HANAI
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
; FILE REFERENCE: 249-202
; CURRENT APPLICATION NUMBER: US/11/131,212
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US/09/971,773
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-308526
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/268,926
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 40
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-11-131-212-40

Query Match      57.5%; Score 13.8; DB 11; Length 45;
Best Local Similarity 88.2%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8  AGCGTGGCCCATGGGG 24
        |||||
Db     27  AGCGTGAGCCATGGTGG 11

RESULT 50
US-10-310-914A-222305
; Sequence 222305, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 222305
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-222305

Query Match      56.7%; Score 13.6; DB 7; Length 20;
Best Local Similarity 70.0%; Pred. No. 5.5e+03;
Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      1  GGGGTCCAGCGTGCGCCATG 20
        |||||
Db      1  GGGGUCCGGCGGGGUCCUG 20

Search completed: February 16, 2006, 02:53:03
Job time : 226.736 secs
```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:51:58 ; Search time 911.686 Seconds  
(without alignments)  
2369.293 Million cell updates/sec

Title: US-09-669-187A-148

Perfect score: 38

Sequence: 1 ggggactttccgtgggactttccaggggactttcc 38

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.in.\*

3: gb.env.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pr.\*

9: gb.ro.\*

10: gb.sts.\*

11: gb.sy.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.htg.\*

15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	38	6	AR088703 Sequence
2	38	100.0	38	6	AX103956 Sequence
3	38	100.0	38	6	AX355389 Sequence
4	38	100.0	38	6	AX547009 Sequence
5	30.8	81.1	43	6	AR035457 Sequence
6	30.2	79.5	46	6	AR035456 Sequence
7	30	78.9	39	6	AR005185 Sequence
8	30	78.9	39	6	AR005186 Sequence
9	30	78.9	39	6	AR038395 Sequence
10	30	78.9	39	6	AR038396 Sequence
11	30	78.9	39	6	AR178131 Sequence
12	30	78.9	39	6	AR178132 Sequence
13	30	78.9	39	6	I58471 Sequence 43
14	30	78.9	39	6	I58472 Sequence 44
15	30	78.9	39	6	I66589 Sequence 43
16	30	78.9	39	6	I66590 Sequence 44
17	30	78.9	39	6	I68236 Sequence 43
18	30	78.9	39	6	I68237 Sequence 44

BD261195 Triterpen  
AR225344 Sequence  
AR473523 Sequence  
AR542759 Sequence  
AR027239 Sequence  
AR035447 Sequence  
AR035451 Sequence  
AR035448 Sequence  
AR035449 Sequence  
AR035450 Sequence  
AR035455 Sequence  
AR049839 Sequence  
AR149733 Sequence  
AR04853 Sequence  
AR035466 Sequence  
AR438116 Sequence  
AR438118 Sequence  
BD081630 Inhibito  
I09458 Sequence 2  
BD249738 Intracell  
AR532727 Sequence  
AX798846 Sequence  
AR035454 Sequence  
AQ846479 Sequence  
AR583386 Sequence  
AR035452 Sequence  
AR035453 Sequence  
AQ846478 Sequence  
AR585153 Sequence  
AR583385 Sequence  
AR397504 Sequence  
AR575406 Sequence  
AR032342 Sequence  
AR032343 Sequence  
AR585154 Sequence  
AR035458 Sequence  
AR035435 Sequence  
AX299019 Sequence  
AX299020 Sequence  
AR026200 Sequence  
AR026280 Sequence  
AR035436 Sequence  
E61343 Probe for d  
I82942 Sequence 44  
I83022 Sequence 12  
AR352029 Sequence  
AR431128 Sequence  
AR431208 Sequence  
AX828921 Sequence  
AX829001 Sequence  
A40180 Sequence 2  
BD062064 Apo-2 rec  
BD085996 Tumor nec  
BD090957 Apo-3 lig  
BD132797 Apo-2bCR.  
AR183747 Sequence  
AR236056 Sequence  
AR241295 Sequence  
AX099766 Sequence  
AX188648 Sequence  
AX188649 Sequence  
CS001237 Sequence  
A40179 Sequence 1  
AR106267 Sequence  
BD008835 Uses of a  
I72377 Sequence 8  
A31989 Synthetic H  
AR131408 Sequence  
BD001814 Immunogen  
AR027240 Sequence  
AR221677 Sequence  
AX798845 Sequence  
AR221678 Sequence

92	20.2	53.2	42	6	AX798848	Sequence	165	14.4	37.9	38	6	AR351569	Sequence
93	19.8	52.1	26	6	AR035444	Sequence	166	14.4	37.9	38	6	AX492879	Sequence
94	19.2	50.5	26	6	AR035437	Sequence	167	14.4	37.9	39	6	AX135021	Sequence
95	19.2	50.5	26	6	AR035443	Sequence	c 168	14.4	37.9	45	6	AX068147	Sequence
c 96	19	50.0	24	6	AR654113	Sequence	169	14.4	37.9	46	6	AR275619	Sequence
97	19	50.0	26	6	AR035438	Sequence	170	14.4	37.9	46	6	AR278099	Sequence
98	19	50.0	26	6	AR035442	Sequence	171	14.4	37.9	46	6	AR409070	Sequence
99	18.6	48.9	39	6	AR005187	Sequence	172	14.4	37.9	46	6	AR616918	Sequence
c 100	18.6	48.9	39	6	AR005188	Sequence	173	14.4	37.9	46	6	AX082449	Sequence
101	18.6	48.9	39	6	AR038397	Sequence	174	14.4	37.9	46	6	AX084800	Sequence
c 102	18.6	48.9	39	6	AR038398	Sequence	175	14.4	37.9	46	6	AX817878	Sequence
103	18.6	48.9	39	6	AR088704	Sequence	176	14.2	37.4	28	6	BD176640	Promoter
104	18.6	48.9	39	6	AR178133	Sequence	c 177	14.2	37.4	31	6	AX248800	Sequence
c 105	18.6	48.9	39	6	AR178134	Sequence	c 178	14.2	37.4	32	6	BD161889	Kl Gene
c 106	18.6	48.9	39	6	IS8473	Sequence	c 179	14.2	37.4	32	6	BD161898	Nonhuman
c 107	18.6	48.9	39	6	IS8474	Sequence	c 180	14.2	37.4	33	6	AX084276	Sequence
c 108	18.6	48.9	39	6	IS8475	Sequence	c 181	14.2	37.4	33	6	AX084276	Sequence
c 109	18.6	48.9	39	6	IS8476	Sequence	c 182	14.2	37.4	35	8	AF505525	Homo sapi
c 110	18.6	48.9	39	6	IS8477	Sequence	c 183	14.2	37.4	35	6	AX686396	Sequence
c 111	18.6	48.9	39	6	IS8478	Sequence	c 184	14.2	37.4	37	6	BD161877	Kl gene
c 112	18.2	47.9	26	6	AR004563	Sequence	c 185	14.2	37.4	39	6	AX306642	Sequence
c 113	17.6	46.3	26	6	AR004564	Sequence	c 186	14.2	37.4	40	6	A79625	Sequence
c 114	17.6	46.3	26	6	AR035441	Sequence	c 187	14.2	37.4	40	6	AR003558	Sequence
c 115	17.4	45.8	47	6	AR035442	Sequence	c 188	14.2	37.4	40	6	AR075338	Sequence
c 116	17.2	45.3	26	6	AR035440	Sequence	c 189	14.2	37.4	40	6	AR087848	Sequence
c 117	17	44.7	17	6	AR438117	Sequence	c 190	14.2	37.4	40	6	AR119903	Sequence
c 118	16.8	44.2	26	6	AR035439	Sequence	c 191	14.2	37.4	40	6	AR154200	Sequence
c 119	16.6	43.7	47	6	AR035439	Sequence	c 192	14.2	37.4	40	6	AR169478	Sequence
c 120	16.4	43.2	38	6	A79871	Sequence	c 193	14.2	37.4	40	6	AR175527	Sequence
c 121	16.4	43.2	38	6	AR011592	Sequence	c 194	14.2	37.4	40	6	AR179302	Sequence
c 122	16.4	43.2	38	6	AR028015	Sequence	c 195	14.2	37.4	40	6	BD134764	Thermoana
c 123	16.4	43.2	38	6	AR157607	Sequence	c 196	14.2	37.4	40	6	BD190485	BD134764
c 124	16.4	43.2	41	6	AX514212	Sequence	c 197	14.2	37.4	40	6	BD191470	Nucleic a
c 125	16.4	43.2	41	6	AX520358	Sequence	c 198	14.2	37.4	40	6	BD240946	Self-cont
c 126	16.2	42.6	40	6	AR004621	Sequence	c 199	14.2	37.4	40	6	BD249410	Electroni
c 127	16.2	42.6	41	6	AX514803	Sequence	c 200	14.2	37.4	40	6	I25354	Sequence
c 128	16.2	42.6	41	6	AX520698	Sequence	c 201	14.2	37.4	40	6	AR195022	Sequence
c 129	16.2	42.6	46	6	E11769	Primer for	c 202	14.2	37.4	40	6	AR352409	Sequence
c 130	16.2	42.6	46	6	I82413	Sequence	c 203	14.2	37.4	40	6	AR352438	Sequence
c 131	16.2	42.6	48	8	HSBFA1B	Sequence	c 204	14.2	37.4	40	6	AR350589	Sequence
c 132	15.8	41.6	28	6	AX431437	Sequence	c 205	14.2	37.4	40	6	AR642772	Sequence
c 133	15.8	41.6	47	6	AR219307	Sequence	c 206	14.2	37.4	40	6	AR648091	Sequence
c 134	15.6	41.1	50	6	CO004477	Sequence	c 207	14.2	37.4	40	6	AX135666	Sequence
c 135	15.4	40.5	25	6	AR203357	Sequence	c 208	14.2	37.4	42	8	HSBTCRV01	Z27179 H.sapiens r
c 136	15.2	40.0	32	6	AX306632	Sequence	c 209	14.2	37.4	44	6	AR172768	Sequence
c 137	15	39.5	15	6	AR035432	Sequence	c 210	14.2	37.4	44	6	AR178712	Sequence
c 138	15	39.5	31	6	AX249048	Sequence	c 211	14.2	37.4	44	6	AR181283	Sequence
c 139	15	39.5	32	6	AX350351	Sequence	c 212	14.2	37.4	44	6	AR199964	Sequence
c 140	15	39.5	33	6	I34944	Sequence	c 213	14.2	37.4	44	6	AR231912	Sequence
c 141	15	39.5	40	6	E08945	Probe. 9/19	c 214	14.2	37.4	44	6	AR343387	Sequence
c 142	15	39.5	45	6	A18604	H. sapiens	c 215	14.2	37.4	44	6	AR349705	Sequence
c 143	15	39.5	45	6	AR063614	Sequence	c 216	14.2	37.4	44	6	AR391176	Sequence
c 144	14.8	38.9	31	6	I37241	Sequence	c 217	14.2	37.4	44	6	AR431619	Sequence
c 145	14.8	38.9	31	6	I37242	Sequence	c 218	14.2	37.4	47	6	AR290084	Sequence
c 146	14.8	38.9	31	6	I37243	Sequence	c 219	14.2	37.4	50	6	AR077264	Sequence
c 147	14.8	38.9	31	6	I94091	Sequence	c 220	14.2	37.4	50	6	CO006807	Sequence
c 148	14.8	38.9	31	6	I94092	Sequence	c 221	14.2	37.4	50	6	CO009108	Sequence
c 149	14.8	38.9	31	6	I94093	Sequence	c 222	14.2	37.4	50	8	HUMTCRVU46	L39584 Homo sapien
c 150	14.8	38.9	34	6	Q0816228	Sequence	c 223	14	36.8	21	6	AR148640	Sequence
c 151	14.6	38.4	23	6	AX023995	Sequence	c 224	14	36.8	21	6	BD124012	Neuroprot
c 152	14.6	38.4	24	6	AX443948	Sequence	c 225	14	36.8	21	6	AR404019	Sequence
c 153	14.6	38.4	25	6	AX447923	Sequence	c 226	14	36.8	23	6	CS048086	Sequence
c 154	14.6	38.4	27	6	CS063410	Sequence	c 227	14	36.8	25	6	AX650582	Sequence
c 155	14.6	38.4	27	6	CS081191	Sequence	c 228	14	36.8	25	6	AX650583	Sequence
c 156	14.6	38.4	31	6	AX249568	Sequence	c 229	14	36.8	25	6	AX650584	Sequence
c 157	14.6	38.4	45	13	MLMLTTRA2	Sequence	c 230	14	36.8	25	6	AX650585	Sequence
c 158	14.6	38.4	47	6	AR284612	Sequence	c 231	14	36.8	27	8	S62577	lamp-2-Lyso
c 159	14.6	38.4	47	6	AX093025	Sequence	c 232	14	36.8	30	6	AX590776	Sequence
c 160	14.6	38.4	48	6	AX223706	Sequence	c 233	14	36.8	31	9	MUSCD3E2	M23371 Mus musculi
c 161	14.6	38.4	50	6	AR392726	Sequence	c 234	14	36.8	32	6	AX766988	Sequence
c 162	14.4	37.9	24	6	BD211083	Quantitat	c 235	14	36.8	33	6	AR021014	Sequence
c 163	14.4	37.9	37	6	I42582	Sequence	c 236	14	36.8	33	6	AR043429	Sequence
c 164	14.4	37.9	38	6	BD177921	Sequence	c 237	14	36.8	33	6	AR062344	Sequence



C 238	14	36.8	33	6	AR183803	AR183803 Sequence
C 239	14	36.8	33	6	AR368186	AR368186 Sequence
C 240	14	36.8	37	6	E10784	PCR primer
C 241	14	36.8	38	6	I38420	Sequence 5
C 242	14	36.8	40	6	AR053668	Sequence
C 243	14	36.8	40	6	CQ918211	Sequence
C 244	14	36.8	40	6	AR258603	Sequence
C 245	14	36.8	40	6	AR364432	Sequence
C 246	14	36.8	41	6	AX513944	Sequence
C 247	14	36.8	41	6	AX519283	Sequence
C 248	14	36.8	45	6	AR157675	Sequence
C 249	14	36.8	45	6	AR157676	Sequence
C 250	14	36.8	45	8	S69452	TCR V gamma
C 251	14	36.8	46	6	BD268660	Isolation
C 252	14	36.8	47	6	A43615	Sequence 5
C 253	14	36.8	47	6	AR288379	Sequence
C 254	14	36.8	47	6	AR289545	Sequence
C 255	14	36.8	47	6	AR290662	Sequence
C 256	14	36.8	50	6	AR214693	Sequence
C 257	14	36.8	50	6	AR282147	Sequence
C 258	13.8	36.3	18	6	CS120586	Sequence
C 259	13.8	36.3	19	6	CS120544	Sequence
C 260	13.8	36.3	20	6	AR315359	Sequence
C 261	13.8	36.3	20	6	AX293963	Sequence
C 262	13.8	36.3	21	6	BD266036	Universal
C 263	13.8	36.3	24	6	AX289330	Sequence
C 264	13.8	36.3	26	6	AR239768	Sequence
C 265	13.8	36.3	26	6	AX279570	Sequence
C 266	13.8	36.3	27	6	AR091132	Sequence
C 267	13.8	36.3	27	6	AR198167	Sequence
C 268	13.8	36.3	27	6	AR260321	Sequence
C 269	13.8	36.3	29	6	CQ827928	Sequence
C 270	13.8	36.3	29	6	CQ831062	Sequence
C 271	13.8	36.3	32	6	I82400	Sequence 48
C 272	13.8	36.3	36	6	AR001104	Sequence
C 273	13.8	36.3	36	6	AR343272	Sequence
C 274	13.8	36.3	36	6	AR401634	Sequence
C 275	13.8	36.3	36	6	AR439958	Sequence
C 276	13.8	36.3	36	6	AR576588	Sequence
C 277	13.8	36.3	36	6	AR609191	Sequence
C 278	13.8	36.3	38	6	AR078082	Sequence
C 279	13.8	36.3	38	6	E35663	Detection o
C 280	13.8	36.3	38	6	I76164	Sequence 8
C 281	13.8	36.3	38	6	AR287028	Sequence
C 282	13.8	36.3	38	6	AR399018	Sequence
C 283	13.8	36.3	38	6	AR601747	Sequence
C 284	13.8	36.3	38	8	HUMTCVD1ES	
C 285	13.8	36.3	39	6	I82405	Sequence 55
C 286	13.8	36.3	39	6	I82406	Sequence 56
C 287	13.8	36.3	40	6	AR3621	Sequence 50
C 288	13.8	36.3	41	6	AR206162	Sequence
C 289	13.8	36.3	41	6	AR595445	Sequence
C 290	13.8	36.3	41	6	AX516152	Sequence
C 291	13.8	36.3	41	6	AX517555	Sequence
C 292	13.8	36.3	42	6	I82396	Sequence 44
C 293	13.8	36.3	42	6	I82397	Sequence 43
C 294	13.8	36.3	42	6	AX538890	Sequence
C 295	13.8	36.3	42	6	AX538891	Sequence
C 296	13.8	36.3	42	8	S80775	gamma delta
C 297	13.8	36.3	47	6	AR291782	Sequence
C 298	13.8	36.3	50	6	CQ003473	Sequence
C 299	13.8	36.3	50	6	CQ005360	Sequence
C 300	13.8	36.3	50	6	CQ008574	Sequence

ALIGNMENTS

RESULT 1	AR088703	Sequence 2 from patent US 5990090.	38 bp	DNA	linear	PAT 07-SEP-2000
LOCUS	AR088703					
DEFINITION	Sequence 2 from patent US 5990090.					
ACCESSION	AR088703					

VERSION	AR088703.1	GI:10015467	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 38)		
AUTHORS	Nabel,G-Jan.		
TITLE	Methods and compositions for treatment of diseases		
JOURNAL	Patent: US 5990090-A 2 23-NOV-1999;		
FEATURES	Location/Qualifiers		
source	1..38		
/organism="unknown"			
/mol_type="unassigned DNA"			
ORIGIN			
Query Match	100.0%;	Score 38; DB 6; Length 38;	
Best Local Similarity	100.0%;	Pred. No. 2.3e-05;	
Matches	38; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GGGGACTTTCGCTGGGACTTTCACGGGGGACTTTCC 38		
Db	1 GGGGACTTTCGCTGGGACTTTCACGGGGGACTTTCC 38		
RESULT 2			PAT 30-APR-2001
LOCUS	AX103956	38 bp DNA	linear
DEFINITION	Sequence 148 from Patent WO0122972.		
ACCESSION	AX103956		
VERSION	AX103956.1	GI:13920153	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Krieg,A.M., Schetter,C. and Vollmer,J.C.		
TITLE	Immunostimulatory nucleic acids		
JOURNAL	Patent: WO 0122972-A 148 05-APR-2001;		
	UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical		
GmbH (DE)			
FEATURES	Location/Qualifiers		
source	1..38		
/organism="synthetic construct"			
/mol_type="unassigned DNA"			
/db_xref="taxon:32630"			
ORIGIN			
Query Match	100.0%;	Score 38; DB 6; Length 38;	
Best Local Similarity	100.0%;	Pred. No. 2.3e-05;	
Matches	38; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GGGGACTTTCGCTGGGACTTTCACGGGGGACTTTCC 38		
Db	1 GGGGACTTTCGCTGGGACTTTCACGGGGGACTTTCC 38		
RESULT 3			PAT 06-FEB-2002
LOCUS	AX355389	38 bp DNA	linear
DEFINITION	Sequence 417 from Patent WO0197843.		
ACCESSION	AX355389		
VERSION	AX355389.1	GI:18620057	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	other sequences; artificial sequences.		
REFERENCE	1		
AUTHORS	Weiner,G. and Hartmann,G.		
TITLE	Methods for enhancing antibody-induced cell lysis and treating		
JOURNAL	Patent: WO 0197843-A 417 27-DEC-2001;		
FEATURES	Location/Qualifiers		

```
source
1. .38
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32830"
/notes="Synthetic oligonucleotide
chimeric phosphorothioate/phosphodiester backbone with
phosphorothioate at 5' and 3' ends"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 38; DB 6; Length 38;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38
|||||
DB 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38

RESULT 4
AX547009
LOCUS AX547009 38 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 148 from Patent WO20053141.
ACCESSION AX547009
VERSION AX547009.1 GI:25812153
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 148 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1. .38
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noe="Synthetic Sequence"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 38; DB 6; Length 38;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38
|||||
DB 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38

RESULT 5
AR035457
LOCUS AR035457 43 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 29 from patent US 5871902.
ACCESSION AR035457
VERSION AR035457.1 GI:5952125
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 43)
AUTHORS Weininger,S. and Weininger,A.M.
TITLE Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
JOURNAL Patent: US 5871902-A 29 16-FEB-1999;
Location/Qualifiers
source
1. .43
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match
Best Local Similarity 81.1%; Score 30.8; DB 6; Length 43;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38
|||||
DB 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38

RESULT 6
AR035456
LOCUS AR035456 46 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 28 from patent US 5871902.
ACCESSION AR035456
VERSION AR035456.1 GI:5952124
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Weininger,S. and Weininger,A.M.
TITLE Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
JOURNAL Patent: US 5871902-A 28 16-FEB-1999;
Location/Qualifiers
source
1. .46
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match
Best Local Similarity 79.5%; Score 30.2; DB 6; Length 46;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTT 35
|||||
DB 6 GGGGACTTTCCGCTGGGGACTTTCCAGGGGAGCGT 40

RESULT 7
AR005185
LOCUS AR005185 39 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 43 from patent US 5747641.
ACCESSION AR005185
VERSION AR005185.1 GI:3966064
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 39)
AUTHORS Frankel,A., Pabo,C., Barsoun,J.G., Fawell,S.E. and
Pepinsky,R.Blake.
TITLE Tat-derived transport polypeptide conjugates
JOURNAL Patent: US 5747641-A 43 05-MAY-1998;
Location/Qualifiers
source
1. .39
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match
Best Local Similarity 78.9%; Score 30; DB 6; Length 39;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38
|||||
DB 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38

RESULT 8
AR005186/c
LOCUS AR005186 39 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 44 from patent US 5747641.
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38
|||||
DB 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGACTTTCC 38
```

ACCESSION AR005186  
VERSION AR005186.1 GI:3966065  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
TITLE Tat-derived transport polypeptide conjugates  
JOURNAL Patent: US 5747641-A 44 05-MAY-1998;  
FEATURES Location/Qualifiers  
source 1. .39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 39 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 2  
|||||  
RESULT 9  
AR038395  
LOCUS AR038395  
DEFINITION Sequence 43 from patent US 5804604.  
ACCESSION AR038395  
VERSION AR038395.1 GI:5957112  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
TITLE Tat-derived transport polypeptides and fusion proteins  
JOURNAL Patent: US 5804604-A 43 08-SEP-1998;  
FEATURES Location/Qualifiers  
source 1. .39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 39 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 2  
|||||  
RESULT 10  
AR038396/c  
LOCUS AR038396  
DEFINITION Sequence 44 from patent US 5804604.  
ACCESSION AR038396  
VERSION AR038396.1 GI:5957113  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
TITLE Tat-derived transport polypeptides and fusion proteins  
JOURNAL Patent: US 5804604-A 44 08-SEP-1998;  
FEATURES Location/Qualifiers  
source 1. .39

ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 39 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 2  
|||||  
RESULT 11  
AR178131  
LOCUS AR178131  
DEFINITION Sequence 43 from patent US 6316003.  
ACCESSION AR178131  
VERSION AR178131.1 GI:17921024  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
TITLE Tat-derived transport polypeptides  
JOURNAL Patent: US 6316003-A 43 13-NOV-2001;  
FEATURES Location/Qualifiers  
source 1. .39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
RESULT 12  
AR178132/c  
LOCUS AR178132  
DEFINITION Sequence 44 from patent US 6316003.  
ACCESSION AR178132  
VERSION AR178132.1 GI:17921025  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
TITLE Tat-derived transport polypeptides  
JOURNAL Patent: US 6316003-A 44 13-NOV-2001;  
FEATURES Location/Qualifiers  
source 1. .39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 39 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 2  
|||||  
RESULT 13  
AR178133/c  
LOCUS AR178133  
DEFINITION Sequence 44 from patent US 6316003.  
ACCESSION AR178133  
VERSION AR178133.1 GI:17921026  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
TITLE Tat-derived transport polypeptides  
JOURNAL Patent: US 6316003-A 44 13-NOV-2001;  
FEATURES Location/Qualifiers  
source 1. .39  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 38  
|||||  
Db 39 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 2  
|||||

RESULT 13  
I58471  
LOCUS I58471 39 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 43 from patent US 5652122.  
ACCESSION I58471  
VERSION I58471.1 GI:2477709  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
Pepinsky,R.Blake.  
TITLE Nucleic acids encoding and methods of making tat-derived transport  
polypeptides  
JOURNAL Patent: US 5652122-A 43 29-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCCTGGGGACTTTCACAGGGGACTTTC 38  
Db 1 GGGGACTTTCCTGGGGACTTTCACAGGGGACTTTC 38  
RESULT 14  
I58472/c  
LOCUS I58472 39 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 44 from patent US 5652122.  
ACCESSION I58472  
VERSION I58472.1 GI:2477710  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
Pepinsky,R.Blake.  
TITLE Nucleic acids encoding and methods of making tat-derived transport  
polypeptides  
JOURNAL Patent: US 5652122-A 44 29-JUL-1997;  
FEATURES Location/Qualifiers  
source 1..39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCCTGGGGACTTTCACAGGGGACTTTC 38  
Db 1 GGGGACTTTCCTGGGGACTTTCACAGGGGACTTTC 38  
RESULT 15  
I66589  
LOCUS I66589 39 bp DNA linear PAT 29-DEC-1997  
DEFINITION Sequence 43 from patent US 5670617.  
ACCESSION I66589  
VERSION I66589.1 GI:2724566  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 39)

AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
Pepinsky,R.Blake.  
TITLE Nucleic acid conjugates of tat-derived transport polypeptides  
JOURNAL Patent: US 5670617-A 43 23-SEP-1997;  
FEATURES Location/Qualifiers  
source 1..39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCCTGGGGACTTTCACAGGGGACTTTC 38  
Db 1 GGGGACTTTCCTGGGGACTTTCACAGGGGACTTTC 38  
RESULT 16  
I66590/c  
LOCUS I66590 39 bp DNA linear PAT 29-DEC-1997  
DEFINITION Sequence 44 from patent US 5670617.  
ACCESSION I66590  
VERSION I66590.1 GI:2724567  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
Pepinsky,R.Blake.  
TITLE Nucleic acid conjugates of tat-derived transport polypeptides  
JOURNAL Patent: US 5670617-A 44 23-SEP-1997;  
FEATURES Location/Qualifiers  
source 1..39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCCTGGGGACTTTCACAGGGGACTTTC 38  
Db 39 GGGGACTTTCCTGGGGACTTTCACAGGGGACTTTC 2  
RESULT 17  
I68236  
LOCUS I68236 39 bp DNA linear PAT 04-FEB-1998  
DEFINITION Sequence 43 from patent US 5674980.  
ACCESSION I68236  
VERSION I68236.1 GI:2830358  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Frankel,A., Pabo,C., Barsoum,J.G., Fawell,S.E. and  
Pepinsky,R.Blake.  
TITLE Fusion protein comprising tat-derived transport moiety  
JOURNAL Patent: US 5674980-A 43 07-OCT-1997;  
FEATURES Location/Qualifiers  
source 1..39  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 78.9%; Score 30; DB 6; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.061;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
QY 1 GGGGACTTTCGGCTGGGGACTTTTCCAGGGGGACTTTTC 38
    |||||
Db 1 GGGGACTTTCGGCTGGGGACTTTTCCACGGGGACTTTC 38
    |||||

RESULT 18
168237/c
LOCUS          39 bp      DNA      linear      PAT 04-FEB-1998
DEFINITION     Sequence 44 from patent US 5674980.
ACCESSION      168237
VERSION        168237.1 GI:2830359
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 39)
AUTHORS       Frankel,A., Fabo,C., Barsoun,J.G., Fawell,S.E. and
              Pepinsky,R.Blake.
TITLE         Fusion protein comprising tat-derived transport moiety
JOURNAL       Patent: US 5674980-A 44 07-OCT-1997;
FEATURES      Location/Qualifiers
              source
              1..39
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      78.9%; Score 30; DB 6; Length 39;
Best Local Similarity 86.8%; Pred.No. 0.061;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTTCCAGGGGGACTTTTC 38
    |||||
Db 39 GGGGACTTTCGGCTGGGGACTTTTCCACGGGGACTTTC 2
    |||||

RESULT 19
BD261195
LOCUS          44 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION     Triterpen compositions and methods for use thereof.
ACCESSION      BD261195
VERSION        BD261195.1 GI:33070965
KEYWORDS       JP 2002515430-A/9.
SOURCE         synthetic construct
ORGANISM       other sequences: artificial sequences.
REFERENCE      1 (bases 1 to 44)
AUTHORS       Arntzen,C.J., Tracey,M.B., Gutterman,J.U., Hoffmann,J.J.,
              Bailey,D.T. and Jayatilake,G.S.
TITLE         Triterpen compositions and methods for use thereof
JOURNAL       Patent: JP 2002515430-A 9 28-MAY-2002;
              RESEARCH DEVELOPMENT FOUNDATION
COMMENT        OS Artificial Sequence
              FN JP 2002515430-A/9
              PD 28-MAY-2002
              PF 19-MAY-1999 JP 2000549243
              PR 19-MAY-1998 US 60/085997,03-SEP-1998 US 60/090666 PI
              CHARLES J ARNTZEN,MARY BLAKE TRACEY,JORDAN U GUTTERMAN,JOSEPH PI
              J HOFFMANN,
              PI DAVID T BAILEY,GAMINI S JAYATILAKE
              PC A61K35/78,A61K35/78,A61K31/7028,A61K31/704,A61P35/00,A61P43/00, PC
              C12N5/04//
              CC C07H15/18,C07H15/256,C12N5/00
              Description of Artificial Sequence:SYNTHETIC PRIMER FH Key
              Location/Qualifiers
              FT source
              1..44
              /organism='Artificial Sequence'.
              FT Location/Qualifiers
              1..44
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

QY 1 GGGGACTTTCGGCTGGGGACTTTTCCAGGGGGACTTTTC 34
    |||||
Db 10 GGGGACTTTCGGCTGGGGACTTTTCCAGGGAGGCT 42
    |||||

RESULT 20
AR225344
LOCUS          44 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION     Sequence 9 from patent US 6444233.
ACCESSION      AR225344
VERSION        AR225344.1 GI:27263287
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 44)
AUTHORS       Arntzen,C.J., Blake,M.E., Gutterman,J.U., Hoffmann,J.J.,
              Jayatilake,G.S. and Bailey,D.T.
TITLE         Triterpene compositions and methods for use thereof
JOURNAL       Patent: US 6444233-A 9 03-SEP-2002;
              Research Development Foundation; Carson City, NV
FEATURES      Location/Qualifiers
              source
              1..44
              /organism="unknown"
              /mol_type="genomic DNA"

ORIGIN
Query Match      78.4%; Score 29.8; DB 6; Length 44;
Best Local Similarity 93.9%; Pred.No. 0.076;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGGACTTTCCAGGGGGACT 34
    |||||
Db 10 GGGACTTTCGGCTGGGGACTTTTCCAGGGAGGCT 42
    |||||

RESULT 21
AR473523
LOCUS          44 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION     Sequence 9 from patent US 6689398.
ACCESSION      AR473523
VERSION        AR473523.1 GI:42711810
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 44)
AUTHORS       Haridas,V. and Gutterman,J.U.
TITLE         Triterpene compositions and methods for use thereof
JOURNAL       Patent: US 6689398-A 9 10-FEB-2004;
              Research Development Foundation; Carson, NV
FEATURES      Location/Qualifiers
              source
              1..44
              /organism="unknown"
              /mol_type="genomic DNA"

ORIGIN
Query Match      78.4%; Score 29.8; DB 6; Length 44;
Best Local Similarity 93.9%; Pred.No. 0.076;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGGACTTTCCAGGGGGACT 34
    |||||
Db 10 GGGACTTTCGGCTGGGGACTTTTCCAGGGAGGCT 42
    |||||

RESULT 22
QY 2 GGGACTTTCGGCTGGGGACTTTCCAGGGGGACT 34
    |||||
Db 10 GGGACTTTCGGCTGGGGACTTTTCCAGGGAGGCT 42
    |||||
```

AR542759  
LOCUS AR542759 44 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 9 from patent US 6746696.  
ACCESSION AR542759  
VERSION AR542759.1 GI:53935323  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 44)  
AUTHORS Arnzen,C.J. and Gutterman,J.U.  
TITLE Triterpene compositions and methods for use thereof  
JOURNAL Patent: US 6746696-A 9 08-JUN-2004;  
Research Development Foundation; Carson City, NV  
FEATURES  
source  
1. .44  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 78.4%; Score 29.8; DB 6; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.076; 2; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GGGACTTTCGGCTGGGACTTTCACGGGGGACT 34  
|||||  
Db 10 GGGACTTTCGGCTGGGACTTTCACGGGGGACT 42  
|||||  
RESULT 23  
LOCUS AR027239 45 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 12 from patent US 5856161.  
ACCESSION AR027239  
VERSION AR027239.1 GI:5938079  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 45)  
AUTHORS Aggarwal,B.B. and Darnay,B.G.  
TITLE Tumor necrosis factor receptor-I-associated protein kinase and methods for its use  
JOURNAL Patent: US 5856161-A 12 05-JAN-1999;  
FEATURES  
source  
1. .45  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 76.8%; Score 29.2; DB 6; Length 45;  
Best Local Similarity 91.2%; Pred. No. 0.14; 3; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GGGACTTTCGGCTGGGACTTTCACGGGGGACTT 35  
|||||  
Db 10 GGGACTTTCGGCTGGGACTTTCACGGGGGACTT 43  
|||||  
RESULT 24  
LOCUS AR035447 45 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 19 from patent US 5871902.  
ACCESSION AR035447  
VERSION AR035447.1 GI:5952115  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 45)  
AUTHORS Weininger,S. and Weininger,A.M.  
TITLE Sequence-specific detection of nucleic acid hybrids using a DNA-binding molecule or assembly capable of discriminating perfect

hybrids from non-perfect hybrids  
JOURNAL Patent: US 5871902-A 19 16-FEB-1999;  
FEATURES  
source  
1. .45  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 76.8%; Score 29.2; DB 6; Length 45;  
Best Local Similarity 91.2%; Pred. No. 0.14; 3; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GGGACTTTCGGCTGGGACTTTCACGGGGGACTT 35  
|||||  
Db 7 GGGACTTTCGGCTGGGACTTTCACGGGGGACTT 40  
|||||  
RESULT 25  
LOCUS AR035451 45 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 23 from patent US 5871902.  
ACCESSION AR035451  
VERSION AR035451.1 GI:5952119  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 45)  
AUTHORS Weininger,S. and Weininger,A.M.  
TITLE Sequence-specific detection of nucleic acid hybrids using a DNA-binding molecule or assembly capable of discriminating perfect hybrids from non-perfect hybrids  
JOURNAL Patent: US 5871902-A 23 16-FEB-1999;  
FEATURES  
source  
1. .45  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 76.8%; Score 29.2; DB 6; Length 45;  
Best Local Similarity 91.2%; Pred. No. 0.14; 3; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GGGACTTTCGGCTGGGACTTTCACGGGGGACTT 35  
|||||  
Db 7 GGGACTTTCGGCTGGGACTTTCACGGGGGACTT 40  
|||||  
RESULT 26  
LOCUS AR035448 46 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 20 from patent US 5871902.  
ACCESSION AR035448  
VERSION AR035448.1 GI:5952116  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 46)  
AUTHORS Weininger,S. and Weininger,A.M.  
TITLE Sequence-specific detection of nucleic acid hybrids using a DNA-binding molecule or assembly capable of discriminating perfect hybrids from non-perfect hybrids  
JOURNAL Patent: US 5871902-A 20 16-FEB-1999;  
FEATURES  
source  
1. .46  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 76.3%; Score 29; DB 6; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.17; 0; Indels 0; Gaps 0;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



ORIGIN		AR438116		AR438116	
Query Match	75.8%; Score 28.8; DB 6; Length 36;	LOCUS	Sequence 9 from patent US 6660906.	32 bp	DNA
Best Local Similarity	93.8%; Pred. No. 0.2;	DEFINITION	Sequence 9 from patent US 6660906.		
Matches	30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	ACCESSION	AR438116		
		VERSION	AR438116.1 GI:40204578		
QY	2 GGGACTTTCGGCTGGGGACTTTCCAGGGGAC 33	KEYWORDS			
Db	4 GGGACTTTCGGCTGGGGACTTTCCAGGGAGC 35	SOURCE	Unknown.		
		ORGANISM	Unknown.		
RESULT 32		REFERENCE	Unclassified.		
AR404853		AUTHORS	1 (bases 1 to 32)		
LOCUS	Sequence 142 from patent US 6630141.	Tsichlis,P.N.			
DEFINITION	36 bp mRNA linear PAT 18-DEC-2003	Tp12 transgenic knockout mice			
ACCESSION	AR404853	Patent: US 660906-A 9 09-DEC-2003;			
VERSION	AR404853.1 GI:40153580	Thomas Jefferson University; Philadelphia, PA;			
KEYWORDS		WOX;			
SOURCE	Unknown.	Location/Qualifiers			
ORGANISM	Unknown.	1. .32			
REFERENCE	Unclassified.	/mol_type="genomic DNA"			
AUTHORS	1 (bases 1 to 36)				
TITLE	Georgopoulos,K.				
JOURNAL	Isolated antibody that binds to an Ikaros polypeptide				
	Patent: US 6630141-A 142 07-OCT-2003;				
	The General Hospital Corporation; Boston, MA				
FEATURES					
source	Location/Qualifiers				
1. .36					
/organism="unknown"					
/mol_type="mRNA"					
ORIGIN		AR438118		AR438118	
Query Match	75.8%; Score 28.8; DB 6; Length 36;	LOCUS	Sequence 11 from patent US 6660906.	32 bp	DNA
Best Local Similarity	93.8%; Pred. No. 0.2;	DEFINITION	Sequence 11 from patent US 6660906.		
Matches	30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	ACCESSION	AR438118		
		VERSION	AR438118.1 GI:40204580		
QY	2 GGGACTTTCGGCTGGGGACTTTCCAGGGGAC 33	KEYWORDS			
Db	4 GGGACTTTCGGCTGGGGACTTTCCAGGGAGC 35	SOURCE	Unknown.		
		ORGANISM	Unknown.		
RESULT 33		REFERENCE	Unclassified.		
AR035466		AUTHORS	1 (bases 1 to 32)		
LOCUS	Sequence 38 from patent US 5871902.	Tsichlis,P.N.			
DEFINITION	37 bp DNA linear PAT 29-SEP-1999	Tp12 transgenic knockout mice			
ACCESSION	AR035466	Patent: US 660906-A 11 09-DEC-2003;			
VERSION	AR035466.1 GI:59521134	Thomas Jefferson University; Philadelphia, PA;			
KEYWORDS		WOX;			
SOURCE	Unknown.	Location/Qualifiers			
ORGANISM	Unknown.	1. .32			
REFERENCE	Unclassified.	/organism="unknown"			
AUTHORS	1 (bases 1 to 37)	/mol_type="genomic DNA"			
TITLE	Weininger,S. and Weininger,A.M.				
JOURNAL	Sequence-specific detection of nucleic acid hybrids using a				
	DNA-binding molecule or assembly capable of discriminating perfect				
	hybrids from non-perfect hybrids				
JOURNAL	Patent: US 5871902-A 38 16-FEB-1999;				
FEATURES	Location/Qualifiers				
source	1. .37				
/organism="unknown"					
/mol_type="unassigned DNA"					
ORIGIN		BD081630		BD081630	
Query Match	74.7%; Score 28.4; DB 6; Length 37;	LOCUS	Inhibition of human immunodeficiency virus (HIV-1) replication.	33 bp	DNA
Best Local Similarity	96.7%; Pred. No. 0.3;	DEFINITION	Inhibition of human immunodeficiency virus (HIV-1) replication.		
Matches	29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	ACCESSION	BD081630		
		VERSION	BD081630.1 GI:22627233		
QY	2 GGGACTTTCGGCTGGGGACTTTCCAGGGG 31	KEYWORDS	JP 2001520017-A/4.		
Db	7 GGGACTTTCGGCTGGGGACTTTCCAGGGAG 36	SOURCE	synthetic construct		
		ORGANISM	other sequences; artificial sequences.		
REFERENCE	1 (bases 1 to 33)				
AUTHORS	Suhadolnik,R.J., Adelson,M.E. and Iacono,K.T.				



TITLE Inhibition of human immunodeficiency virus (HIV-1) replication  
JOURNAL Patent: JP 2001520017-A 4 30-OCT-2001;  
TEMPLE UNIVERSITY OF THE COMMONWEALTH SYSTEM OF HIGHER EDUCATION  
COMMENT OS Artificial Sequence  
PN JP 2001520017-A/4  
PD 30-OCT-2001  
PF 15-OCT-1998 JP 2000516047  
PR 16-OCT-1997 US 60/061984  
PT ROBERT J SUHADOLNIK, MARTIN E ADELSON, KATHRYN T IACONO PC  
C12N15/09, A61K31/513, A61K45/00, A61K45/06, A61K48/00, A61P31/18, PC  
A61P37/04,  
PC  
C12N1/15, C12N1/19, C12N1/21, C12N5/10//A61K35/76, C12N15/00, C12N5/ PC  
00  
CC Description of Artificial Sequence: sense probe CC  
oligonucleotide  
CC corresponding to NF-kappa beta binding site  
FH Key Location/Qualifiers  
FT source 1..33  
FT Location/Qualifiers  
FT /organism='Artificial Sequence'.  
source 1..33  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'  
ORIGIN  
Query Match 73.7%; Score 28; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GGGACTTTCGGCTGGGACTTTCCAGG 29  
DB 5 GGGACTTTCGGCTGGGACTTTCCAGG 32  
RESULT 37  
109458  
LOCUS I09458 34 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 2 from Patent WO 8908147.  
ACCESSION I09458  
VERSION I09458.1 GI:597836  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 34)  
AUTHORS Baeuerle, P.A. and Baltimore, D.  
TITLE ACTIVATION OF NF-KB PRECURSOR  
JOURNAL Patent: WO 8908147-A 2 08-SEP-1989;  
FEATURES Location/Qualifiers  
source 1..34  
/organism='unknown'  
/mol\_type='unassigned DNA'  
ORIGIN  
Query Match 73.7%; Score 28; DB 6; Length 34;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GGGACTTTCGGCTGGGACTTTCCAGG 29  
DB 6 GGGACTTTCGGCTGGGACTTTCCAGG 33  
RESULT 38  
BD249738  
LOCUS BD249738 35 bp DNA linear PAT 17-JUL-2003  
DEFINITION Intracellular targeted delivery of compounds by 70 kD heat shock protein.  
ACCESSION BD249738  
VERSION BD249738.1 GI:33059508  
KEYWORDS JP 2002530426-A/1.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Fujihara, S.M. and Nadler, S.G.  
TITLE Intracellular targeted delivery of compounds by 70 kD heat shock protein.  
JOURNAL Patent: JP 2002530426-A 1 17-SEP-2002;  
BRISTOL MYERS SQUIBB CO  
COMMENT OS Homo sapiens (human)  
PN JP 2002530426-A/1  
PD 17-SEP-2002  
PF 17-SEP-1999 JP 2000583940  
PR 24-NOV-1998 US 60/109872  
PT SHERI M FUJIHARA, STEVEN G NADLER  
PC A61K38/00, A61K47/48, A61K48/00, A61P3/10, A61P9/00, A61P11/06, PC  
A61P19/02  
PC A61P29/00, A61P29/00, A61P35/00, C12N15/09, A61K37/02, C12N15/00 CC  
Intracellular targeted delivery of compounds by 70 kD heat shock protein  
FH Key Location/Qualifiers  
FT source 1..35  
FT Location/Qualifiers  
FT /organism='Homo sapiens (human)'.  
source 1..35  
/organism='Homo sapiens'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'  
ORIGIN  
Query Match 73.7%; Score 28; DB 6; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCGGCTGGGACTTTCCAGG 28  
DB 8 GGGGACTTTCGGCTGGGACTTTCCAGG 35  
RESULT 39  
AR532727  
LOCUS AR532727 35 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 4 from patent US 6730302.  
ACCESSION AR532727  
VERSION AR532727.1 GI:53922132  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Fujihara, S.M. and Nadler, S.G.  
TITLE Intracellular targeted delivery of compounds by 70 kD heat shock protein.  
JOURNAL Patent: US 6730302-A 4 04-MAY-2004;  
Bristol-Myers Squibb Company; Princeton, NJ  
FEATURES Location/Qualifiers  
source 1..35  
/organism='unknown'  
/mol\_type='genomic DNA'  
ORIGIN  
Query Match 73.7%; Score 28; DB 6; Length 35;  
Best Local Similarity 100.0%; Pred. No. 0.44;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCGGCTGGGACTTTCCAGG 28  
DB 8 GGGGACTTTCGGCTGGGACTTTCCAGG 35  
RESULT 40  
AX798846

```
LOCUS AX798846 42 bp DNA linear PAT 08-OCT-2003
DEFINITION Sequence 2 from Patent WO03053468.
ACCESSION AX798846
VERSION AX798846.1 GI:37604920
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1 van Lint,C., Burny,A., Quivy,V. and Adam,E.
AUTHORS Method for obtaining the elimination of integrated and functional
TITLE viruses from infected mammal cells
JOURNAL Patent: WO 03053468-A 2 03-JUL-2003;
UNIVERSITE LIBRE DE BRUXELLES (BE)
FEATURES
Location/Qualifiers
1..42
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="mutagenic oligonucleotide primer"
ORIGIN
Query Match 73.7%; Score 28; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGCTGGGACTTTCACGGG 29
Db 15 GGGACTTTCGCTGGGACTTTCACGGG 42
RESULT 41
AR035454
LOCUS AR035454 45 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 26 from patent US 5871902.
ACCESSION AR035454
VERSION AR035454.1 GI:5952122
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 45)
AUTHORS Weininger,S. and Weininger,A.M.
TITLE Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
JOURNAL Patent: US 5871902-A 26 16-FEB-1999;
FEATURES Location/Qualifiers
1..45
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 72.6%; Score 27.6; DB 6; Length 45;
Best Local Similarity 88.2%; Pred. No. 0.67;
Matches 30; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 GGGACTTTCGCTGGGACTTTCACGGGACTT 35
Db 7 GGGACTTTCGCTGGGACTTTCACGAGGCGT 40
RESULT 42
CQ846479/c
LOCUS CQ846479 35 bp DNA linear PAT 02-AUG-2004
DEFINITION Sequence 10 from Patent EP1433485.
ACCESSION CQ846479
VERSION CQ846479.1 GI:50895715
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
Lipton,J. and Catania,A.
AUTHORS A uro-genital condition treatment system
TITLE Patent: EP 1433485-A 10 30-JUN-2004;
JOURNAL Zengen, Inc. (US)
FEATURES Location/Qualifiers
1..35
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide probe for NF-kB (antisense)"
ORIGIN
Query Match 72.1%; Score 27.4; DB 6; Length 35;
Best Local Similarity 96.6%; Pred. No. 0.8;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGACTTTCGCTGGGACTTTCACGGG 29
Db 32 GGGGACTTTCGCTGGGACTTTCACATGG 4
RESULT 43
AR589386/c
LOCUS AR589386 35 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 6 from patent US 6803044.
ACCESSION AR589386
VERSION AR589386.1 GI:56636662
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Catania,A.P. and Lipton,J.M.
TITLE Antimicrobial and anti-inflammatory peptides for use in human
immunodeficiency virus
JOURNAL Patent: US 6803044-A 6 12-OCT-2004;
Zengen, Inc.; Woodland Hills, CA
FEATURES Location/Qualifiers
1..35
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 72.1%; Score 27.4; DB 6; Length 35;
Best Local Similarity 96.6%; Pred. No. 0.8;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGACTTTCGCTGGGACTTTCACGGG 29
Db 32 GGGGACTTTCGCTGGGACTTTCACATGG 4
RESULT 44
AR035452
LOCUS AR035452 44 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 24 from patent US 5871902.
ACCESSION AR035452
VERSION AR035452.1 GI:5952120
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Weininger,S. and Weininger,A.M.
TITLE Sequence-specific detection of nucleic acid hybrids using a
DNA-binding molecule or assembly capable of discriminating perfect
hybrids from non-perfect hybrids
JOURNAL Patent: US 5871902-A 24 16-FEB-1999;
FEATURES Location/Qualifiers
1..44
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
```

Query Match 72.1%; Score 27.4; DB 6; Length 44;  
Best Local Similarity 83.8%; Pred. No. 0.81;  
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGGACTTTCCGCTGGGACTTTCCAGGGGACTTTCC 38  
|||||  
Db 7 GGGACTTTCCGCTGGGACTTTCCAGGGGAGCGTGGCC 43

RESULT 45  
LOCUS AR035453  
DEFINITION Sequence 25 from patent US 5871902.  
ACCESSION AR035453  
VERSION AR035453.1 GI:5952121  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 44)  
AUTHORS Weininger, S. and Weininger, A. M.  
TITLE Sequence-specific detection of nucleic acid hybrids using a DNA-binding molecule or assembly capable of discriminating perfect hybrids from non-perfect hybrids  
JOURNAL Patent: US 5871902-A 25 16-FEB-1999;  
FEATURES Location/Qualifiers  
source 1..44  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 71.6%; Score 27.2; DB 6; Length 44;  
Best Local Similarity 90.8%; Pred. No. 0.99;  
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTTCCGCTGGGACTTTCCAGGGGAC 33  
|||||  
Db 7 GGGACTTTCCGCTGGGACTTTCCGGGGAGGC 38

RESULT 46  
LOCUS CQ846478  
DEFINITION Sequence 9 from Patent EPI433485.  
ACCESSION CQ846478  
VERSION CQ846478.1 GI:50895714  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Lipton, J. and Catania, A.  
TITLE A uro-genital condition treatment system  
JOURNAL Patent: EP 1433485-A 9 30-JUN-2004;  
Zengen, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..35  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide probe for NF-kB (sense)"

ORIGIN  
Query Match 69.5%; Score 26.4; DB 6; Length 35;  
Best Local Similarity 96.4%; Pred. No. 2.1;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACTTTCCGCTGGGACTTTCCAGG 28  
|||||  
Db 8 GGGACTTTCCGCTGGGACTTTCCATG 35

RESULT 47  
LOCUS AR585153  
DEFINITION Sequence 9 from patent US 680291.  
ACCESSION AR585153  
VERSION AR585153.1 GI:56628768  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Lipton, J. M. and Catania, A. P.  
TITLE Uro-genital condition treatment system  
JOURNAL Patent: US 680291-A 9 05-OCT-2004;  
Zengen, Inc.; Woodland Hills, CA  
FEATURES Location/Qualifiers  
source 1..35  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 69.5%; Score 26.4; DB 6; Length 35;  
Best Local Similarity 96.4%; Pred. No. 2.1;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACTTTCCGCTGGGACTTTCCAGG 28  
|||||  
Db 8 GGGACTTTCCGCTGGGACTTTCCATG 35

RESULT 48  
LOCUS AR589385  
DEFINITION Sequence 5 from patent US 6803044.  
ACCESSION AR589385  
VERSION AR589385.1 GI:56636661  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Catania, A. P. and Lipton, J. M.  
TITLE Antimicrobial and anti-inflammatory peptides for use in human immunodeficiency virus  
JOURNAL Patent: US 6803044-A 5 12-OCT-2004;  
Zengen, Inc.; Woodland Hills, CA  
FEATURES Location/Qualifiers  
source 1..35  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 69.5%; Score 26.4; DB 6; Length 35;  
Best Local Similarity 96.4%; Pred. No. 2.1;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGACTTTCCGCTGGGACTTTCCAGG 28  
|||||  
Db 8 GGGACTTTCCGCTGGGACTTTCCATG 35

RESULT 49  
LOCUS AR397504  
DEFINITION Sequence 5 from patent US 6617171.  
ACCESSION AR397504  
VERSION AR397504.1 GI:40134392  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Faustman, D. L. and Hayashi, T.

TITLE Methods for diagnosing and treating autoimmune disease  
JOURNAL Patent: US 6617171-A 5 09-SEP-2003;  
The General Hospital Corporation; Boston, MA  
FEATURES  
source 1. .32  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 68.4%; Score 26; DB 6; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GGGACTTTCGGCTGGGACTTTCCAG 27  
Db 7 GGGACTTTCGGCTGGGACTTTCCAG 32  
RESULT 50  
AR575406  
LOCUS AR575406 32 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 1 from patent US 6773705.  
ACCESSION AR575406  
VERSION AR575406.1 GI:56576396  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Faustman,D.L. and Hayashi,T.  
TITLE Methods for diagnosing and treating autoimmune disease  
JOURNAL Patent: US 6773705-A 1 10-AUG-2004;  
General Hospital Corporation; Boston, MA  
FEATURES  
source 1. .32  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 68.4%; Score 26; DB 6; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GGGACTTTCGGCTGGGACTTTCCAG 27  
Db 7 GGGACTTTCGGCTGGGACTTTCCAG 32

Search completed: February 15, 2006, 18:55:57  
Job time : 924.686 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:25:23 ; Search time 285.413 Seconds  
(without alignments)  
884.241 Million cell updates/sec

Title: US-09-669-187A-148  
Perfect score: 38  
Sequence: 1 ggggactttccgtgggactttccaggggactttccc 38

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : N\_Geneseq\_21.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	38	3	Aaz32919 Kappa-B-P
2	38	100.0	38	4	Aaf99023 Immunosti
3	38	100.0	38	6	Abst77664 Angiogene
4	38	100.0	38	6	AbL39015 Immunosti
5	38	100.0	38	9	Acd99455 Immunosti
6	38	100.0	38	9	Adb36525 Immunosti
7	38	100.0	38	13	Adu89464 Allergic
8	30.8	81.1	43	2	Aat30609 Target bi
9	30.2	79.5	46	2	Aat30608 Target bi
10	30	78.9	39	2	Aaq58049 Oligonucl
11	30	78.9	39	2	Aaq58050 Oligonucl
12	30	78.9	39	2	Aat84584 NF-kappa
13	30	78.9	39	2	Aat88240 NF-kappaB
14	30	78.9	39	2	Aat88239 NF-kappaB
15	30	78.9	39	2	Aat89779 Transcrip
16	30	78.9	39	2	Aat89780 Transcrip
17	30	78.9	39	2	Aav56615 NF-kappaB
18	30	78.9	39	2	Aav56616 NF-kappaB
19	30	78.9	39	6	Aad26647 NF-kB wil

Aad26648	NF-kB wil	39	6	AAD26648	78.9	30	20	C
Aaz48474	HIV LTR N	44	3	Aaz48474	78.4	29.8	21	
AbL61552	HIV LTR N	44	3	ABL61552	78.4	29.8	22	
Aat30599	Target bi	45	2	AAT30599	76.8	29.2	23	
Aat30603	Target bi	45	2	AAT30603	76.8	29.2	24	
Aax28079	HIV-LTR O	45	2	AAX28079	76.8	29.2	25	
Adh12178	HIV-1 LTR	45	12	ADH12178	76.8	29.2	26	
Aad00136	EMSA prob	45	14	AD200136	76.8	29.2	27	
Aea06160	Oligo fro	45	14	AEA06160	76.8	29.2	28	
Aat30607	Target bi	46	2	AAT30607	76.3	29	29	
Aat30602	Target bi	46	2	AAT30602	76.3	29	30	
Aat30601	Target bi	46	2	AAT30601	76.3	29	31	
Aat30600	Target bi	46	2	AAT30600	76.3	29	32	
Aav67098	HIV LTR #	36	2	AAV67098	75.8	28.8	33	
Aaq61543	HIV long	37	2	AAQ61543	74.7	28.4	34	
Aat30615	Probe nuc	37	2	AAT30615	74.7	28.4	35	
Aav45402	HIV LTR b	37	2	AAV45402	74.7	28.4	36	
Aad17457	Human imm	32	5	AAD17457	73.7	28	37	
Aad17455	Nuclear f	32	5	AAD17455	73.7	28	38	
Aax34336	HIV probe	33	2	AAX34336	73.7	28	39	
Aan90922	Part of t	34	1	AAN90922	73.7	28	40	
Aac66959	Lymphoid	34	4	AAC66959	73.7	28	41	
Adt77252	HIV enhan	34	13	ADT77252	73.7	28	42	
Aaa61055	Electroph	35	3	AAA61055	73.7	28	43	
Acf05495	HIV-1 LAI	42	9	ACF05495	73.7	28	44	
Aat30606	Target bi	45	2	AAT30606	72.6	27.6	45	
Aaa99616	NF-kB oli	35	3	AAA99616	72.1	27.4	46	C
Acc47366	NF-kappaB	35	10	ACC47366	72.1	27.4	47	
Aat30604	Target bi	44	2	AAT30604	71.6	27.2	48	
Aat30605	Target bi	44	2	AAT30605	71.6	27.2	49	
Aaa99615	NF-kB oli	35	3	AAA99615	69.5	26.4	50	
Acc47365	NF-kappaB	35	10	ACC47365	69.5	26.4	51	
Adx83925	Novel KpV	35	14	ADX83925	68.4	26	52	
Adu81628	Peroxisom	26	14	ADU81628	68.4	26	53	
Aaq04699	HIV enhan	27	2	AAQ04699	68.4	26	54	
Aat34697	Vector fr	32	2	AAT34697	68.4	26	55	
Adr31220	Hiv type	32	13	ADR31220	68.4	26	56	
Aeb25862	HIV-1 enh	32	14	AEB25862	68.4	26	57	
Adx83926	Novel KpV	35	14	ADX83926	67.9	25.8	58	
Aeb01104	Nuclear f	38	14	AEBO1104	67.9	25.8	59	
Aat30610	Target bi	48	2	AAT30610	66.3	25.2	60	
Aat30587	Target bi	27	2	AAT30587	65.8	25	61	
AbL58385	NF-kappaB	25	6	ABL58385	63.2	24	62	
AbL58384	NF-kappaB	25	6	ABL58384	63.2	24	63	C
Aat30588	Target bi	27	2	AAT30588	63.2	24	64	
Aat40192	HIV targe	27	2	AAT40192	63.2	24	65	
Aad62572	PCR prime	27	10	AAD62572	63.2	24	66	
Adf43595	HIV detec	27	10	ADF43595	63.2	24	67	
Adf75964	DNA PCR p	27	10	ADF75964	63.2	24	68	
Adf76044	RNA PCR p	27	10	ADF76044	63.2	24	69	
Aaq73477	NF KB tra	28	2	AAQ73477	63.2	24	70	C
Aaq74525	Primer fo	28	2	AAQ74525	63.2	24	71	
Aaq74616	Primer fo	28	2	AAQ74616	63.2	24	72	
Aav84353	Human NF	29	2	AAV84353	63.2	24	73	
Aax59847	NF-kappaB	29	2	AAX59847	63.2	24	74	
Aav72528	NF-kappaB	29	2	AAV72528	63.2	24	75	
Aax56005	NF-kappaB	29	2	AAX56005	63.2	24	76	
Aaf84483	NF-kappaB	29	4	AAF84483	63.2	24	77	
Aah24297	NF-kappa-	29	4	AAH24297	63.2	24	78	
AbS53576	32P-label	29	6	ABS53576	63.2	24	79	
AbL41731	Nucleotid	29	6	ABL41731	63.2	24	80	
Abx15510	32P-label	29	8	ABX15510	63.2	24	81	
Abx16405	Necrosis	29	8	ABX16405	63.2	24	82	
Ada49696	Oligonucl	29	9	ADA49696	63.2	24	83	
Aad64043	32P-label	29	10	AAD64043	63.2	24	84	
Adg98732	NF-kappa	29	10	ADG98732	63.2	24	85	
Abx15843	Radiolabe	29	10	ABX15843	63.2	24	86	
Abx13180	Human Nuc	29	10	ABX13180	63.2	24	87	
Abx15467	32P-label	29	10	ABX15467	63.2	24	88	
AcA61694	Nuclear f	29	10	ACA61694	63.2	24	89	
Ado40441	NF-kappaB	29	12	ADO40441	63.2	24	90	
Aeb34893	Oligonucl	30	14	AEB34893	63.2	24	91	
Aaq73476	NF KB tra	37	2	AAQ73476	63.2	24	92	

93	23	60.5	23	2	AAT95708	Aat95708 DNA from
94	23	60.5	23	2	AAV04923	Aav04923 Primer LT
95	23	60.5	23	2	AAV09864	Aav09864 Primer LT
96	23	60.5	23	2	AAV15221	Aav15221 PCR prime
97	23	60.5	23	3	AAA90157	Aaa90157 PCR prime
98	23	60.5	23	3	AAI72530	Aai72530 Nested PC
99	23	60.5	23	8	ABX11223	Abx11223 HIV-1 PCR
100	22.4	58.9	25	2	AAQ10479	Aaq10479 Phosphorot
101	22	57.9	22	2	AAQ06947	Aaq06947 Mny11 nuc
102	22	57.9	22	2	AAT98055	Aat98055 Human or
103	21.4	56.3	29	10	AD82904	Ad82904 EMSA prob
104	21.4	56.3	45	14	AEA06161	Aea06161 Mutated o
105	21	55.3	25	2	AAT91829	Aat91829 Probe 1
106	20.6	54.2	45	9	ACF05494	Acf05494 HIV-1 LAI
107	20.2	53.2	26	2	AAT91830	Aat91830 Probe 2 u
108	20.2	53.2	30	3	AAT90467	Aaz90467 NF-kappaB
109	20.2	53.2	30	3	AAZ90466	Aaz90466 NF-kappaB
110	20.2	53.2	31	12	ADQ94608	Adq94608 HIV-1 3'
111	20.2	53.2	31	14	AEA11054	Aea11054 STAT5 bin
112	20.2	53.2	42	9	ACF05487	Acf05487 HIV-1 LAI
113	19.8	52.1	26	2	AAT30586	Aat30586 Target bi
114	19.2	50.5	24	2	AAQ3979	Aaq3979 HIV-1 LTR
115	19.2	50.5	26	2	AAT30595	Aat30595 Target bi
116	19.2	50.5	26	2	AAT30589	Aat30589 Target bi
117	19	50.0	19	10	ADG36512	Adg36512 HIV siNA
118	19	50.0	19	10	ADG36584	Adg36584 HIV siNA
119	19	50.0	19	10	ADG35846	Adg35846 HIV siNA
120	19	50.0	19	10	ADG35733	Adg35733 HIV siNA
121	19	50.0	19	10	ADG36501	Adg36501 HIV siNA
122	19	50.0	19	10	ADG35713	Adg35713 HIV siNA
123	19	50.0	19	10	ADG35774	Adg35774 HIV siNA
124	19	50.0	19	10	ADG35818	Adg35818 HIV siNA
125	19	50.0	19	10	ADG36471	Adg36471 HIV siNA
126	19	50.0	19	10	ADG35779	Adg35779 HIV siNA
127	19	50.0	19	10	ADG35763	Adg35763 HIV siNA
128	19	50.0	19	10	ADG36556	Adg36556 HIV siNA
129	19	50.0	19	10	ADG36517	Adg36517 HIV siNA
130	19	50.0	19	10	ADG36451	Adg36451 HIV siNA
131	19	50.0	24	14	ADZ65007	Adz65007 HIV-1 str
132	19	50.0	26	2	AAT30590	Aat30590 Target bi
133	19	50.0	26	2	AAT30594	Aat30594 Target bi
134	18.6	48.9	39	2	AAQ44332	Aaq44332 Oligonuc
135	18.6	48.9	39	2	AAQ44331	Aaq44331 Oligonuc
136	18.6	48.9	39	2	AAT94585	Aat94585 Mutant NF
137	18.6	48.9	39	2	AAT98241	Aat98241 NF-kappaB
138	18.6	48.9	39	2	AAT98242	Aat98242 NF-kappaB
139	18.6	48.9	39	2	AAT9781	Aat9781 Transcrip
140	18.6	48.9	39	2	AAT99782	Aat99782 Transcrip
141	18.6	48.9	39	2	AAV56618	Aav56618 NF-kappaB
142	18.6	48.9	39	2	AAV56617	Aav56617 NF-kappaB
143	18.6	48.9	39	3	AZ32920	Aaz32920 Mutant ka
144	18.6	48.9	39	6	ADZ26649	Adz26649 NF-kB mut
145	18.6	48.9	39	6	ADZ26650	Adz26650 NF-kB mut
146	18.2	47.9	26	2	AAQ73641	Aaq73641 Oligonuc
147	17.8	46.3	45	14	AEb63578	Aeb63578 PAG PCR p
148	17.6	46.3	26	2	AAQ73642	Aaq73642 Oligonuc
149	17.6	46.3	26	2	AAT30593	Aat30593 Target bi
150	17.6	46.3	30	10	ADZ28997	Adz28997 PCR prime
151	17.6	46.3	41	9	ACC41977	Acc41977 Human KcN
152	17.2	45.3	26	2	AAT30592	Aat30592 Target bi
153	17	44.7	17	5	AAI7456	Aai7456 Nuclear f
154	16.8	44.2	26	2	AAT30591	Aat30591 Target bi
155	16.8	44.2	30	10	AD82905	Ad82905 Control p
156	16.8	44.2	41	9	ACC41989	Acc41989 Human HER
157	16.4	43.2	18	6	AD40603	Ad40603 HIV-1 LTR
158	16.4	43.2	38	2	AAT31915	Aat31915 Plasmid l
159	16.4	43.2	38	2	AAT59208	Aat59208 5' primer
160	16.4	43.2	38	2	AAV23093	Aav23093 5' PCR pr
161	16.4	43.2	38	2	AAQ00768	Aaq00768 5' nested
162	16.4	43.2	38	5	AAQ09598	Aaq09598 Influenza
163	16.4	43.2	48	2	AAV35898	Aav35898 PCR prime
164	16.4	43.2	48	4	ABK43418	Abk43418 Necrosis
165	16.2	42.6	40	2	AAV16820	Aav16820 Mycobacte

166	16.2	42.6	46	2	AAT34424	Aat34424 Primer fo
167	15.8	41.6	28	6	ABK94866	Abk94866 Fat regul
168	15.8	41.6	32	14	ADY62240	Ady62240 FeLV p15E
169	15.8	41.6	45	2	AAT35082	Aat35082 Human inc
170	15.8	41.6	47	3	AAc87820	Aac87820 Zymogen a
171	15.8	41.6	47	4	AAf55294	Aaf55294 Primer us
172	15.6	41.1	25	9	ACI53845	Aci53845 Human mic
173	15.6	41.1	37	10	ADK68360	Adk68360 HCMV glyc
174	15.6	41.1	41	6	ABV75580	Abv75580 SR protei
175	15.6	41.1	50	4	AAL29909	Aal29909 Human SNP
176	15.4	40.5	25	5	AAc85573	Aac85573 Human 5-H
177	15.4	40.5	25	9	ACI95695	Aci95695 Human mic
178	15.2	40.0	23	2	AAQ41413	Aaq41413 Sequence
179	15.2	40.0	32	6	ABK13491	Abk13491 DT390 mut
180	15.2	40.0	41	6	ABZ43626	Abz43626 Human car
181	15.2	40.0	41	6	ABZ49774	Abz49774 Human car
182	15.2	40.0	48	5	ADV62542	Adv62542 HBV amber
183	15.2	40.0	48	8	ACD56028	Acd56028 HBV amber
184	15.2	40.0	48	12	ADM63789	Adm63789 Hepatitis
185	15.2	40.0	50	6	ABZ05973	Abz05973 Human leu
186	15	39.5	15	2	AAT30584	Aat30584 Target bi
187	15	39.5	25	9	ACI89487	Aci89487 Human mic
188	15	39.5	25	9	ACI89486	Aci89486 Human mic
189	15	39.5	32	6	ABK13733	Abk13733 Rabbit SM
190	15	39.5	33	2	AAQ52069	Aaq52069 Breast ca
191	15	39.5	39	11	ADM47297	Adm47297 NOVX olig
192	15	39.5	39	14	AEb86140	Aeb86140 Optimized
193	15	39.5	40	2	AAQ87916	Aaq87916 Human his
194	15	39.5	41	6	ABL42091	AbL42091 Probe #1
195	15	39.5	41	6	ABL42090	AbL42090 Primer #4
196	15	39.5	41	6	ABZ44217	Abz44217 Human NDU
197	15	39.5	41	6	ABZ50114	Abz50114 Human NDU
198	14.8	38.9	22	10	ADD43631	AdD43631 Oligonuc
199	14.8	38.9	25	9	ACI74187	Aci74187 Human mic
200	14.8	38.9	31	2	AAQ93717	Aaq93717 Human str
201	14.8	38.9	31	2	AAQ93716	Aaq93716 Human str
202	14.8	38.9	31	2	AAQ93715	Aaq93715 Human str
203	14.8	38.9	31	2	AAx63622	Aax63622 Human str
204	14.8	38.9	31	2	AAx63623	Aax63623 Human str
205	14.8	38.9	31	2	AAx63624	Aax63624 Human str
206	14.8	38.9	34	10	ABE25941	Abe25941 GalNAC-tr
207	14.8	38.9	34	14	ADX58204	Adx58204 Polyepi
208	14.8	38.9	37	8	ACA07953	Aca07953 Necrosis
209	14.8	38.9	39	12	ADM13533	Adm13533 GFP circu
210	14.8	38.9	41	12	ADP48407	Adp48407 Green flu
211	14.8	38.9	44	4	AAI65082	Aai65082 Oligonuc
212	14.8	38.9	45	10	ADP18224	Adp18224 DNA-bindi
213	14.8	38.9	45	10	ADF18224	Adf18224 DNA-bindi
214	14.8	38.9	48	2	AAQ34624	Aaq34624 GS3A prom
215	14.6	38.4	23	3	Aaz88805	Aaz88805 Human HLA
216	14.6	38.4	24	6	ABQ04752	Abq04752 Oligonuc
217	14.6	38.4	24	6	ABQ11121	Abq11121 Oligonuc
218	14.6	38.4	24	6	ABQ04793	Abq04793 Oligonuc
219	14.6	38.4	24	6	ABQ11080	Abq11080 Oligonuc
220	14.6	38.4	24	6	ABQ00396	Abq00396 Oligonuc
221	14.6	38.4	25	6	ABQ12616	Abq12616 Oligonuc
222	14.6	38.4	25	6	ABQ12657	Abq12657 Oligonuc
223	14.6	38.4	27	14	ADZ09950	Adz09950 Probe use
224	14.6	38.4	31	2	AAx06159	Aax06159 Human bia
225	14.6	38.4	31	4	AAI31159	Aai31159 Human sin
226	14.6	38.4	33	12	ADJ93097	Adj93097 rpsf prom
227	14.6	38.4	41	12	ADH06035	Adh06035 Gene poly
228	14.6	38.4	41	12	ADH05189	Adh05189 Gene poly
229	14.6	38.4	41	12	ADH90976	Adh90976 1-beta-me
230	14.6	38.4	41	12	ADH91822	Adh91822 1-beta-me
231	14.6	38.4	47	4	AAF80304	Aaf80304 Primer us
232	14.6	38.4	48	5	ABK09148	Abk09148 Human CD2
233	14.6	38.4	48	5	ADV62275	Adv62275 HBV amber
234	14.6	38.4	48	5	ACN36290	Acn36290 WNV minus
235	14.6	38.4	48	8	ACN36290	Acn36290 WNV minus
236	14.6	38.4	48	8	ACI09532	Aci09532 Necrosis
237	14.6	38.4	48	8	ACD55444	Acd55444 HBV amber
238	14.6	38.4	48	8	ACD55761	Acd55761 HBV amber

C 239	14.6	38.4	48	11	ADU55277	Adl55277 Human INK
C 240	14.6	38.4	48	12	ADM63489	Adm63489 Hepatitis
C 241	14.6	38.4	48	12	ADM63658	Adm63658 Hepatitis
C 242	14.6	38.4	50	2	AAV06347	Aav06347 Phosphati
C 243	14.4	37.9	24	3	AAZ36082	Aaz36082 Forward p
C 244	14.4	37.9	25	9	ACI09133	Act09133 Human mic
C 245	14.4	37.9	25	9	ACK19148	Ack19148 Human mic
C 246	14.4	37.9	25	9	ACI55943	Act55943 Human mic
C 247	14.4	37.9	32	6	AAI42267	Aai42267 Human pol
C 248	14.4	37.9	38	6	ABS70875	Abst70875 Hepatitis
C 249	14.4	37.9	39	4	AH24489	Aah24489 TRIM adap
C 250	14.4	37.9	41	6	ABS60719	Abst60719 Human DNA
C 251	14.4	37.9	41	6	ABZ43358	Abz43358 Human N-m
C 252	14.4	37.9	41	6	ABZ48698	Abz48698 Human N-m
C 253	14.4	37.9	45	4	Aaf67676	Aaf67676 Chicken i
C 254	14.4	37.9	46	4	Aaf63534	Aaf63534 aveC muta
C 255	14.4	37.9	46	5	AAS00545	Aas00545 S. avermi
C 256	14.4	37.9	46	10	ADG83558	Adg83558 Streptomy
C 257	14.4	37.9	50	6	ABZ02656	Abz02656 Human leu
C 258	14.4	37.9	50	6	ABZ00443	Abz00443 Human leu
C 259	14.2	37.4	21	13	ADU28731	Adu28731 Knock-dow
C 260	14.2	37.4	28	6	ABQ82499	Abq82499 Spo11B ge
C 261	14.2	37.4	32	6	ABK87827	Abk87827 Interleuk
C 262	14.2	37.4	32	14	ADY51614	Ady51614 Transcrip
C 263	14.2	37.4	33	4	AAf74484	Aaf74484 Clone 179
C 264	14.2	37.4	34	10	ADC98706	Adc98706 Double-st
C 265	14.2	37.4	35	6	ABT08597	Abt08597 Human nov
C 266	14.2	37.4	35	12	ADO09962	Ado09962 Human NOV
C 267	14.2	37.4	37	6	ABK87815	Abk87815 Human Kai
C 268	14.2	37.4	39	6	ABK13495	Abk13495 DT390 mut
C 269	14.2	37.4	40	2	AAT39933	Aat39933 SI primer
C 270	14.2	37.4	40	2	AAT61522	Aat61522 Mycobacte
C 271	14.2	37.4	40	2	AAT93008	Aat93008 M. tuberc
C 272	14.2	37.4	40	2	AAT64794	Aat64794 Primer S2
C 273	14.2	37.4	40	2	AAT90466	Aat90466 PCR prime
C 274	14.2	37.4	40	2	AAT61537	Aat61537 Mycobacte
C 275	14.2	37.4	40	2	AAV18912	Aav18912 Aval PCR
C 276	14.2	37.4	40	2	AAV71893	Aav71893 Mycobacte
C 277	14.2	37.4	40	3	AAZ94293	Aaz94293 Composite
C 278	14.2	37.4	40	3	AAC64840	Aac64840 Novel str
C 279	14.2	37.4	40	3	AAC63161	Aac63161 Novel str
C 280	14.2	37.4	40	3	AAC65251	Aac65251 Allele-ep
C 281	14.2	37.4	40	3	AAC65184	Aac65184 Novel str
C 282	14.2	37.4	40	4	AAH27107	Aah27107 Primer S2
C 283	14.2	37.4	40	5	AAC63642	Aac63642 Surface a
C 284	14.2	37.4	40	5	AAC64902	Aac64902 Novel str
C 285	14.2	37.4	40	6	ABL54131	Ab154131 Mycobacte
C 286	14.2	37.4	40	6	ABQ78694	Abq78694 SDA prime
C 287	14.2	37.4	40	8	ACC58630	Acc58630 Mycobacte
C 288	14.2	37.4	40	9	ACF57180	Acf57180 M. tuberc
C 289	14.2	37.4	40	10	ADP11059	Adp11059 Mtb DNA P
C 290	14.2	37.4	40	11	ADY50544	Ady50544 Novel nuc
C 291	14.2	37.4	40	13	ADU04902	Adu04902 Composite
C 292	14.2	37.4	41	6	ABN85235	Abn85235 Protein a
C 293	14.2	37.4	44	2	AAV39051	Aav39051 Intronic
C 294	14.2	37.4	48	5	ADV07518	Adv07518 Human BAC
C 295	14.2	37.4	50	2	AAT89217	Aat89217 Specific
C 296	14.2	37.4	50	4	AAI32239	Aai32239 Human SNP
C 297	14.2	37.4	50	4	AAI34540	Aai34540 Human SNP
C 298	14	36.8	19	13	ADT01206	Adt01206 Novel mut
C 299	14	36.8	21	2	AAZ25681	Aaz25681 Transcrip
C 300	14	36.8	21	12	ADP48377	Adp48377 NF-kappaB

## ALIGNMENTS

RESULT 1  
AAZ32919  
ID AAZ32919 standard; DNA; 38 BP.

XX  
AC AAZ32919;  
XX

DT 09-FEB-2000 (first entry)  
XX Kappa-B-PT sequence (SEQ ID 2), used to inhibit NF-kappa-B.  
DE Kappa-B-PT sequence; NF-kappa-B; nuclear factor kappa B; adhesion;  
KW differentiation; phosphorothioate; treatment; immune disorder;  
KW inflammatory disease; cancer; viral infection;  
KW immunoglobulin kappa B sequence; rheumatoid arthritis; ischaemia;  
KW reperfusion injury; restenosis; transplant rejection; Crohn's disease;  
KW ulcerative colitis; psoriasis; glomerulonephritis; leukaemia; melanoma;  
KW sarcoma; lymphoma; HIV; HTLV; herpes virus; poison ivy; poison oak;  
KW poison sumac; ds.  
XX Synthetic.  
OS Key  
FH Location/Qualifiers  
FT modified\_base 1..10  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "Optionally phosphorothioate linkages"  
FT protein\_bind 2..11  
FT /tag= b  
FT /bound\_moiety= "NF-kappa-B"  
FT protein\_bind 16..25  
FT /tag= b  
FT /bound\_moiety= "NF-kappa-B"  
FT protein\_bind 29..38  
FT /tag= b  
FT /bound\_moiety= "NF-kappa-B"  
XX US5990090-A.  
XX 23-NOV-1999.  
XX 27-FEB-1996; 96US-00607519.  
XX 20-SEP-1993; 93US-00123188.  
(UNMI ) UNIV MICHIGAN.  
XX Nabel GU;  
XX WPI; 2000-022803/02.  
XX Composition useful for the treatment of immune and inflammatory diseases,  
XX cancer and viral infections.  
XX Claim 1; Col 4; 14pp; English.  
XX This sequence represents the kappa-B-PT sequence (SEQ ID 2) which  
XX contains three immunoglobulin kappa-B sequences (AAZ32918) which are  
XX bound by activated NF-kappa-B (nuclear factor kappa-B). It can inhibit NF  
XX -kappa-B binding to endogenous kappa-B enhancer/promoter elements, thus  
XX inhibiting transcription of genes that comprise such elements. NF-kappa-B  
XX is involved in the induction of cell adhesion associated with  
XX differentiation or activation. For example, the human promyelotic  
XX leukaemia cell line (HL-60 cells) can be induced to differentiate into  
XX monocytoid cells with concomitant expression of the leukocyte adhesion  
XX glycoprotein CD11b by treatment with phorbol esters. However, this  
XX differentiation and adhesion can be inhibited by prior incubation of the  
XX HL-60 cells with this sequence which specifically binds NF-kappa-B. In  
XX contrast, use of a mutant kappa-B-PT sequence (AAZ32920) had no effect on  
XX differentiation and adhesion. Compositions containing the kappa-B-PT  
XX sequence may be used for the treatment of immune and inflammatory  
XX diseases, cancer and viral infections. In particular it can be used to  
XX treat rheumatoid arthritis, ischaemia/reperfusion injury, restenosis,  
XX transplant rejection, Crohn's disease, ulcerative colitis, psoriasis,  
XX glomerulonephritis, leukaemia, melanoma, sarcoma, lymphomas and HIV,  
XX HTLV, herpes virus infections and reaction to poison ivy, poison oak and  
XX poison sumac  
XX Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;

Query Match		100.0%;	Score 38;	DB 3;	Length 38;				
Best Local Similarity		100.0%;	Pred. No. 2e-05;						
Matches		38;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;				
QY	1	GGGGACTTTC	CGCTGGGGACTTTC	CCAGGGGACTTTCC	38				
DB	1	GGGGACTTTC	CGCTGGGGACTTTC	CCAGGGGACTTTCC	38				
RESULT 2									
AAAF99023									
ID	AAF99023	standard; DNA; 38 BP.							
XX	AC	AAAF99023;							
XX	DT	12-JUN-2001 (first entry)							
XX	DE	Immunostimulatory nucleic acid #139.							
XX	KW	Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;							
KW	immunostimulatory; tumour; viral infection; bacterial infection;								
KW	fungal infection; parasitic infection; cancer; asthma;								
KW	infectious disease; allergy; immune deficiency; phosphorothioate; ss.								
XX	OS	Synthetic.							
XX	PN	WO200122972-A2.							
XX	PD	05-APR-2001.							
XX	PF	25-SEP-2000; 2000WO-US026383.							
XX	PR	25-SEP-1999; 99US-0156113P.							
PR	27-SEP-1999;	99US-0156135P.							
PR	23-AUG-2000;	2000US-0227436P.							
XX	(IOWA ) UNIV IOWA RES FOUND.								
PA	(COLE-) COLEY PHARM GMBH.								
PI	Krieg AM, Schetter C, Vollmer J;								
XX	WPI; 2001-273485/28.								
XX	Vaccinating against tumors, infectious diseases, allergies and asthma								
PT	using immunostimulatory Py-rich and TG nucleic acids.								
XX	Claim 101; Page 41; 338pp; English.								
XX	The present invention relates to a method for stimulating an immune								
CC	response. The method comprises administering an immunostimulatory nucleic								
CC	acid to a non-rodent subject in sufficient quantity to stimulate an								
CC	immune response. The present sequence is one such immunostimulatory								
CC	nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich								
CC	(py-rich) or thymidine (T) rich. The method is used to vaccinate subjects								
CC	against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae								
CC	and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,								
CC	haemophilus, campylobacter, clostridium, Escherichia coli and/or								
CC	staphylococcus), fungal antigens and/or parasitic antigens. The method is								
CC	also useful for preventing cancer, asthma, infectious disease, allergy or								
CC	immune deficiency. The present sequence can also be used to redirect a								
CC	Th2 to a Th1 immune response and to activate immune cells. Note: the								
CC	present sequence may have a phosphorothioate backbone								
XX	Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;								
Query Match		100.0%;	Score 38;	DB 4;	Length 38;				
Best Local Similarity		100.0%;	Pred. No. 2e-05;						
Matches		38;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;				
QY	1	GGGGACTTTC	CGCTGGGGACTTTC	CCAGGGGACTTTCC	38				
DB	1	GGGGACTTTC	CGCTGGGGACTTTC	CCAGGGGACTTTCC	38				
RESULT 4									
ABL39015									
ID	ABL39015	standard; DNA; 38 BP.							
XX	AC	ABL39015;							
XX									

Query Match		100.0%;	Score 38;	DNA; 38 BP.	
ID	ABS77664	standard; DNA; 38 BP.			
XX	AC	ABS77664;			
XX	DT	13-DEC-2002 (first entry)			
XX	DE	Angiogenesis inhibitory oligonucleotide #148.			
XX	KW	Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;			
KW	tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;				
KW	diabetic retinopathy; retinopathy of prematurity; macular degeneration;				
KW	corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;				
KW	rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;				
KW	plaque neovascularisation; telangiectasia; haemophilic joint;				
KW	angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;				
KW	scleroderma; hypertrophic scar.				
XX	OS	Synthetic.			
XX	PN	WO200253141-A2.			
XX	PD	11-JUL-2002.			
XX	PF	14-DEC-2001; 2001WO-US048458.			
XX	PR	14-DEC-2000; 2000US-0255534P.			
XX	PA	(COLE-) COLEY PHARM GROUP INC.			
XX	PI	Bratzler RL;			
XX	DR	WPI; 2002-566690/60.			
XX	PT	Inhibiting angiogenesis in a subject, involves administering at least one			
PT	antiangiogenic nucleic acid molecule to the subject.				
XX	PS	Claim 2; Page 22; 276pp; English.			
XX	CC	The invention relates to inhibiting angiogenesis in a subject, comprising			
CC	administering at least one antiangiogenic nucleic acid molecule. Also				
CC	included is a kit comprising a first container housing the antiangiogenic				
CC	nucleic acids, and instructions for administering them to a subject				
CC	having a condition characterised by unwanted angiogenesis. The method is				
CC	useful for inhibiting angiogenesis associated with solid tumour growth,				
CC	tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,				
CC	diabetic retinopathy, retinopathy of prematurity, macular degeneration,				
CC	corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,				
CC	rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque				
CC	neovascularisation, telangiectasia, haemophilic joints, angiofibroma,				
CC	wound granulation, intestinal adhesions, atherosclerosis, scleroderma and				
CC	hypertrophic scars. The present sequence is an antiangiogenic nucleic				
CC	acid of the invention				
XX	Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;				
Query Match		100.0%;	Score 38;	DB 6;	Length 38;
Best Local Similarity		100.0%;	Pred. No. 2e-05;		
Matches		38;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	GGGGACTTTC	CGCTGGGGACTTTC	CCAGGGGACTTTCC	38
DB	1	GGGGACTTTC	CGCTGGGGACTTTC	CCAGGGGACTTTCC	38
RESULT 4					
ABL39015					
ID	ABL39015	standard; DNA; 38 BP.			
XX	AC	ABL39015;			
XX					



DT 16-APR-2002 (first entry)  
XX Immunostimulatory nucleic acid SEQ ID NO: 417.  
DE  
XX  
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; ss.  
XX  
XX Synthetic.  
XX  
XX WO200197843-A2.  
XX  
XX 27-DEC-2001.  
XX  
XX 22-JUN-2001; 2001WO-US020154.  
XX  
XX 22-JUN-2000; 2000US-0213346P.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX  
XX Weiner G, Hartmann G;  
PI  
XX WPI; 2002-154611/20.  
XX  
XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer.  
XX  
XX Disclosure; Page 201; 312pp; English.  
XX  
XX The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention  
XX  
XX Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 38; DB 6; Length 38;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCGGTGGGACTTTCAGGGGACTTTCC 38  
DB 1 GGGGACTTTCGGTGGGACTTTCAGGGGACTTTCC 38  
RESULT 5  
ACD99455  
ID ACD99455 standard; DNA; 38 BP.  
XX  
XX ACD99455;  
XX  
XX 25-SEP-2003 (first entry)  
XX  
XX Immunostimulatory nucleic acid #141.  
DE  
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX  
XX Synthetic.  
XX

PN US2003050268-A1.  
XX  
XX 13-MAR-2003.  
XX  
XX 29-MAR-2002; 2002US-00112653.  
XX  
XX 29-MAR-2001; 2001US-0279642P.  
XX  
XX (KRIE/) KRIEG A M.  
XX (BERG/) BERG D J.  
XX  
XX Krieg AM, Berg DJ;  
XX  
XX WPI; 2003-521815/49.  
XX  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX  
XX Disclosure; Page 12; 229pp; English.  
XX  
XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
XX Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 38; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGACTTTCGGTGGGACTTTCAGGGGACTTTCC 38  
DB 1 GGGGACTTTCGGTGGGACTTTCAGGGGACTTTCC 38  
RESULT 6  
ADB36525  
ID ADB36525 standard; DNA; 38 BP.  
XX  
XX ADB36525;  
XX  
XX 04-DEC-2003 (first entry)  
XX  
XX Immunostimulatory nucleic acid #139.  
XX  
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX  
XX Synthetic.  
XX  
XX US2003087848-A1.  
XX  
XX 08-MAY-2003.  
XX  
XX 02-FEB-2001; 2001US-00776479.  
XX  
XX 03-FEB-2000; 2000US-0179991P.  
XX  
XX (BRAT/) BRATZLER R L.  
XX (PETE/) PETERSEN D M.  
XX (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
XX  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
XX

PT nucleic acid alone or in combination with an asthma/allergy medicament.

XX Disclosure; Page 7; 221pp; English.

CC The invention relates to a method of treating or preventing allergy or

CC asthma which comprises administering to a subject a poly-G nucleic acid

CC in an aerosol formulation. The methods and compositions of the present

CC invention are useful for diagnosing and/or treating asthma and allergy

CC especially in a hypo-responsive subject. The present sequence represents

CC an immunostimulatory nucleic acid of the invention.

XX

SQ Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 38; DB 9; Length 38;

Best Local Similarity 100.0%; Pred. No. 2e-05;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38

Db 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38

RESULT 7

ADU89464

ID ADU89464 standard; DNA; 38 BP.

XX

AC ADU89464;

XX

DT 10-FEB-2005 (first entry)

XX

DE Allergic response suppressor oligonucleotide #148.

XX

DE ss: antiasthmatic; antiallergic; dermatological; antiinflammatory;

KW antibacterial; virucide; immunoglobulin E antagonist; allergy;

KW immunostimulant; asthma; rhinitis; urticaria; dermatitis;

KW bacterial infection; viral infection.

XX

OS Synthetic.

XX

XX US2004235774-A1.

PN

XX 25-NOV-2004.

PD

XX

PF 23-APR-2004; 2004US-00831778.

XX

PR 03-FEB-2000; 2000US-0179991P.

PR

PR 02-FEB-2001; 2001US-00776479.

XX

XX (BRAT/) BRATZLER R L.

PA (PETE/) PETERSEN D M.

PA (FOUR/) FOURON Y.

XX

PI Bratzler RL, Petersen DM, Fouron Y;

XX

XX WPI; 2004-833006/82.

DR

XX

XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic

PT dermatitis in a subject, comprises administering a first and second dose

PT of an immunostimulatory nucleic acid.

XX

XX Disclosure; SEQ ID NO 148; 235pp; English.

SS

XX The invention relates to a method of suppressing a symptom of an allergic

CC response in a subject by administering a first and second dose of an

CC immunostimulatory nucleic acid that comprises a nucleotide sequence

CC comprising 5'-cg-3', and where the second dose is administered from 1 day

CC to 8 weeks after the first dose. The methods and compositions of the

CC present invention are useful for the treatment or prevention of asthma

CC and allergy, including rhinitis, urticaria and atopic dermatitis, using

CC an immunostimulatory nucleic acid alone or in combination with other

CC medicaments. They can also be used in preventing bacterial and viral

CC infections. This sequence represents an oligonucleotide used in the

CC method of the invention.

XX

SQ Sequence 38 BP; 4 A; 10 C; 14 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 38; DB 13; Length 38;

Best Local Similarity 100.0%; Pred. No. 2e-05;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38

Db 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38

RESULT 8

AAT30609

ID AAT30609 standard; DNA; 43 BP.

XX

AC AAT30609;

XX

DT 19-FEB-1997 (first entry)

XX

DE Target binding region #29.

XX

KW Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;

KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;

KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;

KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;

KW virus; ss.

XX

OS Synthetic.

XX

XX WO9617956-A2.

PN

XX 13-JUN-1996.

PD

XX 07-DEC-1995; 95WO-US015944.

PF

XX 09-DEC-1994; 94US-00353476.

PR

XX (GENE-) GENE POOL INC.

PA

PI Weininger S, Weininger AM;

XX

XX WPI; 1996-287199/29.

DR

XX

XX Probe nucleic acids, target binding assemblies, etc - for detection and

PT localisation of specific nucleic acid sequences, esp. HIV and HPV.

XX

XX Disclosure; Page 73; 172pp; English.

PS

XX AAT30581-T30614 represent target binding regions (TBR) of a probe of the

CC invention. The probe of the invention contains a TBR, a booster binding

CC region (BBR), and an optional support or attachment (OSA). The target

CC binding assembly (TBA) recognised by the probe, contains at least one

CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an

CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see

CC AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007),

CC and an OSA. The assembly sequence and asymmetry sequences are responsible

CC for the folding and association of the NARs. The NARs (see AAR95965-

CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus

CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding

CC units. The linker sequence is an oligopeptide, which does not interfere

CC with NAR function, but provides stability and control over the spacing of

CC the NAR from the rest of the TBA. The OSA is an attached support or

CC indicator, or other means of localisation of the probe. The probe can be

CC used in a method for detecting or localising a specific target nucleic

CC acid sequence (TNA). The method is highly sensitive, and has a high

CC degree of specificity. The method can be used for detecting specific

CC nucleic acid sequences, including those found in human cells, in HIV,

CC HPV, and other nucleic acid containing systems, including bacteria and

CC viruses

XX

SQ Sequence 43 BP; 6 A; 12 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 81.1%; Score 30.8; DB 2; Length 43;  
Best Local Similarity 94.1%; Pred. No. 0.015;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGACTTCCAGGGGACT 34  
DB 6 GGGGACTTCCGCTGGGACTTCCAGGGGAGGCT 39

RESULT 9  
AAAT30608  
ID AAAT30608 standard; DNA; 46 BP.  
XX AC  
XX AAT30608;  
DT 19-FEB-1997 (first entry)  
DE Target binding region #28.  
XX Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;  
KW TATA; human papillomavirus; HPV E2; human immunodeficiency virus;  
KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
KW virus; ss.  
XX Synthetic.  
XX WO9617956-A2.  
PN 13-JUN-1996.  
PD 07-DEC-1995; 9SWO-US015944.  
PF 09-DEC-1994; 94US-00353476.  
PR (GENE-) GENE POOL INC.  
PA Weininger S, Weininger AM;  
PI WPI; 1996-287199/29.  
XX Probe nucleic acids, target binding assemblies, etc - for detection and  
PT localisation of specific nucleic acid sequences, esp. HIV and HPV.  
XX Disclosure; Page 73; 172pp; English.

AAAT30581-T30614 represent target binding regions (TBR) of a probe of the  
invention. The probe of the invention contains a TBR, a booster binding  
region (BBR), and an optional support or attachment (OSA). The target  
binding assembly (TBA) recognised by the probe, contains at least one  
nucleic acid recognition unit (NAR), and optionally a linker sequence, an  
assembly sequence (see AAR95994-R95998), an asymmetry sequence (see  
AAR95999-R95006), a nuclear localisation signal sequence (see AAR96007),  
and an OSA. The assembly sequence and asymmetry sequences are responsible  
for the folding and association of the NARs. The NARs (see AAR95995-  
R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus  
(HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding  
units. The linker sequence is an oligopeptide, which does not interfere  
with NAR function, but provides stability and control over the spacing of  
the NAR from the rest of the TBA. The OSA is an attached support or  
indicator, or other means of localisation of the probe. The probe can be  
used in a method for detecting or localising a specific target nucleic  
acid sequence (TNA). The method is highly sensitive, and has a high  
degree of specificity. The method can be used for detecting specific  
nucleic acid sequences, including those found in human cells in HIV,  
HPV, and other nucleic acid containing systems, including bacteria and  
viruses

XX Sequence 46 BP; 7 A; 10 C; 20 G; 9 T; 0 U; 0 Other;

Query Match 79.5%; Score 30.2; DB 2; Length 46;  
Best Local Similarity 91.4%; Pred. No. 0.026;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGACTTCCAGGGGACTT 35  
DB 6 GGGGACTTCCGCTGGGACTTCCAGGGAGCGT 40

RESULT 10  
AAQ58049  
ID AAQ58049 standard; DNA; 39 BP.  
XX AC  
XX AAQ58049;  
DT 25-MAR-2003 (revised)  
DT 23-SEP-1994 (first entry)  
XX  
DE Oligonucleotide NF1.  
XX HIV; tat; transport; moiety; conjugate; cargo molecule;  
KW cytoplasmic delivery; nuclear delivery; cysteine-rich region;  
KW transactivation; disulphide aggregation; ss.  
XX Synthetic.  
XX WO9404686-A1.  
PN 03-MAR-1994.  
PD 19-AUG-1993; 93WO-US007833.  
PF 21-AUG-1992; 92US-00934375.  
PR (BIOJ) BIOGEN INC.  
PA Barsoum JG, Fawell SE, Pepinsky RB;  
PI WPI; 1994-083202/10.  
XX Transport of cargo moieties into cells - using genetic fusions of  
PT chemical conjugates comprising a portion of HIV tat protein as transport  
XX peptide.  
XX Claim 21; Page 116; 153pp; English.

The sequences given in AAQ58049-50 form a double stranded DNA molecule  
which was used as the cargo moiety in the conjugate of the invention.  
This oligonucleotide fragment was linked to a peptide fragment of the HIV  
tat protein which was used as transport moieties. These conjugates are  
used as cargo molecules for the efficient cytoplasmic and nuclear  
delivery of biologically active non-tat proteins, nucleic acids and other  
molecules which are not inherently capable of entering a target cell. The  
tat basic region amino acid sequence carries cargo molecules by covalent  
attachment. The reduced size of the transport peptides minimises  
interference with the biological activity of the cargo molecule. By  
virtue of the absence of the cysteine-rich region (residues 22-36) of the  
tat protein, problems of spurious trans-activation and disulphide  
aggregation are solved. The reduced transport peptide size also enhances  
uptake efficiency. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;

Query Match 78.9%; Score 30; DB 2; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.03;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGACTTCCAGGGGACTTTC 38  
DB 1 GGGGACTTCCGCTGGGACTTCCAGGGGACTTTC 38

RESULT 11  
AAQ58050/c  
ID AAQ58050 standard; DNA; 39 BP.  
XX

AC AAQ58050;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 23-SEP-1994 (first entry)  
 XX  
 DE  
 XX  
 XX  
 XX  
 KW HIV; tat; transport; moiety; conjugate; cargo molecule;  
 KW cytoplasmic delivery; nuclear delivery; cysteine-rich region;  
 KW transactivation; disulphide aggregation; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9404686-A1.  
 XX  
 XX  
 PD 03-MAR-1994.  
 XX  
 PF 19-AUG-1993; 93WO-US007833.  
 XX  
 PR 21-AUG-1992; 92US-00934375.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PI Barsoum JG, Fawell SE, Pepinsky RB;  
 XX WPI; 1994-083202/10.  
 XX  
 PT Transport of cargo moieties into cells - using genetic fusions of  
 PT chemical conjugates comprising a portion of HIV tat protein as transport  
 PT peptide.  
 XX  
 PS Claim 21; Page 116; 153pp; English.  
 CC  
 CC The sequences given in AAQ58049-50 form a double stranded DNA molecule  
 CC which was used as the cargo moiety in the conjugate of the invention.  
 CC This oligonucleotide fragment was linked to a peptide fragment of the HIV  
 CC tat protein which was used as transport moieties. These conjugates are  
 CC used as cargo molecules for the efficient cytoplasmic and nuclear  
 CC delivery of biologically active non-tat proteins, nucleic acids and other  
 CC molecules which are not inherently capable of entering a target cell. The  
 CC tat basic region amino acid sequence carries cargo molecules by covalent  
 CC attachment. The reduced size of the transport peptides minimises  
 CC interference with the biological activity of the cargo molecule. By  
 CC virtue of the absence of the cysteine-rich region (residues 22-36) of the  
 CC tat protein, problems of spurious trans- activation and disulphide  
 CC aggregation are solved. The reduced transport peptide size also enhances  
 CC uptake efficiency. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;  
 Query Match 78.9%; Score 30; DB 2; Length 39;  
 Best Local Similarity 86.8%; Pred. No. 0.03;  
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 GGGGACTTTCGCTGGGACTTTCACGGGGGACTTTC 38  
 |||||  
 Db 39 GGGGACTTTCGCTGGGACTTTCACGGGGGACTTTC 2  
 |||||  
 RESULT 12  
 AAT84584  
 ID AAT84584 standard; DNA; 39 BP.  
 XX  
 AC AAT84584;  
 XX  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 16-DEC-1997 (first entry)  
 XX  
 DE NF-kappa B binding site.  
 XX  
 KW HIV; tat protein; transport protein; cargo delivery;  
 KW NF-kappa B binding site; ds.  
 XX

OS Synthetic.  
 XX  
 PN US5652122-A.  
 XX  
 PD 29-JUL-1997.  
 XX  
 XX  
 PF 25-MAY-1995; 95US-00450257.  
 XX  
 PR 21-DEC-1989; 89US-00454450.  
 PR 02-JAN-1991; 91US-00636662.  
 PR 21-AUG-1992; 92US-00934375.  
 PR 19-AUG-1993; 93WO-US007833.  
 PR 24-NOV-1993; 93US-00158015.  
 PR 28-APR-1994; 94US-00235403.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.  
 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 PI Pepinsky RB, Barsoum JG, Pabo C, Fawell SE, Frankel A;  
 XX WPI; 1997-392943/36.  
 DR  
 XX  
 XX  
 PT New DNA constructs for transporting molecules to cells - encode a fusion  
 PT protein comprising a modified HIV tat protein and a carboxy-terminal  
 PT cargo moiety.  
 XX  
 PS Example 17; Col 97; 76pp; English.  
 XX  
 CC This double-stranded DNA sequence, comprising oligonucleotides NF1 (sense  
 CC strand) and NF2 (antisense strand), corresponds to the wild-type NF-kappa  
 CC B binding site. It was used in the preparation of transport polypeptide-  
 CC DNA conjugates. Such conjugates, in which modified HIV tat protein is  
 CC used as transport polypeptide, can be used to deliver cargo molecules to  
 CC cells in vivo or in vitro. (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;  
 Query Match 78.9%; Score 30; DB 2; Length 39;  
 Best Local Similarity 86.8%; Pred. No. 0.03;  
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 GGGGACTTTCGCTGGGACTTTCACGGGGGACTTTC 38  
 |||||  
 Db 1 GGGGACTTTCGCTGGGACTTTCACGGGGGACTTTC 38  
 |||||  
 RESULT 13  
 AAT8240/c  
 ID AAT8240 standard; DNA; 39 BP.  
 XX  
 AC AAT8240;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-JAN-1998 (first entry)  
 XX  
 DE NF-kappaB transcriptional activation inhibitor NF2.  
 XX  
 KW Chemical conjugate; transport polypeptide; tat protein; nucleic acid;  
 KW delivery; cytoplasm; cell nucleus; therapy; prophylaxis; diagnosis;  
 KW spurious transactivation; HIV-1; disulphide aggregation; NF-kappaB;  
 KW inhibition; NF2; human immunodeficiency virus type 1;  
 KW transcriptional activation; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX US5670617-A.  
 PN  
 XX  
 PD 23-SEP-1997.  
 XX  
 XX 25-MAY-1995; 95US-00450246.

```
XX 21-DEC-1989; 89US-00454450.
PR 02-JAN-1991; 91US-00636662.
PR 21-AUG-1992; 92US-00934375.
PR 19-AUG-1993; 93WO-US007833.
PR 24-NOV-1993; 93US-00158015.
PR 28-APR-1994; 94US-00235403.
XX
XX (BIOJ ) BIOGEN INC.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
XX
XX Barsom JG, Fawell SE, Frankel A, Pepinsky RB, Pabo C;
XX WPI; 1997-479523/44.
XX
XX Conjugate for intracellular delivery - comprising transport moiety having
PT amino acids 49-57 of human immunodeficiency virus tat protein and nucleic
PT acid cargo moiety.
XX
XX Claim 3; Col 97-98; 77pp; English.
XX
XX A novel covalently linked chemical conjugate, comprises a transport
CC polypeptide moiety consisting of at least residues 49-57 of human
CC immunodeficiency virus (HIV) tat protein, but not residues 22-36 and 73-
CC 86, and a cargo moiety comprising a single or double stranded nucleic
CC acid, e.g. the present sequence. The conjugate can be used to deliver
CC cargo moieties into the cytoplasm and nuclei of cells for therapeutic,
CC prophylactic and diagnostic applications. In an example conjugates to
CC inhibit transcriptional activation by NF-kappaB were prepared, the
CC oligonucleotides used were NF1-4 (AAT88239-42). NF1 and NF2 for a duplex
CC a duplex corresponding to the wild type NF-KB binding site, while NF2 and NF4 form
CC was then reacted with bismaleimidoethane activated tat 32-72. The
CC products were tested as in Science 250, 997-1000 (1990) for inhibition of
CC NF-KB transcriptional activation. The results showed that the tat
CC transport polypeptide significantly enhanced the inhibition. The HIV tat
CC protein is readily taken up into cells and the cell nucleus. The reduced
CC size of the transport polypeptides minimises interference with the
CC biological activity of the cargo molecule. In addition, by virtue of the
CC absence of the cysteine rich region of the HIV tat protein, the transport
CC polypeptides solve the potential problems of spurious transactivation and
CC disulphide aggregation. (Updated on 25-MAR-2003 to correct PF field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 78.9%; Score 30; DB 2; Length 39;
XX Best Local Similarity 86.8%; Pred. No. 0.03;
XX Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38
Db 39 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 2
XX
RESULT 14
AAT88239
ID AAT88239 standard; DNA; 39 BP.
XX
XX AAT88239;
XX
XX 25-MAR-2003 (revised)
DT 20-JAN-1998 (first entry)
XX
XX NF-kappaB transcriptional activation inhibitor NF1.
XX
XX Chemical conjugate; transport polypeptide; tat protein; nucleic acid;
KW delivery; cytoplasm; cell nucleus; therapy; prophylaxis; diagnosis;
KW spurious transactivation; HIV-1; disulphide aggregation; NF-kappaB;
KW inhibition; NF1; human immunodeficiency virus type 1;
KW transcriptional activation; ss.
```

```
XX Synthetic.
OS Homo sapiens.
XX
XX US5670617-A.
XX
XX 23-SEP-1997.
PD
XX
XX 25-MAY-1995; 95US-00450246.
XX
XX 21-DEC-1989; 89US-00454450.
PR 02-JAN-1991; 91US-00636662.
PR 21-AUG-1992; 92US-00934375.
PR 19-AUG-1993; 93WO-US007833.
PR 24-NOV-1993; 93US-00158015.
PR 28-APR-1994; 94US-00235403.
XX
XX (BIOJ ) BIOGEN INC.
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
XX
XX Barsom JG, Fawell SE, Frankel A, Pepinsky RB, Pabo C;
XX WPI; 1997-479523/44.
XX
XX Conjugate for intracellular delivery - comprising transport moiety having
PT amino acids 49-57 of human immunodeficiency virus tat protein and nucleic
PT acid cargo moiety.
XX
XX Claim 3; Col 97-98; 77pp; English.
XX
XX A novel covalently linked chemical conjugate, comprises a transport
CC polypeptide moiety consisting of at least residues 49-57 of human
CC immunodeficiency virus (HIV) tat protein, but not residues 22-36 and 73-
CC 86, and a cargo moiety comprising a single or double stranded nucleic
CC acid, e.g. the present sequence. The conjugate can be used to deliver
CC cargo moieties into the cytoplasm and nuclei of cells for therapeutic,
CC prophylactic and diagnostic applications. In an example conjugates to
CC inhibit transcriptional activation by NF-kappaB were prepared, the
CC oligonucleotides used were NF1-4 (AAT88239-42). NF1 and NF2 for a duplex
CC a duplex corresponding to the wild type NF-KB binding site, while NF2 and NF4 form
CC was then reacted with bismaleimidoethane activated tat 32-72. The
CC products were tested as in Science 250, 997-1000 (1990) for inhibition of
CC NF-KB transcriptional activation. The results showed that the tat
CC transport polypeptide significantly enhanced the inhibition. The HIV tat
CC protein is readily taken up into cells and the cell nucleus. The reduced
CC size of the transport polypeptides minimises interference with the
CC biological activity of the cargo molecule. In addition, by virtue of the
CC absence of the cysteine rich region of the HIV tat protein, the transport
CC polypeptides solve the potential problems of spurious transactivation and
CC disulphide aggregation. (Updated on 25-MAR-2003 to correct PF field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 78.9%; Score 30; DB 2; Length 39;
XX Best Local Similarity 86.8%; Pred. No. 0.03;
XX Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38
Db 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38
XX
RESULT 15
AAT89779
ID AAT89779 standard; DNA; 39 BP.
XX
XX AAT89779;
AC
XX 25-MAR-2003 (revised)
DT
```

```

DT 20-MAR-1998 (first entry)
XX DE
XX DE Transcription factor NF-kappaB oligonucleotide NF1.
XX KW Human Immunodeficiency Virus; HIV Type 1; Tat protein; cargo molecule;
XX KW intracellular delivery; fusion protein; therapeutic; prophylactic;
XX KW diagnostic; transport polypeptide; E2 repressor protein; ss.
XX OS Synthetic.
XX XX
XX PN US5674980-A.
XX PD 07-OCT-1997.
XX XX
XX PF 25-MAY-1995; 95US-00450098.
XX XX
XX PR 21-DEC-1989; 89US-00454450.
XX PR 02-JAN-1991; 91US-00636662.
XX PR 21-AUG-1992; 92US-00934375.
XX PR 19-AUG-1993; 93WO-US007833.
XX PR 24-NOV-1993; 93US-00158015.
XX PR 28-APR-1994; 94US-00235403.
XX XX
XX PA (PABO/) PABO C.
XX PA (FRAN/) FRANKEL A.
XX PA (FAWE/) FAWELL S E.
XX PA (PEPI/) PEPINSKY R B.
XX PA (BARS/) BARSOUM J G.
XX XX
XX PI Barsoum JG, Fawell SE, Frankel A, Pepinsky RB, Pabo C;
XX PI WPI; 1997-502388/46.
XX DR
XX XX
XX PT Fusion proteins containing truncated HIV tat sequences - useful for
XX PT intracellular delivery of viral repressor proteins.
XX XX
XX PS Example 17; Col 95-96; 77pp; English.
XX XX
XX CC This oligonucleotide primer is used with AAT89780 to form a duplex
XX CC corresponding to the wild type transcription factor NF-kappaB binding
XX CC site which is used in the construction of a transport polypeptide-DNA
XX CC conjugate. This conjugate is used in a novel method for delivery of
XX CC biologically active cargo molecules into the cytoplasm and nuclei of
XX CC eukaryotic cells. The tat protein from immunodeficiency virus (e.g. HIV-
XX CC 1, HIV-2, SIV) is readily taken up into cells when present
XX CC extracellularly and can be modified to covalently link to cargo proteins
XX CC e.g. E2 repressor proteins producing a fusion protein without the
XX CC problems of spurious trans-activation and disulphide aggregation. These
XX CC transport polypeptides also minimise interference with the biological
XX CC activity of the cargo molecule. This is applicable for therapeutic,
XX CC prophylactic or diagnostic intracellular delivery of small molecules and
XX CC macromolecules e.g. proteins, nucleic acids and polysaccharides. (Updated
XX CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
XX CC PA field.)
XX XX
XX SQ Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;

Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCTCGCTGGGGACTTTCCAGGGGGACTTTCC 38
Db 1 GGGGACTTTCCTCGCTGGGGACTTTCCAGGGGGACTTTCC 38

RESULT 16
AAT89780/c
ID AAT89780 standard; DNA; 39 BP.
XX ID
XX AC AAT89780;
XX AC
XX DT 25-MAR-2003 (revised)

DT 20-MAR-1998 (first entry)
XX DE
XX DE Transcription factor NF-kappaB oligonucleotide NF2.
XX KW Human Immunodeficiency Virus; HIV Type 1; Tat protein; cargo molecule;
XX KW intracellular delivery; fusion protein; therapeutic; prophylactic;
XX KW diagnostic; transport polypeptide; E2 repressor protein; ss.
XX OS Synthetic.
XX XX
XX PN US5674980-A.
XX PD 07-OCT-1997.
XX XX
XX PF 25-MAY-1995; 95US-00450098.
XX XX
XX PR 21-DEC-1989; 89US-00454450.
XX PR 02-JAN-1991; 91US-00636662.
XX PR 21-AUG-1992; 92US-00934375.
XX PR 19-AUG-1993; 93WO-US007833.
XX PR 24-NOV-1993; 93US-00158015.
XX PR 28-APR-1994; 94US-00235403.
XX XX
XX PA (PABO/) PABO C.
XX PA (FRAN/) FRANKEL A.
XX PA (FAWE/) FAWELL S E.
XX PA (PEPI/) PEPINSKY R B.
XX PA (BARS/) BARSOUM J G.
XX XX
XX PI Barsoum JG, Fawell SE, Frankel A, Pepinsky RB, Pabo C;
XX PI WPI; 1997-502388/46.
XX DR
XX XX
XX PT Fusion proteins containing truncated HIV tat sequences - useful for
XX PT intracellular delivery of viral repressor proteins.
XX XX
XX PS Example 17; Col 95-96; 77pp; English.
XX XX
XX CC This oligonucleotide primer is used with AAT89779 to form a duplex
XX CC corresponding to the wild type transcription factor NF-kappaB binding
XX CC site which is used in the construction of a transport polypeptide-DNA
XX CC conjugate. This conjugate is used in a novel method for delivery of
XX CC biologically active cargo molecules into the cytoplasm and nuclei of
XX CC eukaryotic cells. The tat protein from immunodeficiency virus (e.g. HIV-
XX CC 1, HIV-2, SIV) is readily taken up into cells when present
XX CC extracellularly and can be modified to covalently link to cargo proteins
XX CC e.g. E2 repressor proteins producing a fusion protein without the
XX CC problems of spurious trans-activation and disulphide aggregation. These
XX CC transport polypeptides also minimise interference with the biological
XX CC activity of the cargo molecule. This is applicable for therapeutic,
XX CC prophylactic or diagnostic intracellular delivery of small molecules and
XX CC macromolecules e.g. proteins, nucleic acids and polysaccharides. (Updated
XX CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
XX CC PA field.)
XX XX
XX SQ Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCTCGCTGGGGACTTTCCAGGGGGACTTTCC 38
Db 39 GGGGACTTTCCTCGCTGGGGACTTTCCAGGGGGACTTTCC 2

RESULT 17
AAV56615
ID AAV56615 standard; DNA; 39 BP.
XX ID
XX AC AAV56615;
XX AC
XX DT 25-MAR-2003 (revised)

```

```
DT 24-NOV-1998 (first entry)
DE NF-kappaB binding site phosphorothioate primer NF1.
XX
XX TAT protein; cargo molecule; therapy; diagnosis; transport protein;
KW fusion protein; human papillomavirus E2 repressor; target cell;
KW phosphorothioate; primer; ss.
XX
XX Synthetic.
XX
XX US5804604-A.
XX
XX 08-SEP-1998.
XX
XX 25-MAY-1995; 95US-00450236.
XX
XX 21-DEC-1989; 89US-00454450.
XX 02-JAN-1991; 91US-00636662.
XX 19-AUG-1993; 93WO-US007833.
XX 24-NOV-1993; 93US-00158015.
XX 28-APR-1994; 94US-00235403.
XX
XX (BIOJ ) BIOGEN INC.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
XX
XX Fawell SE, Barsoum JG, Pepinsky RB, Pabo C, Frankel A;
XX WPI; 1998-505702/43.
XX
XX HIV tat-derived transport fusion proteins - used to deliver biological
PT active molecules e.g. peptide(s) or nucleic acids, specifically into
PT cytoplasm or nuclei of cells.
XX
XX Example 17; Col 95-96; 83pp; English.
XX
XX This sequence is a phosphorothioate primer used in a method for the
CC delivery of biologically active cargo molecules into the cytoplasm and
CC nuclei of cells, for therapeutic, prophylactic or diagnostic purposes.
CC This is accomplished by the presence of a small, basic section of the tat
CC transport protein from human immunodeficiency virus (HIV) Type I. This is
CC used as it is this protein which is observed to cause human cells in
CC culture to take up HIV. The method involves the use of a cargo moiety in
CC combination with a transport moiety usually in the form of a fusion
CC protein. The cargo moiety is a human papillomavirus E2 repressor that
CC retains its biological activity after delivery into a target cell and
CC where the transport moiety is one of following HIV tat protein fragments
CC (a) aa 47-58, (b) aa 47-72, (c) 38-72, (d) aa 38-58, (e) aa 37-58, (f) aa
CC 1-21 and 38-72, (g) aa 47-62 or aa 38-62. The proteins allow delivery of
CC specific peptides into cells at high concentrations due to use of
CC existing transporters. Previous methods of delivery include bombardment
CC and transforming, which only allow a fraction of the cell population to
CC be infected and can additionally damage cells as they cause physical
CC opening of the cell walls/membranes to allow entry. (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX
XX Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
SQ
Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTCC 38
Db 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTC 38
RESULT 18
AAV56616/c
ID AAV56616 standard; DNA; 39 BP.
XX
XX AAV56616;
AC
XX
```

```
DT 25-MAR-2003 (revised)
DT 24-NOV-1998 (first entry)
XX
XX NF-kappaB binding site phosphorothioate primer NF2.
DE
XX
XX TAT protein; cargo molecule; therapy; diagnosis; transport protein;
KW fusion protein; human papillomavirus E2 repressor; target cell;
KW phosphorothioate; primer; ss.
XX
XX Synthetic.
XX
XX US5804604-A.
XX
XX 08-SEP-1998.
XX
XX 25-MAY-1995; 95US-00450236.
XX
XX 21-DEC-1989; 89US-00454450.
XX 02-JAN-1991; 91US-00636662.
XX 19-AUG-1993; 93WO-US007833.
XX 24-NOV-1993; 93US-00158015.
XX 28-APR-1994; 94US-00235403.
XX
XX (BIOJ ) BIOGEN INC.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.
XX
XX Fawell SE, Barsoum JG, Pepinsky RB, Pabo C, Frankel A;
XX WPI; 1998-505702/43.
XX
XX HIV tat-derived transport fusion proteins - used to deliver biological
PT active molecules e.g. peptide(s) or nucleic acids, specifically into
PT cytoplasm or nuclei of cells.
XX
XX Example 17; Col 97-98; 83pp; English.
XX
XX This sequence is a phosphorothioate primer used in a method for the
CC delivery of biologically active cargo molecules into the cytoplasm and
CC nuclei of cells, for therapeutic, prophylactic or diagnostic purposes.
CC This is accomplished by the presence of a small, basic section of the tat
CC transport protein from human immunodeficiency virus (HIV) Type I. This is
CC used as it is this protein which is observed to cause human cells in
CC culture to take up HIV. The method involves the use of a cargo moiety in
CC combination with a transport moiety usually in the form of a fusion
CC protein. The cargo moiety is a human papillomavirus E2 repressor that
CC retains its biological activity after delivery into a target cell and
CC where the transport moiety is one of following HIV tat protein fragments
CC (a) aa 47-58, (b) aa 47-72, (c) 38-72, (d) aa 38-58, (e) aa 37-58, (f) aa
CC 1-21 and 38-72, (g) aa 47-62 or aa 38-62. The proteins allow delivery of
CC specific peptides into cells at high concentrations due to use of
CC existing transporters. Previous methods of delivery include bombardment
CC and transforming, which only allow a fraction of the cell population to
CC be infected and can additionally damage cells as they cause physical
CC opening of the cell walls/membranes to allow entry. (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX
XX Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
SQ
Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.03;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTCC 38
Db 39 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTC 2
RESULT 19
AAD26647
ID AAD26647 standard; DNA; 39 BP.
XX
XX AAD26647;
AC
```

```
XX 26-MAR-2002 (first entry)
XX NF-kB wild type binding site generating NF1 phosphorothioate oligo.
XX
XX Human immunodeficiency virus; HIV-1; tat; therapeutic; toxin; enzyme;
XX regulatory factor; prophylactic; extracellular fusion protein; drug;
XX NFkB; nuclear factor kappa B; phosphorothioate backbone; ds.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 1..39
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX
XX US6316003-B1.
XX
XX 13-NOV-2001.
XX
XX 28-APR-1994; 94US-00235403.
XX
XX 21-DEC-1989; 89US-00454450.
XX 02-JAN-1991; 91US-00636662.
XX 21-AUG-1992; 92US-00934375.
XX 19-AUG-1993; 93WO-US007833.
XX 24-NOV-1993; 93US-00158015.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (UYUO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX (BIOJ ) BIOGEN INC.
XX
XX Frankel A, Pabo C, Barsom JG, Fawell SE, Pepinsky RB;
XX WPI; 2002-088872/12.
XX
XX Delivering biologically active cargo molecules such as polypeptides,
XX nucleic acids into cells by using transport polypeptides which comprise
XX human immunodeficiency virus transactivator protein linked to cargo
XX molecules.
XX
XX Example 17; Col 95; 78pp; English.
XX
XX The invention relates to a method for delivering a biologically active
XX cargo molecule of interest into a cell. The method comprises presenting
XX to the cell an extracellular fusion protein or a covalently linked
XX conjugate consisting of a cargo moiety and a transport moiety having
XX amino acids 49-57 of human immunodeficiency virus (HIV) transactivator
XX (tat) protein and lacking amino acids 22-36 and 73-86 of HIV tat protein.
XX The method is useful for delivering a molecule of interest such as
XX polypeptides, antigen, monoclonal antibody, single- or double-stranded
XX nucleic acid, a therapeutic, prophylactic and diagnostic molecule to a
XX cell in vitro or in vivo. The method delivers proteins or peptides,
XX including regulatory factors, enzymes, drugs or toxins into the cytoplasm
XX and cell nucleus. The method is useful for diagnostic, prophylactic or
XX therapeutic intracellular delivery of small and macro molecules. The
XX present sequence is a phosphorothioate oligonucleotide used for generating
XX nuclear factor kappa B (NFkB) wild type binding site used in the
XX exemplification of the invention
XX
XX Sequence 39 BP; 4 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 78.9%; Score 30; DB 6; Length 39;
XX Best Local Similarity 86.8%; Pred. No. 0.03;
XX Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
XX
XX 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
XX
```

```
AAID26648/c
ID AAD26648 standard; DNA; 39 BP.
XX
XX AAD26648;
AC
XX
XX 26-MAR-2002 (first entry)
XX
XX NF-KB wild type binding site generating NF2 phosphorothioate oligo.
XX
XX Human immunodeficiency virus; HIV-1; tat; therapeutic; toxin; enzyme;
XX regulatory factor; prophylactic; extracellular fusion protein; drug;
XX NFkB; nuclear factor kappa B; phosphorothioate backbone; ds.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 1..39
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone"
XX
XX US6316003-B1.
XX
XX 13-NOV-2001.
XX
XX 28-APR-1994; 94US-00235403.
XX
XX 21-DEC-1989; 89US-00454450.
XX 02-JAN-1991; 91US-00636662.
XX 21-AUG-1992; 92US-00934375.
XX 19-AUG-1993; 93WO-US007833.
XX 24-NOV-1993; 93US-00158015.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (UYUO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX (BIOU ) BIOGEN INC.
XX
XX Frankel A, Pabo C, Barsom JG, Fawell SE, Pepinsky RB;
XX WPI; 2002-088872/12.
XX
XX Delivering biologically active cargo molecules such as polypeptides,
XX nucleic acids into cells by using transport polypeptides which comprise
XX human immunodeficiency virus transactivator protein linked to cargo
XX molecules.
XX
XX Example 17; Col 97; 78pp; English.
XX
XX The invention relates to a method for delivering a biologically active
XX cargo molecule of interest into a cell. The method comprises presenting
XX to the cell an extracellular fusion protein or a covalently linked
XX conjugate consisting of a cargo moiety and a transport moiety having
XX amino acids 49-57 of human immunodeficiency virus (HIV) transactivator
XX (tat) protein and lacking amino acids 22-36 and 73-86 of HIV tat protein.
XX The method is useful for delivering a molecule of interest such as
XX polypeptides, antigen, monoclonal antibody, single- or double-stranded
XX nucleic acid, a therapeutic, prophylactic and diagnostic molecule to a
XX cell in vitro or in vivo. The method delivers proteins or peptides,
XX including regulatory factors, enzymes, drugs or toxins into the cytoplasm
XX and cell nucleus. The method is useful for diagnostic, prophylactic or
XX therapeutic intracellular delivery of small and macro molecules. The
XX present sequence is a phosphorothioate oligonucleotide used for generating
XX nuclear factor kappa B (NFkB) wild type binding site used in the
XX exemplification of the invention
XX
XX Sequence 39 BP; 10 A; 14 C; 11 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 78.9%; Score 30; DB 6; Length 39;
XX Best Local Similarity 86.8%; Pred. No. 0.03;
XX Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
XX
XX 1 GGGGACTTTCCGCTGGGGACTTTCCAGGGGGACTTTCC 38
XX
```



Db 39 GGGGACTTTCCGCTGGGGACTTTCCACGGGGGAGCTTTC 2

RESULT 21

AA248474

ID AAZ48474 standard; DNA; 44 BP.

XX AC AAZ48474;

XX AC

DT 15-SEP-2003 (revised)

DT 28-MAR-2000 (first entry)

XX HIV LTR NF-kB oligonucleotide.

XX Triterpene glycoside; antitumor; cytotoxic; antioxidant; contraceptive; antihelminthic; expectorant; diuretic; anti-inflammatory; cardiac; anti-ulcer; analgesic; sedative; immunomodulator; antipyretic; cancer; vasotropic; Acacia victoriae; angiogenesis; antifungal; cholesterol; cardiovascular effector; HIV; NF-kappaB; ds.

XX Human immunodeficiency virus 1.

OS

PN WO959578-A1.

XX 25-NOV-1999.

PF 19-MAY-1999; 99WO-US011041.

PR 19-MAY-1998; 98US-0085997P.

PR 03-SEP-1998; 98US-0099066P.

XX (RERE-) RES DEV FOUND.

PI Arntzen CJ, Tracey MB, Guterman JU, Hoffmann JJ, Bailey DT;

PI Jayatilake GS;

XX WPI; 2000-105567/09.

XX Mixture containing triterpene glycosides, useful for treating variety of tumor cells.

XX Example 27; Page 199; 312pp; English.

XX The invention relates to a mixture comprising one or more triterpene glycosides isolated from Acacia victoriae. The composition is used for the treatment of cancer, inhibiting the initiation and promotion of mammalian epithelial cells (such as skin, colon, uterine, ovarian, pancreatic, prostate, renal, lung, bladder or breast cells), for preventing the abnormal proliferation of mammalian epithelial cells (such as crypt or colon cells), and/or regulating angiogenesis. The triterpene glycosides may also be used as a solvent, an antioxidant, antifungal or antiviral agent, piscicide, molluscicides, contraceptive, antihelminthic, angiogenesis regulator, UV-protectant, expectorant, diuretic, anti-inflammatory agent, regulator of cholesterol metabolism, cardiovascular effector, anti-ulcer agent, analgesic, sedative, immunomodulator, antipyretic, as an agent for decreasing capillary fragility, combating the effects of aging, increasing skin collagen, enhancing penile function and improving cognition and memory. The present sequence represents an 32p-labelled NF-kappaB oligo from HIV long terminal repeat used in electrophoretic mobility shift assay. (Updated on 15-SEP-2003 to standardise OS field)

XX Sequence 44 BP; 7 A; 9 C; 16 G; 12 T; 0 U; 0 Other;

Query Match 78.4%; Score 29.8; DB 3; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.037;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCCGCTGGGGACTTTTCACGGGGGACT 34

Db 10 GGGACTTTCCGCTGGGGACTTTTCACGGGGGACT 42

RESULT 22

ABL61552

ID ABL61552 standard; DNA; 44 BP.

XX AC ABL61552;

XX AC

DT 20-SEP-2002 (first entry)

XX HIV-LTR NFkappaB DNA.

XX DE

XX NFkappaB; antiinflammatory; antiarteriosclerotic; antirheumatic; antiarthritic; osteopathic; antiparkinsonian; nootropic; monoterpene; neuroprotective; antiparkinsonian. Barretts esophagitis; osteoarthritis; inflammatory bowel disease; chronic pancreatitis; chronic prostatitis; familial polyposis; actinic keratosis; rheumatoid arthritis; multiple sclerosis; Parkinson's disease; Alzheimer's disease; ds.

XX Human immunodeficiency virus.

OS

XX Key modified\_base 1 Location/Qualifiers

FT FT /\*tag= a

FT FT /mod\_base= OTHER

FT FT /note= "32P labelled"

XX WO200255016-A2.

XX 18-JUL-2002.

XX 19-NOV-2001; 2001WO-US043286.

XX 17-NOV-2000; 2000US-0249710P.

PR 17-SEP-2001; 2001US-0322859P.

XX (RERE-) RES DEV FOUND.

XX Guterman JU, Haridas V;

PI WPI; 2002-557793/59.

XX Inhibiting inflammation used for treating e.g. osteoarthritis and multiple sclerosis comprises administering monoterpene composition inhibiting nuclear factor kappaB.

XX Example 28; Page 349; 349pp; English.

XX This sequence represents a novel method for inhibiting inflammation which comprises administering a monoterpene composition that inhibits NFkappaB. The products of the invention have antiinflammatory, antiarteriosclerotic, antirheumatic, antiarthritic, osteopathic, antiparkinsonian, nootropic, neuroprotective and antiparkinsonian activity. The method described can be used for treating inflammatory diseases, particularly premalignant inflammatory disease (e.g. Barretts esophagitis, inflammatory bowel disease, chronic pancreatitis, chronic prostatitis, familial polyposis and actinic keratosis), arteriosclerosis, rheumatoid arthritis, osteoarthritis, multiple sclerosis, Parkinson's disease and Alzheimer's disease. This sequence represents a 32p-labelled NFkappaB oligonucleotide used in an electrophoretic mobility shift assay to detect the biological characteristics of active triterpenes

XX Sequence 44 BP; 7 A; 9 C; 16 G; 12 T; 0 U; 0 Other;

Query Match 78.4%; Score 29.8; DB 6; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.037;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCCGCTGGGGACTTTTCACGGGGGACT 34

Db 10 GGGACTTTCCGCTGGGGACTTTTCACGGGGGACT 42

RESULT 23

AAT30599

ID AAT30599 standard; DNA; 45 BP.  
 AC AAT30599;  
 XX  
 XX  
 XX 19-FEB-1997 (first entry)  
 DT  
 XX Target binding region #19.  
 DE  
 XX Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;  
 XX TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;  
 KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
 KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
 KW virus; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9617956-A2.  
 PN  
 XX 13-JUN-1996.  
 XX  
 PD  
 XX 07-DEC-1995; 95WO-US015944.  
 PF  
 XX 09-DEC-1994; 94US-00353476.  
 PR  
 XX (GENE-) GENE POOL INC.  
 PA  
 XX Weininger S, Weininger AM;  
 PI  
 XX WPI; 1996-287199/29.  
 DR  
 XX Probe nucleic acids, target binding assemblies, etc - for detection and  
 PT localisation of specific nucleic acid sequences, esp. HIV and HPV.  
 XX  
 XX Disclosure; Page 70; 172pp; English.  
 PS  
 CC AAT30581-T30614 represent target binding regions (TBR) of a probe of the  
 CC invention. The probe of the invention contains a TBR, a booster binding  
 CC region (BBR), and an optional support or attachment (OSA). The target  
 CC binding assembly (TBA) recognised by the probe, contains at least one  
 CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an  
 CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see  
 CC AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007),  
 CC and an OSA. The assembly sequence and asymmetry sequences are responsible  
 CC for the folding and association of the NARs. The NARs (see AAR95965-  
 CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus  
 CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding  
 CC units. The linker sequence is an oligopeptide, which does not interfere  
 CC with NAR function, but provides stability and control over the spacing of  
 CC the NAR from the rest of the TBA. The OSA is an attached support or  
 CC indicator, or other means of localisation of the probe. The probe can be  
 CC used in a method for detecting or localising a specific target nucleic  
 CC acid sequence (TNA). The method is highly sensitive, and has a high  
 CC degree of specificity. The method can be used for detecting specific  
 CC nucleic acid sequences, including those found in human cells, in HIV,  
 CC HPV, and other nucleic acid containing systems, including bacteria and  
 CC viruses  
 XX  
 XX Sequence 45 BP; 7 A; 12 C; 16 G; 10 T; 0 U; 0 Other;  
 SQ  
 Query Match 76.8%; Score 29.2; DB 2; Length 45;  
 Best Local Similarity 91.2%; Pred. No. 0.064;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GGGACTTTCCGCTGGGGACTTTCCAGGGGACTT 35  
 DB 7 GGGACTTTCCGCTGGGGACTTTCCAGGGGAGCGT 40  
 RESULT 24  
 AAT30603  
 ID AAT30603 standard; DNA; 45 BP.  
 XX  
 XX AAT30603;  
 AC

XX  
 DT 19-FEB-1997 (first entry)  
 XX  
 DE Target binding region #23.  
 XX  
 KW Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;  
 KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;  
 KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
 KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
 KW virus; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9617956-A2.  
 PN  
 XX 13-JUN-1996.  
 XX  
 PD  
 XX 07-DEC-1995; 95WO-US015944.  
 PF  
 XX 09-DEC-1994; 94US-00353476.  
 PR  
 XX (GENE-) GENE POOL INC.  
 PA  
 XX Weininger S, Weininger AM;  
 PI  
 XX WPI; 1996-287199/29.  
 DR  
 XX Probe nucleic acids, target binding assemblies, etc - for detection and  
 PT localisation of specific nucleic acid sequences, esp. HIV and HPV.  
 XX  
 XX Disclosure; Page 71; 172pp; English.  
 PS  
 CC AAT30581-T30614 represent target binding regions (TBR) of a probe of the  
 CC invention. The probe of the invention contains a TBR, a booster binding  
 CC region (BBR), and an optional support or attachment (OSA). The target  
 CC binding assembly (TBA) recognised by the probe, contains at least one  
 CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an  
 CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see  
 CC AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007),  
 CC and an OSA. The assembly sequence and asymmetry sequences are responsible  
 CC for the folding and association of the NARs. The NARs (see AAR95965-  
 CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus  
 CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding  
 CC units. The linker sequence is an oligopeptide, which does not interfere  
 CC with NAR function, but provides stability and control over the spacing of  
 CC the NAR from the rest of the TBA. The OSA is an attached support or  
 CC indicator, or other means of localisation of the probe. The probe can be  
 CC used in a method for detecting or localising a specific target nucleic  
 CC acid sequence (TNA). The method is highly sensitive, and has a high  
 CC degree of specificity. The method can be used for detecting specific  
 CC nucleic acid sequences, including those found in human cells, in HIV,  
 CC HPV, and other nucleic acid containing systems, including bacteria and  
 CC viruses  
 XX  
 XX Sequence 45 BP; 8 A; 11 C; 16 G; 10 T; 0 U; 0 Other;  
 SQ  
 Query Match 76.8%; Score 29.2; DB 2; Length 45;  
 Best Local Similarity 91.2%; Pred. No. 0.064;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GGGACTTTCCGCTGGGGACTTTCCAGGGGACTT 35  
 DB 7 GGGACTTTCCGCTGGGGACTTTCCAGGGGAGCGT 40  
 RESULT 25  
 AAX28079  
 ID AAX28079 standard; DNA; 45 BP.  
 XX  
 AC AAX28079;  
 XX  
 XX 17-OCT-2003 (revised)  
 DT  
 DT 10-JUN-1999 (first entry)

```
XX HIV-LTR oligonucleotide.
DE
XX Inhibitor; activator; NF-kappaB transcription factor; toxic shock;
KW septic shock; graft versus host disease; curcumin; diferuloylmethane;
KW radiation damage; atherosclerosis; cancer; HIV infection; HIV-LTR; ss.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX US5891924-A.
PN
XX
XX 06-APR-1999.
PD
XX
XX 26-SEP-1996; 96US-00712932.
PF
XX
XX 26-SEP-1996; 96US-00712932.
PR
XX
XX (RERE-) RES DEV FOUND.
PA
XX Aggarwal BB;
PI
XX WPI; 1999-253918/21.
DR
XX Inhibiting activation of NFkappaB with curcumin used for treatment of
PT e.g. septic shock or guest versus host reaction.
PT
XX
XX Example 3; Col 5; 21pp; English.
PS
XX This sequence represents a HIV-LTR oligonucleotide used to test the
CC method of the invention. The method is for inhibition of activation of
CC the NF-kappaB transcription factor (A), for treatment of toxic or septic
CC shock or graft versus host reactions in humans, comprises administration
CC of curcumin (I; diferuloylmethane). (I) is used to treat toxic or septic
CC shock and graft versus host reactions in humans. (I) may be used to
CC inhibit activation of (A) e.g. in cases of radiation damage,
CC atherosclerosis, cancer and human immune deficiency virus (HIV)
CC infection. (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;
SQ
Query Match 76.8%; Score 29.2; DB 2; Length 45;
Best Local Similarity 91.2%; Pred. No. 0.064;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GGACATTTCCGCTGGGACTTTCCAGGGGACTT 35
Db 10 GGACATTTCCGCTGGGACTTTCCAGGGGCGT 43
RESULT 26
ADH12178
ID ADH12178 standard; DNA; 45 BP.
XX
XX ADH12178;
AC
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX HIV-1 LTR NF-kappa-B sequence used as EMSA probe.
DE
XX Multiple myeloma; proliferation inhibition; apoptosis induction;
KW curcumin; diferuloylmethane; chemotherapy potentiator;
KW I-kappa-B kinase inhibitor; I-kappa-B-alpha phosphorylation suppressor;
KW NF-kappa-B suppressor; I-kappa-B-alpha; Bcl-2; Bcl-XL; cyclin D1;
KW interleukin-6; IL-6; cell cycle arrest; cytosstatic; NF-kappa-B;
KW HIV-1 LTR; long terminal repeat; electrophoretic mobility shift assay;
KW EMSA; probe; ds.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO200400229-A2.
PN
XX
XX 31-DEC-2003.
PD
XX
XX
```

---

```
PF 24-JUN-2003; 2003WO-US019837.
XX
PR 24-JUN-2002; 2002US-0390926P.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Aggarwal B;
XX
XX WPI; 2004-156362/15.
XX
XX Inhibiting proliferation of multiple myeloma cells comprises
PT administering curcumin and optionally with vincristine,
PT bichloroethylnitrosourea, melphalan, cyclophosphamide, adriamycin,
PT prednisone or dexamethasone.
XX
XX Example 3; SEQ ID NO 4; 77pp; English.
XX
XX The invention relates to a method for inhibiting the proliferation of,
CC and inducing apoptosis in multiple myeloma cells comprising
CC administration of curcumin (diferuloylmethane). The invention also
CC relates to a method for increasing the cytotoxic effects of a
CC chemotherapeutic agent (e.g., vincristine, bichloroethylnitrosourea,
CC melphalan, cyclophosphamide, adriamycin, prednisone or dexamethasone)
CC against multiple myeloma cells (preferably CD138+ plasma cells) comprises
CC administration of the chemotherapeutic agent and curcumin. Curcumin
CC increases the cytotoxic effects of the chemotherapeutic agent against
CC multiple myeloma cells. It suppresses constitutive I-kappa-B-alpha
CC phosphorylation through inhibition of I-kappa-B kinase activity, and
CC downregulates the expression of NF-kappa-B-regulated gene products (e.g.
CC I-kappa-B-alpha, Bcl-2, Bcl-XL, cyclin D1 and interleukin-6), leading to
CC suppression of proliferation and arrest of cells at the G1/S phase of the
CC cell cycle. The methods of the invention are used for the treatment of
CC multiple myeloma. The present sequence represents an NF-kappa-B binding
CC sequence derived from the HIV-1 long terminal repeat (LTR) which was used
CC as a probe in electrophoretic mobility shift assay (EMSA) of NF-kappa-B
CC in an example of the invention.
XX
XX Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;
SQ
Query Match 76.8%; Score 29.2; DB 12; Length 45;
Best Local Similarity 91.2%; Pred. No. 0.064;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GGACATTTCCGCTGGGACTTTCCAGGGGACTT 35
Db 10 GGACATTTCCGCTGGGACTTTCCAGGGGCGT 43
RESULT 27
ADZ00136
ID ADZ00136 standard; DNA; 45 BP.
XX
XX ADZ00136;
AC
XX
XX 30-JUN-2005 (first entry)
DT
XX
XX EMSA probe for detecting NF-kappaB activation in curcumin treated cells.
DE
XX osteopathic; osteogenesis; nuclear factor kappa B; cancer; breast tumor;
KW myeloma; osteoporosis; Paget's disease; rheumatoid arthritis;
KW head and neck tumor; probe; ss.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX US2005080023-A1.
PN
XX
XX 14-APR-2005.
PD
XX
XX 25-AUG-2004; 2004US-00925608.
PF
XX
XX 26-AUG-2003; 2003US-0497841P.
PR
XX
XX (AGGA/) AGGARWAL B B.
PA
```

XX Aggarwal BB;  
XX WPI; 2005-295074/30.  
XX  
XX Use of compounds comprising diferuloylmethane, guggulsterone, 1'-  
PT acetoxychavicol or their analogues to e.g. reduce/inhibit osteoclast  
PT development induced by the receptor for activation of nuclear factor  
PT kappa B ligand.  
XX  
PS Example 7; SEQ ID NO 1; 43pp; English.  
XX  
CC The invention relates to a method of reducing or inhibiting osteoclast  
CC development induced by the receptor for activation of nuclear factor  
CC kappa B ligand (RANKL) by contacting the osteoclast or its precursor with  
CC compounds (i) comprising diferuloylmethane, guggulsterone, 1'-  
CC acetoxychavicol or their analogues. (i) is useful for reducing or  
CC inhibiting osteoclast development induced by RANKL, inhibiting the  
CC formation of osteoclasts in an individual and reducing osteolytic  
CC activity and bone loss in an individual having breast cancer, multiple  
CC myeloma, post-menopausal osteoporosis, Paget's disease, rheumatoid  
CC arthritis or head and neck squamous cell carcinoma. The diferuloylmethane  
CC (curcumin) is safe to humans. This sequence corresponds to an  
CC electrophoresis shift assay (EMSA) probe used to analyze NF-kappaB  
CC activation in curcumin-treated or untreated cells. The sequence is  
CC derived from the human immunodeficiency virus 1 long terminal repeat.  
XX  
SQ Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;  
  
Query Match 76.8%; Score 29.2; DB 14; Length 45;  
Best Local Similarity 91.2%; Pred. No. 0.064;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 GGGACTTTCGCTGGGAGCTTTCAGGGGACTT 35  
Db 10 GGGACTTTCGCTGGGAGCTTTCAGGGGAGCT 43  
  
RESULT 28  
AEA06160  
ID AEA06160 standard; DNA; 45 BP.  
XX  
AC AEA06160;  
XX  
DT 28-JUL-2005 (first entry)  
XX  
DE Oligo from HIV long terminal repeat containing NF-kappaB binding site.  
XX  
KW Nuclear factor-kappa B; NF-kappaB; NF-kappaB inhibitor;  
KW apoptosis stimulation; cancer; cytostatic; HIV long terminal repeat; ss.  
XX  
OS Human immunodeficiency virus.  
XX  
FH Key Location/Qualifiers  
FT protein\_bind 10..17  
FT /\*tag= a  
FT /bound\_moiety= "NF-kappaB"  
FT protein\_bind 24..32  
FT /\*tag= b  
FT /bound\_moiety= "NF-kappaB"  
XX  
PN WO2005046708-A1.  
XX  
PD 26-MAY-2005.  
XX  
XX 04-NOV-2004; 2004WO-US036777.  
XX  
XX 06-NOV-2003; 2003US-0517852P.  
XX  
XX (RERE-) RES DEV FOUND.  
XX  
XX Aggarwal BB, Singh S;  
XX

DR WPI; 2005-372280/38.  
XX  
PT New cell permeable nuclear factor kappaB inhibitor comprising a peptide  
PT fragment and a protein transduction domain, useful for treating cancer.  
XX  
XX Example 2; SEQ ID NO 1; 47pp; English.  
XX  
CC The present invention relates to cell permeable nuclear factor (NF)-  
CC kappaB, and specifically to polypeptides that selectively inhibit NF-  
CC kappaB activation, downregulate NF-kappaB mediated gene expression and  
CC enhance apoptosis induced by TNF and other apoptotic stimuli. The  
CC inhibitor comprises (i) a peptide fragment of the p65 subunit of NF-  
CC kappaB, where the peptide comprises phosphorylation site(s) of the p65  
CC subunit and (ii) a protein transduction domain which is able to transport  
CC the polypeptide across cell membrane. The protein transduction domain is  
CC derived from a protein or domain selected from third helix of the  
CC antenapedia homeodomain (SEQ ID NO:3), herpes virus structural protein,  
CC or HIV tat protein. Also disclosed is an isolated DNA encoding the  
CC inhibitor. Provided is a method of inhibiting the DNA binding activity of  
CC NF-kappaB; a method of increasing the level of apoptosis; and a method of  
CC treating cancer. Inhibiting the DNA binding activity of NF-kappaB in a  
CC cell comprises contacting a cell with the inhibitor above, where the  
CC inhibitor suppresses NF-kappaB binding to DNA. Activity is induced by an  
CC agent, e.g. TNF, LPS, IL-1, okadaic acid, phorbol myristate acetate  
CC (PMA), hydrogen peroxide, cigarette smoke condensate, TNF receptor 1, TNF  
CC receptor-associated death domain (TRADD), TNF receptor-associated factor-  
CC 2 (TRAF2), NF-kappaB-inducing kinase (NIK), or IkappaBalpha kinase (IKK).  
CC The present sequence is a 45-mer double-stranded oligonucleotide from the  
CC HIV long terminal repeat containing NF-kappaB binding site, used to form  
CC a DNA-protein complex to examine the specificity of binding of NF-kappaB  
CC to the DNA.  
XX  
SQ Sequence 45 BP; 7 A; 9 C; 17 G; 12 T; 0 U; 0 Other;  
  
Query Match 76.8%; Score 29.2; DB 14; Length 45;  
Best Local Similarity 91.2%; Pred. No. 0.064;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 GGGACTTTCGCTGGGAGCTTTCAGGGGACTT 35  
Db 10 GGGACTTTCGCTGGGAGCTTTCAGGGGAGCT 43  
  
RESULT 29  
AAT30607  
ID AAT30607 standard; DNA; 46 BP.  
XX  
AC AAT30607;  
XX  
DT 19-FEB-1997 (first entry)  
XX  
DE Target binding region #27.  
XX  
KW Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;  
KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;  
KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
KW virus; ss.  
XX  
OS Synthetic.  
XX  
PN WO9617956-A2.  
XX  
PD 13-JUN-1996.  
XX  
XX 07-DEC-1995; 95WO-US015944.  
XX  
XX 09-DEC-1994; 94US-00353476.  
XX  
XX (GENE-) GENE POOL INC.  
XX  
XX Weininger S, Weininger AM;  
XX

```
DR WPI; 1996-287199/29.
XX
XX Probe nucleic acids, target binding assemblies, etc - for detection and
PT localisation of specific nucleic acid sequences, esp. HIV and HPV.
XX
XX Disclosure; Page 72; 172pp; English.
XX
XX AAT30581-T30614 represent target binding regions (TBR) of a probe of the
CC invention. The probe of the invention contains a TBR, a booster binding
CC region (BBR), and an optional support or attachment (OSA). The target
CC binding assembly (TBA) recognised by the probe, contains at least one
CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an
CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see
CC AAR95999-R96006), a nuclear localisation signal sequence (see
CC AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007),
CC and an OSA. The assembly sequence and asymmetry sequences are responsible
CC for the folding and association of the NARs. The NARs (see AAR95965-
CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus
CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding
CC units. The linker sequence is an oligopeptide, which does not interfere
CC with NAR function, but provides stability and control over the spacing of
CC the NAR from the rest of the TBA. The OSA is an attached support or
CC indicator, or other means of localisation of the probe. The probe can be
CC used in a method for detecting or localising a specific target nucleic
CC acid sequence (TNA). The method is highly sensitive, and has a high
CC degree of specificity. The method can be used for detecting specific
CC nucleic acid sequences, including those found in human cells, in HIV,
CC HPV, and other nucleic acid containing systems, including bacteria and
CC viruses
XX
XX Sequence 46 BP; 8 A; 11 C; 17 G; 10 T; 0 U; 0 Other;
SQ
Query Match 76.3%; Score 29; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGCTGGGACTTTCACGGG 30
Db |||||
7 GGGACTTTCGCTGGGACTTTCACGGG 35
RESULT 30
AAT30602
ID AAT30602 standard; DNA; 46 BP.
XX
XX AAT30602;
AC
XX
XX 19-FEB-1997 (first entry)
DT
XX
XX Target binding region #22.
DE
XX
XX Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;
KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
KW virus; ss.
XX
XX Synthetic.
OS
XX
XX WO9617956-A2.
PN
XX
XX 13-JUN-1996.
PD
XX
XX 07-DEC-1995; 95WO-US015944.
PF
XX
XX 09-DEC-1994; 94US-00353476.
PR
XX
XX (GENE-) GENE POOL INC.
PA
XX
XX Weininger S, Weininger AM;
PI
XX
XX WPI; 1996-287199/29.
DR
XX
XX Probe nucleic acids, target binding assemblies, etc - for detection and
PT localisation of specific nucleic acid sequences, esp. HIV and HPV.
XX
XX Disclosure; Page 70; 172pp; English.
PS
```

---

```
PT localisation of specific nucleic acid sequences, esp. HIV and HPV.
XX
XX Disclosure; Page 71; 172pp; English.
XX
XX AAT30581-T30614 represent target binding regions (TBR) of a probe of the
CC invention. The probe of the invention contains a TBR, a booster binding
CC region (BBR), and an optional support or attachment (OSA). The target
CC binding assembly (TBA) recognised by the probe, contains at least one
CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an
CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see
CC AAR95999-R96006), a nuclear localisation signal sequence (see
CC AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007),
CC and an OSA. The assembly sequence and asymmetry sequences are responsible
CC for the folding and association of the NARs. The NARs (see AAR95965-
CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus
CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding
CC units. The linker sequence is an oligopeptide, which does not interfere
CC with NAR function, but provides stability and control over the spacing of
CC the NAR from the rest of the TBA. The OSA is an attached support or
CC indicator, or other means of localisation of the probe. The probe can be
CC used in a method for detecting or localising a specific target nucleic
CC acid sequence (TNA). The method is highly sensitive, and has a high
CC degree of specificity. The method can be used for detecting specific
CC nucleic acid sequences, including those found in human cells, in HIV,
CC HPV, and other nucleic acid containing systems, including bacteria and
CC viruses
XX
XX Sequence 46 BP; 8 A; 11 C; 17 G; 10 T; 0 U; 0 Other;
SQ
Query Match 76.3%; Score 29; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGCTGGGACTTTCACGGG 30
Db |||||
7 GGGACTTTCGCTGGGACTTTCACGGG 35
RESULT 31
AAT30601
ID AAT30601 standard; DNA; 46 BP.
XX
XX AAT30601;
AC
XX
XX 19-FEB-1997 (first entry)
DT
XX
XX Target binding region #21.
DE
XX
XX Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;
KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
KW virus; ss.
XX
XX Synthetic.
OS
XX
XX WO9617956-A2.
PN
XX
XX 13-JUN-1996.
PD
XX
XX 07-DEC-1995; 95WO-US015944.
PF
XX
XX 09-DEC-1994; 94US-00353476.
PR
XX
XX (GENE-) GENE POOL INC.
PA
XX
XX Weininger S, Weininger AM;
PI
XX
XX WPI; 1996-287199/29.
DR
XX
XX Probe nucleic acids, target binding assemblies, etc - for detection and
PT localisation of specific nucleic acid sequences, esp. HIV and HPV.
XX
XX Disclosure; Page 70; 172pp; English.
PS
```



CC a delta A element, an NFkB element or an Ikaros binding oligonucleotide  
CC consensus sequence; (c) it competitively inhibits the binding of a  
CC naturally occurring Ikaros isoform to any of a delta A element, an NFkB  
CC element or an Ikaros binding oligonucleotide consensus sequence; (d) it  
CC competitively inhibits Ikaros binding to Ikaros responsive elements; or  
CC (e) it inhibits protein-protein interactions of transcriptional complexes  
CC formed with naturally occurring Ikaros isoforms. The proteins, provided  
CC that they stimulate gene transcription under the control of delta A  
CC elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to  
CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,  
CC competitively inhibit binding of naturally occurring Ikaros isoforms to  
CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,  
CC competitively inhibit Ikaros binding to Ikaros-responsive elements and/or  
CC inhibit protein-protein interactions of transcriptional complexes with  
CC naturally occurring Ikaros isoforms, can be used to treat immune system  
CC disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.  
CC Alzheimer's disease. AAV66975 to AAV67118 represent oligonucleotides  
CC given in the present invention  
XX  
SQ Sequence 36 BP; 6 A; 9 C; 14 G; 7 T; 0 U; 0 Other;

Query Match 75.8%; Score 28.8; DB 2; Length 36;  
Best Local Similarity 93.8%; Pred. No. 0.088; Indels 0; Gaps 0;  
Matches 30; Conservative 0; Mismatches 2;

QY 2 GGGACTTTCGGCTGGGGACTTTCACGGGGAC 33  
|||||  
DB 4 GGGACTTTCGGCTGGGGACTTTCACGGGGAC 35

## RESULT 34

AAQ61543  
ID AAQ61543 standard; cDNA; 37 BP.

XX AAQ61543;

XX 25-MAR-2003 (revised)

DT 21-OCT-1994 (first entry)

XX HIV long terminal repeat sequence comprising Ikaros binding site.

XX Ikaros; zinc finger; protein; immune disorder; therapy; treatment;  
KW corpus striatum; regulatory gene; enhancer; regulatory element;  
KW gene expression; HIV; human immunodeficiency virus; ss.

XX Human immunodeficiency virus.

XX WO9406814-A1.

XX 31-MAR-1994.

XX 14-SEP-1993; 93WO-US008743.

XX 14-SEP-1992; 92US-00946233.

XX (GENE) GEN HOSPITAL CORP.

XX Georgopoulos K;

XX WPI; 1994-118387/14.

XX I-cell pathway regulatory gene, Ikaros - encodes family of unique zinc  
PT finger proteins, useful for treating immune system disorders.

XX Disclosure; Page 29; 112pp; English.

XX The Ikaros gene encodes a zinc finger protein which can be used in a  
CC therapeutic composition to treat animals with an immune system disorder.  
CC It may also be used for assessing whether a subject is at risk for an  
CC immune disorder. It is of particular use in treating a disorder of the  
CC corpus striatum. Heterologous genes may be expressed by placing them  
CC under the control of an Ikaros responsive control element and contacting  
CC the element with an Ikaros protein. Potential high affinity binding sites

CC for the Ikaros proteins were found in the enhancer and promoter regions  
CC of the TCR-alpha, -beta and -delta, the CD3-delta, -epsilon and -gamma  
CC genes, the SL3 and HIV long terminal repeat and in the regulatory domains  
CC of other T cell restricted antigens. Related sequences to the Ikaros  
CC motif were also found in the purine boxes of the IL2 gene in the in the  
CC LYP site of the TDT promoter as well as in the NFkB variant sites of the  
CC HIV long terminal repeat. See also AAQ61504-Q61543. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX

SQ Sequence 37 BP; 6 A; 9 C; 15 G; 7 T; 0 U; 0 Other;

Query Match 74.7%; Score 28.4; DB 2; Length 37;  
Best Local Similarity 96.7%; Pred. No. 0.13; Indels 0; Gaps 0;  
Matches 29; Conservative 0; Mismatches 1;

QY 2 GGGACTTTCGGCTGGGGACTTTCACGGGGG 31  
|||||  
DB 4 GGGACTTTCGGCTGGGGACTTTCACGGGGG 33

## RESULT 35

AAAT30615  
ID AAAT30615 standard; cDNA; 37 BP.

XX AAAT30615;

XX 21-FEB-1997 (first entry)

DE Probe nucleic acid PNA1.

XX Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;

KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;

KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;

KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;

XX virus; ss.

XX Synthetic.

XX WO9617956-A2.

XX 13-JUN-1996.

XX 07-DEC-1995; 95WO-US015944.

XX 09-DEC-1994; 94US-00353476.

XX (GENE-) GENE POOL INC.

XX Weininger S, Weininger AM;

XX WPI; 1996-287199/29.

XX Probe nucleic acids, target binding assemblies, etc - for detection and  
PT localisation of specific nucleic acid sequences, esp. HIV and HPV.

XX Disclosure; Page 76; 172pp; English.

XX AAAT30615-T30634 represent probe nucleic acids of the invention. The probe  
CC of the invention contains a target binding region (TBR), a booster  
CC binding region (BBR), and an optional support or attachment (OSA). The  
CC target binding assembly (TBA) recognised by the TBR (see AAR30581-T30614)  
CC of the probe, contains at least one nucleic acid recognition unit (NAR),  
CC and optionally a linker sequence, an assembly sequence (see AAR95994-  
CC R95998), an asymmetry sequence (see AAR95999-R96006), a nuclear  
CC localisation signal sequence (see AAR96007), and an OSA. The assembly  
CC sequence and asymmetry sequences are responsible for the folding and  
CC association of the NARs. The NARs (see AAR95965-R95993) are selected from  
CC NF-kappa-B, SPI, TATA, human papillomavirus (HPV) E2, HPV LTR, human  
CC immunodeficiency virus (HIV) LTR and Tat binding units. The linker  
CC sequence is an oligopeptide, which does not interfere with NAR function,  
CC but provides stability and control over the spacing of the NAR from the  
CC rest of the TBA. The OSA is an attached support or indicator, or other  
CC means of localisation of the probe. The probe can be used in a method for

CC detecting or localising a specific target nucleic acid sequence (TNA).  
CC The method is highly sensitive, and has a high degree of specificity. The  
CC method can be used for detecting specific nucleic acid sequences,  
CC including those found in human cells, in HIV, HPV, and other nucleic acid  
CC containing systems, including bacteria and viruses  
XX  
SQ Sequence 37 BP; 7 A; 9 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 74.7%; Score 28.4; DB 2; Length 37;  
Best Local Similarity 96.7%; Pred. No. 0.13;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCAGGGG 31  
|||||  
DB 7 GGGACTTTCGCTGGGACTTTCAGGGG 36  
|||||

RESULT 36  
AAV45402  
ID AAV45402 standard; DNA; 37 BP.  
XX  
AC AAV45402;  
XX  
DT 11-JAN-1999 (first entry)  
XX  
DE HIV LTR binding site for Ikaros.  
XX  
KW Ikaros; mIK; transcription factor; mouse; lymphocyte;  
KW cell differentiation; T cell; cancer; immunodeficiency;  
KW Alzheimer's disease; therapy; diagnosis; HIV; ss.  
XX  
OS Human immunodeficiency virus.  
XX  
PN CA2194256-A.  
XX  
PD 05-MAR-1998.  
XX  
PF 02-JAN-1997; 97CA-02194256.  
XX  
PR 05-SEP-1996; 96US-00711417.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
XX  
PI Georgopoulos K;  
XX  
DR WPI; 1998-378292/33.  
XX

PT New nucleic acid encoding Ikaros protein involved in early  
PT differentiation of lymphocytes - existing in several isoforms, and  
PT related products, used to treat e.g. immune diseases or cancer and to  
PT control cell differentiation.  
XX  
PS Disclosure; Page 39; 158pp; English.  
XX

CC This oligonucleotide from the HIV long terminal repeat was identified as  
CC a potential high affinity binding site for Ikaros (see AAW70963-71). It  
CC partially includes a core motif GGAA found in consensus recognition  
CC sites of murine Ikaros isoforms mIK-1, mIK-2 and mIK-3 (see AAV52830-32).  
CC High affinity binding sites for Ikaros have been found in enhancer and  
CC promoter regions of the regulatory domains of the TCR antigen complex,  
CC the CD3 genes, the SL3 and HIV long terminal repeat and in the regulatory  
CC domains of other T cell restricted antigens (see AAV45358-402) by gel  
CC retardation assay. Ikaros is involved in early differentiation of  
CC lymphocytes. The invention provides Ikaros nucleic acids (see AAV42805-11  
CC and AAV42840) and polypeptides, vectors and host cells. These are used to  
CC treat T and B cell diseases, to control expression of heterologous genes  
CC placed under control of an Ikaros-responsive element, to treat nervous  
CC system diseases and to modulate cell division, amplification or  
CC differentiation, especially in haematopoietic cells  
XX

SQ Sequence 37 BP; 6 A; 9 C; 15 G; 7 T; 0 U; 0 Other;

Query Match 74.7%; Score 28.4; DB 2; Length 37;

Best Local Similarity 96.7%; Pred. No. 0.13;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GGGACTTTCGCTGGGACTTTCAGGGG 31  
|||||  
DB 4 GGGACTTTCGCTGGGACTTTCAGGGG 33  
|||||

RESULT 37  
AAD17457  
ID AAD17457 standard; DNA; 32 BP.  
XX  
AC AAD17457;  
XX  
DT 10-DEC-2001 (first entry)  
XX  
DE Human immunodeficiency virus LTR NF-kB-specific double-stranded oligo.  
XX  
KW Tpl2; serine threonine kinase; tumour necrosis factor; TNFalpha; NF-kB;  
KW inflammatory disease; therapy; rheumatoid arthritis; endotoxin shock;  
KW research tool; LPS; lipopolysaccharide; nuclear factor kappa B; HIV;  
KW Human immunodeficiency virus; ds.  
XX  
OS Human immunodeficiency virus.  
XX  
PN WO200166559-A1.  
XX  
PD 13-SEP-2001.  
XX  
PF 08-MAR-2001; 2001WO-US007588.  
XX  
PR 08-MAR-2000; 2000US-00522775.  
XX  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
PI Tschlis PN;  
XX  
DR WPI; 2001-582266/65.  
XX

PT Knock-out animal resistant to lipopolysaccharide-induced endotoxin shock  
PT and tumor necrosis factor alpha-mediated inflammatory disease, comprises  
PT a functionally disrupted endogenous Tpl2 gene.  
XX  
PS Example 8; Page 55; 98pp; English.  
XX  
CC The invention relates to an animal with a structurally intact Tpl2 gene  
CC but functionally disrupted endogenous Tpl2 (a protooncogene which encodes  
CC a cytoplasmic serine threonine protein kinase). The animal has increased  
CC resistance to lipopolysaccharide-induced endotoxin shock or tumour  
CC necrosis factor (TNF) alpha-mediated inflammatory diseases. Tpl2 protein  
CC and DNA are useful for identifying compounds that agonise or inhibit the  
CC function of Tpl2 protein. Tpl2 is useful for treating rheumatoid  
CC arthritis. TNFalpha-mediated inflammatory diseases or LPS induced  
CC endotoxin shock, may be treated by transfecting bone marrow derived cells  
CC invitro with a DNA construct which encodes sequences that interferes with  
CC the expression of function of the endogenous Tpl2 in the cells and  
CC administering the cells to an animal. The knock out animals and the  
CC constructs used to generate the animals are useful in the development of  
CC compositions and methods of treating inflammation. Tpl2 agonist and  
CC antagonist are useful as targets for the development of novel therapeutic  
CC agents which eliminate the functional role of Tpl2 and as research tools  
CC to facilitate the elucidation of the mechanistic action of the novel  
CC genetic and protein interactions involved in inflammatory disorders. Tpl2  
CC polynucleotide sequences facilitate the discovery and development of anti  
CC endotoxin shock and/or antiinflammatory compounds. The present sequence  
CC is human immunodeficiency virus LTR NF-kB-specific (nuclear factor kappa  
CC B) double-stranded oligonucleotide used in the exemplification of the  
CC invention  
XX

SQ Sequence 32 BP; 6 A; 8 C; 11 G; 7 T; 0 U; 0 Other;

Query Match 73.7%; Score 28; DB 5; Length 32;

Best Local Similarity 100.0%; Pred. No. 0.18;



```
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGGCTGGGACTTTCAGGG 29
Db 5 GGGACTTTCGGCTGGGACTTTCAGGG 32
RESULT 38
AADI7455
ID AAD17455 standard; DNA; 32 BP.
XX
AC AAD17455;
XX
DT 10-DEC-2001 (first entry)
XX
DE Nuclear factor kappa B binding site probe generating oligo #1.
XX
KW Tpl2; serine threonine kinase; tumour necrosis factor; TNFalpha; NF-kB;
KW inflammatory disease; therapy; rheumatoid arthritis; endotoxin shock;
KW research tool; LPS; lipopolysaccharide; nuclear factor kappa B; ss.
XX
OS Unidentified.
XX
PN WO20016559-A1.
XX
PD 13-SEP-2001.
XX
PF 08-MAR-2001; 2001WO-US007588.
XX
PR 08-MAR-2000; 2000US-00522775.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Tschlis PN;
XX
DR WPI; 2001-582266/65.
XX
PT Knock-out animal resistant to lipopolysaccharide-induced endotoxin shock
PT and tumor necrosis factor alpha-mediated inflammatory disease, comprises
PT a functionally disrupted endogenous Tpl2 gene.
XX
PS Example 8; Page 50; 98pp; English.
XX
CC The invention relates to an animal with a structurally intact Tpl2 gene
CC but functionally disrupted endogenous Tpl2 (a protooncogene which encodes
CC a cytoplasmic serine threonine protein kinase). The animal has increased
CC resistance to lipopolysaccharide-induced endotoxin shock or tumour
CC necrosis factor (TNF) alpha-mediated inflammatory diseases. Tpl2 protein
CC and DNA are useful for identifying compounds that agonise or inhibit the
CC function of Tpl2 protein. Tpl2 is useful for treating rheumatoid
CC arthritis. TNFalpha-mediated inflammatory diseases or LPS induced
CC endotoxin shock, may be treated by transfecting bone marrow derived cells
CC invitro with a DNA construct which encodes sequences that interferes with
CC the expression of function of the endogenous Tpl2 in the cells and
CC administering the cells to an animal. The knock out animals and the
CC constructs used to generate the animals are useful in the development of
CC compositions and methods of treating inflammation. Tpl2 agonist and
CC antagonists are useful as targets for the development of novel therapeutic
CC agents which eliminate the functional role of Tpl2 and as research tools
CC to facilitate the elucidation of the mechanistic action of the novel
CC genetic and protein interactions involved in inflammatory disorders. Tpl2
CC polynucleotide sequences facilitate the discovery and development of anti
CC endotoxin shock and/or antiinflammatory compounds. The present sequence
CC is an oligonucleotide used for generating nuclear factor kappa B (NF-kB)
CC DNA binding site probe used in the exemplification of the invention
XX
SQ Sequence 32 BP; 6 A; 8 C; 11 G; 7 T; 0 U; 0 Other;
Query Match 73.7%; Score 28; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGGCTGGGACTTTCAGGG 29
```

```
Db 5 GGGACTTTCGGCTGGGACTTTCAGGG 32
RESULT 39
AAX34336
ID AAX34336 standard; DNA; 33 BP.
XX
AC AAX34336;
XX
DT 06-JUL-1999 (first entry)
XX
DE HIV probe corresponding to NF-kappaB binding site.
XX
KW Primer; PCR; amplification; HIV-1; genome; vector; inhibition;
KW replication; gene expression; infection; probe; hybridisation; ss.
XX
OS Synthetic.
OS Human immunodeficiency virus 1.
XX
PN WO9919496-A1.
XX
PD 22-APR-1999.
XX
PF 15-OCT-1998; 98WO-US021880.
XX
PR 16-OCT-1997; 97US-0061984P.
XX
PA (UTEM ) UNIV TEMPLE.
XX
PI Suhadolnik RJ, Adelson ME, Iacono KT;
XX
DR WPI; 1999-277646/23.
XX
PT New vectors for inhibiting HIV replication.
XX
PS Example 1; Page 25; 65pp; English.
XX
CC Primers AAX34333-X34336 were used to amplify region of the human
CC immunodeficiency virus type 1 (HIV-1) genome for the construction of new
CC vectors for inhibiting HIV replication comprise a PKR or 2',5'-
CC oligoadenylate synthetase coding region and a regulatory element
CC activated in the presence of HIV trans-acting factors. Using the
CC constructs, antiviral gene expression is activated upon HIV infection
CC resulting in the death of HIV infected cells, thus preventing viral
CC replication and the subsequent infection of neighbouring cells
XX
SQ Sequence 33 BP; 7 A; 8 C; 11 G; 7 T; 0 U; 0 Other;
Query Match 73.7%; Score 28; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGGCTGGGACTTTCAGGG 29
Db 5 GGGACTTTCGGCTGGGACTTTCAGGG 32
RESULT 40
AAN90922
ID AAN90922 standard; DNA; 34 BP.
XX
AC AAN90922;
XX
DT 09-SEP-2004 (revised)
DT 25-MAR-2003 (revised)
DT 30-JAN-1990 (first entry)
XX
DE Part of the kappa light chain enhancer.
XX
KW Nuclear factor kappa B inhibitor complex; HIV enhancer;
KW immunoglobulin kappa light chain enhancer; transcription factor; ds.
XX
```

```
OS Homo sapiens.
OS Unidentified.
PN WO8908147-A.
XX
XX
XX 08-SEP-1989.
XX
XX 01-MAR-1989; 89WO-US000820.
XX
XX 01-MAR-1988; 88US-00162680.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA
XX
XX
XX WPI; 1989-278306/38.
XX
XX Altering gene expression in a cell - by controlling dissociation of
PT nuclear factor kappa B inhibitor complex to prevent or cause binding to
PT an enhancer, e.g. HIV-dna.
XX
XX Disclosure; Fig 1; 69pp; English.
XX
XX The sequence is part of the HIV LTR enhancer. Tag a and tag b represent
CC binding sites for NF-KB. (Updated on 25-MAR-2003 to correct PA field.)
CC
CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX
XX Sequence 34 BP; 7 A; 8 C; 11 G; 8 T; 0 U; 0 Other;
SQ
Query Match 73.7%; Score 28; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGGCTGGGGACTTTCACGGG 29
Db 6 GGGACTTTCGGCTGGGGACTTTCACGGG 33
RESULT 41
AAC66959
ID AAC66959 standard; DNA; 34 BP.
XX
AC AAC66959;
XX
DT 27-MAR-2001 (first entry)
XX
DE Lymphoid cell nuclear factor related sequence #6.
XX
XX Lymphoid cell nuclear factor; immunoglobulin gene transcription; Ig gene;
KW IgNF-A; IgNF-E; IgNF-B; IgNF-kappaB; PCR primer; ss.
XX
OS Unidentified.
XX
XX US6150090-A.
PN
XX
XX 21-NOV-2000.
PD
XX
XX 05-JUN-1995; 95US-00463397.
PF
XX
XX 09-JAN-1986; 86US-00817441.
PR
XX 24-DEC-1986; 86US-00946365.
PR
XX 12-FEB-1988; 88US-00155207.
PR
XX 01-MAR-1988; 88US-00162680.
PR
XX 05-DEC-1988; 88US-00280173.
PR
XX 03-MAR-1989; 89US-00318901.
PR
XX 21-APR-1989; 89US-00341436.
PR
XX 13-NOV-1991; 91US-00791898.
PR
XX 06-APR-1995; 95US-00418266.
PR
XX (HARD ) HARVARD COLLEGE.
PA
PA (WASI ) MASSACHUSETTS INST TECHNOLOGY.
PA
PA (WHED ) WHITEHEAD INST.
XX
XX Sharp PA, Singh H, Sen R, Baldwin AS, Clerc RG, Baltimore D;
PI
```

```
PI Fan C, Maniatis TP, Baeuerle PA, Lebowitz JH, Lenardo MJ;
PI Corcoran LM, Staudt L;
XX
XX WPI; 2001-060011/07.
XX
XX Identifying an NF-kappa B modulator, useful for analyzing protein DNA
PT interactions in cells or in identifying transcriptional regulatory
PT factors by detecting NF-kappa B or IKB DNA binding activity level or
PT cytoplasmic localization.
XX
XX Disclosure; Fig 14; 66pp; English.
XX
XX The present invention provides assays for identifying compounds which
CC modulate NF-kappaB. NF-kappaB, along with IgNF-A, IgNF-E and IgNF-B, is a
CC lymphoid cell nuclear factor which regulates the transcription of the
CC immunoglobulin genes. The modulators are useful in the control of
CC activation of host cells
XX
XX Sequence 34 BP; 7 A; 8 C; 11 G; 8 T; 0 U; 0 Other;
SQ
Query Match 73.7%; Score 28; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GGGACTTTCGGCTGGGGACTTTCACGGG 29
Db 6 GGGACTTTCGGCTGGGGACTTTCACGGG 33
RESULT 42
ADT77252
ID ADT77252 standard; DNA; 34 BP.
XX
AC ADT77252;
XX
DT 13-JAN-2005 (first entry)
XX
DE HIV enhancer NF-KB binding site.
XX
XX necrosis factor kappa B; NF-kappaB;
KW transcriptional regulatory DNA element; immunoglobulin;
KW transcription enhancer; immunoassay; IgNF-B; HIV enhancer; ds.
XX
XX Human immunodeficiency virus.
XX
XX US2004214757-A1.
PN
XX
XX 28-OCT-2004.
PD
XX
XX 04-JAN-2002; 2002US-00037341.
PF
XX
XX 09-JAN-1986; 86US-00817441.
PR
XX 24-DEC-1986; 86US-00946365.
PR
XX 12-FEB-1988; 88US-00155207.
PR
XX 01-MAR-1988; 88US-00162680.
PR
XX 05-DEC-1988; 88US-00280173.
PR
XX 03-MAR-1989; 89US-00318901.
PR
XX 21-APR-1989; 89US-00341436.
PR
XX 13-NOV-1991; 91US-00791898.
PR
XX 06-APR-1995; 95US-00418266.
PR
XX 05-JUN-1995; 95US-00464364.
XX
XX (BALT/) BALTIMORE D.
PA
XX (SENR/) SEN R.
PA
XX (SHAR/) SHARP P A.
PA
XX (SING/) SINGH H.
PA
XX (STAU/) STAUDT L.
PA
XX (LEBO/) LEBOWITZ J H.
PA
XX (BALD/) BALDWIN A S.
PA
XX (CLER/) CLERC R G.
PA
XX (CORC/) CORCORAN L M.
PA
XX (BAEU/) BAEUERLE P A.
PA
XX (LENA/) LENARDO M J.
```



CC to 377 of the coding strand sequence of the HIV-1 LAI 5' long terminal  
 CC repeat (LTR), and including an added KpnI restriction site. This was used  
 CC as 5' primer, with the 3' primer given in ACP05496, to amplify a 186 bp  
 CC fragment of the 5' LTR (nucleotides 345-531) for use in the plasmid  
 CC construct pLTR(345-531)-luc. This plasmid was used to demonstrate the  
 CC trichostatin-A (TSA) inducibility of HIV-1 LTRs and also to show that  
 CC intact kappaB sites are required for maximal TSA inducibility of the HIV-  
 CC 1 promoter. The invention relates to the use of a deacetylase inhibitor  
 CC (e.g. TSA) combined with one or more compounds used in a viral treatment  
 CC for the manufacture of a medicament for obtaining elimination of  
 CC integrated, functional and pathogenic viruses, e.g. HIV-1, in a mammal  
 CC cell, including a human cell. This allows significant elimination and  
 CC possible suppression of the presence of virus in a patient and therefore  
 CC improves long-term control of viral infections in patients receiving  
 CC highly active antiretroviral therapy (HAART) treatment

XX  
 SQ Sequence 42 BP; 7 A; 11 C; 15 G; 9 T; 0 U; 0 Other;  
 Query Match 73.7%; Score 28; DB 9; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 0.19;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCACGGG 29  
 |||||  
 DB 15 GGGACTTTCGGCTGGGACTTTCACGGG 42

RESULT 45  
 AAT30606  
 ID AAT30606 standard; DNA; 45 BP.  
 XX  
 AC AAT30606;  
 XX  
 DT 19-FEB-1997 (first entry)  
 XX  
 DE Target binding region #26.  
 XX  
 KW Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SPI;  
 KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;  
 KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
 KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
 KW virus; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9617956-A2.  
 XX  
 PD 13-JUN-1996.  
 XX  
 PF 07-DEC-1995; 95WO-US015944.  
 XX  
 PR 09-DEC-1994; 94US-00353476.  
 XX  
 PA (GENE-) GENE POOL INC.  
 XX  
 PI Weininger S, Weininger AM;  
 XX  
 DR WPI; 1996-287199/29.  
 XX  
 PT Probe nucleic acids, target binding assemblies, etc - for detection and  
 PT localisation of specific nucleic acid sequences, esp. HIV and HPV.  
 XX  
 PS Disclosure; Page 72; 172pp; English.  
 XX  
 CC AAT30581-T30614 represent target binding regions (TER) of a probe of the  
 CC invention. The probe of the invention contains a TER, a booster binding  
 CC region (BBR), and an optional support or attachment (OSA). The target  
 CC binding assembly (TBA) recognised by the probe, contains at least one  
 CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an  
 CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see  
 CC AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007),  
 CC and an OSA. The assembly sequence and asymmetry sequences are responsible  
 CC for the folding and association of the NARs. The NARs (see AAR95995-

CC R95993) are selected from NF-kappa-B, SPI, TATA, human papillomavirus  
 CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding  
 CC units. The linker sequence is an oligopeptide, which does not interfere  
 CC with NAR function, but provides stability and control over the spacing of  
 CC the NAR from the rest of the TBA. The OSA is an attached support or  
 CC indicator, or other means of localisation of the probe. The probe can be  
 CC used in a method for detecting or localising a specific target nucleic  
 CC acid sequence (TNA). The method is highly sensitive, and has a high  
 CC degree of specificity. The method can be used for detecting specific  
 CC nucleic acid sequences, including those found in human cells, in HIV,  
 CC HPV, and other nucleic acid containing systems, including bacteria and  
 CC viruses

XX  
 SQ Sequence 45 BP; 9 A; 11 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 72.6%; Score 27.6; DB 2; Length 45;  
 Best Local Similarity 88.2%; Pred. No. 0.27;  
 Matches 30; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCACGGGACTT 35  
 |||||  
 DB 7 GGGACTTTCGGCTGGGACTTTCACGAGGGCGT 40

RESULT 46  
 AAA99616/c  
 ID AAA99616 standard; DNA; 35 BP.  
 XX  
 AC AAA99616;  
 XX  
 DT 22-JAN-2001 (first entry)  
 XX  
 DE NF-kB oligonucleotide #2.  
 XX  
 KW NF-kB; alpha-melanocyte stimulating hormone; alpha-MSH; antibacterial;  
 KW fungicide; virucide; antiinflammatory; vaginitis; cystitis; urethritis;  
 KW balanoposthitis; toxic shock syndrome; sexually transmitted disease;  
 KW probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XN WO200056353-A2.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PF 23-MAR-2000; 2000WO-US007846.  
 XX  
 PR 24-MAR-1999; 99US-0126233P.  
 XX  
 PA (ZENG-) ZENGEN INC.  
 XX  
 PI Lipton J, Catania A;  
 XX  
 DR WPI; 2000-628219/60.  
 XX

PT Treating uro-genital conditions, such as vaginitis, cystitis, urethritis,  
 PT or balanoposthitis comprises using alpha-melanocyte stimulating hormone  
 PT or a derivative of it.

PS Example 9; Page 15; 37pp; English.

XX The present sequence is an oligonucleotide used to determine the level of  
 CC NF-kB activity in human U1 cells treated with alpha-melanocyte  
 CC stimulating hormone (alpha-MSH). Alpha-MSH and its derivatives were shown  
 CC to inhibit TNF-alpha induced NF-kB activation and binding. Alpha-MSH and  
 CC its derivatives have potent antipruritic and antiinflammatory properties,  
 CC yet they have extremely low toxicity. A uro-genital condition treatment  
 CC system has been developed that comprises a carrier and a polypeptide  
 CC including a sequence derived from alpha-MSH. The system may be used to  
 CC treat a uro-genital condition such as vaginitis, cystitis, urethritis, or  
 CC balanoposthitis. It may also be used to prevent toxic shock syndrome and  
 CC infection from sexually transmitted diseases, and to treat an antibiotic  
 CC resistant microorganism. The polypeptides used in the treatment system

CC can reduce the viability of microbes, reduce the germination of yeast,  
CC kill microbes, treat inflammation associated with microbial infection,  
CC increase the accumulation of cAMP in microbes and inhibit replication and  
CC expression of viral pathogens

XX SQ Sequence 35 BP; 9 A; 11 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 72.1%; Score 27.4; DB 3; Length 35;  
Best Local Similarity 96.6%; Pred. No. 0.32;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGTGGGGACTTTCACGGG 29  
|||  
Db 32 GGGGACTTTCGGTGGGGACTTTCACATGG 4

## RESULT 47

ACC47366/c  
ID ACC47366 standard; DNA; 35 BP.

XX AC ACC47366;

DT 11-AUG-2003 (first entry)

XX NF-kappaB DNA binding site negative strand.

DE MSH; alpha-melanocyte stimulating hormone; alpha-MSH; cancer; cytostatic;  
KW NF-kappaB; ss.

XX Synthetic.

XX WO2003020223-A2.

XX 13-MAR-2003.

XX 05-SEP-2002; 2002WO-US028257.

XX 05-SEP-2001; 2001US-0317514P.

XX (LIPT/) LIPTON J.

XX (CATA/) CATANIA A P.

XX Lipton J, Catania AP;

XX WPI; 2003-290144/28.

XX Use of alpha-melanocyte stimulating hormone to combat cancer and in  
PT inhibiting cancer cell proliferation.

XX Example 4; Page 14; 27pp; English.

CC The invention relates to the use of alpha-melanocyte stimulating hormone  
CC (MSH), its derivative, or both, to combat cancer and in inhibiting cancer  
CC cell proliferation by administering the above alpha-MSH to a patient with  
CC cancer. The alpha-MSH is useful for combating cancer and for inhibiting  
CC cancer cell proliferation, where the cancer is mesothelioma, and is  
CC selected from Hodgkin lymphoma, non-Hodgkin lymphoma, squamous cell  
CC carcinoma, breast cancer and colorectal cancer. Sequences ACC47365-366  
CC represent positive and negative strands of NF-kappaB DNA binding site,  
CC used in DNA binding assays for determining alpha-MSH inhibition of NF-  
CC kappaB in cancer cells

XX SQ Sequence 35 BP; 9 A; 11 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 72.1%; Score 27.4; DB 10; Length 35;  
Best Local Similarity 96.6%; Pred. No. 0.32;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGTGGGGACTTTCACGGG 29  
|||  
Db 32 GGGGACTTTCGGTGGGGACTTTCATGG 4

## RESULT 48

AAT30604

ID AAT30604 standard; DNA; 44 BP.

XX AC AAT30604;

XX 19-FEB-1997 (first entry)

XX Target binding region #24.

DE Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;  
KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;  
KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;  
KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;  
KW virus; ss.

XX Synthetic.

XX WO9617956-A2.

XX 13-JUN-1996.

XX 07-DEC-1995; 95WO-US015944.

XX 09-DEC-1994; 94US-00353476.

XX (GENE-) GENE POOL INC.

XX Weininger S, Weininger AM;

XX WPI; 1996-287199/29.

XX Probe nucleic acids, target binding assemblies, etc - for detection and  
PT localisation of specific nucleic acid sequences, esp. HIV and HPV.

XX Disclosure; Page 71; 172pp; English.

XX AAT30581-T30614 represent target binding regions (TBR) of a probe of the  
CC invention. The probe of the invention contains a TBR, a booster binding  
CC region (BBR), and an optional support or attachment (OSA). The target  
CC binding assembly (TBA) recognised by the probe, contains at least one  
CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an  
CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see  
CC AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007),  
CC and an OSA. The assembly sequence and asymmetry sequences are responsible  
CC for the folding and association of the NARs. The NARs (see AAR95965-  
CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus  
CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding  
CC units. The linker sequence is an oligopeptide, which does not interfere  
CC with NAR function, but provides stability and control over the spacing of  
CC the NAR from the rest of the TBA. The OSA is an attached support or  
CC indicator, or other means of localisation of the probe. The probe can be  
CC used in a method for detecting or localising a specific target nucleic  
CC acid sequence (TNA). The method is highly sensitive, and has a high  
CC degree of specificity. The method can be used for detecting specific  
CC nucleic acid sequences, including those found in human cells, in HIV,  
CC HPV, and other nucleic acid containing systems, including bacteria and  
CC viruses

XX SQ Sequence 44 BP; 6 A; 12 C; 16 G; 10 T; 0 U; 0 Other;

Query Match 72.1%; Score 27.4; DB 2; Length 44;  
Best Local Similarity 83.8%; Pred. No. 0.33;  
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGTGGGGACTTTCACGGGGACTTTC 38  
|||  
Db 7 GGGACTTTCGGTGGGGACTTTCGGGGACGCGTGCC 43

## RESULT 49

AAT30605

ID AAT30605 standard; DNA; 44 BP.

```
XX AC AAT30605;
XX DT 19-FEB-1997 (first entry)
XX DE Target binding region #25.
XX KW Target binding assembly; nucleic acid recognition unit; NF-kappa-B; SP1;
XX KW TATA; human papillomavirus; HPV; HPV E2; human immunodeficiency virus;
XX KW HIV LTR; Tat binding unit; probe; assembly sequence; asymmetry sequence;
XX KW nuclear localisation signal sequence; human cell; HPV LTR; HIV; bacteria;
XX KW virus; ss.
XX OS Synthetic.
XX PN W09617956-A2.
XX PD 13-JUN-1996.
XX PF 07-DEC-1995; 95WO-US015944.
XX PR 09-DEC-1994; 94US-00353476.
XX PA (GENE-) GENE POOL INC.
XX PI Weininger S, Weininger AM;
XX DR WPI; 1996-287199/29.
XX PT Probe nucleic acids, target binding assemblies, etc - for detection and
XX PT localisation of specific nucleic acid sequences, esp. HIV and HPV.
XX PS Disclosure; Page 72; 172pp; English.
XX CC AAT30581-T30614 represent target binding regions (TBR) of a probe of the
XX CC invention. The probe of the invention contains a TBR, a booster binding
XX CC region (BBR), and an optional support or attachment (OSA). The target
XX CC binding assembly (TBA) recognised by the probe, contains at least one
XX CC nucleic acid recognition unit (NAR), and optionally a linker sequence, an
XX CC assembly sequence (see AAR95994-R95998), an asymmetry sequence (see
XX CC AAR95999-R96006), a nuclear localisation signal sequence (see AAR96007),
XX CC and an OSA. The assembly sequence and asymmetry sequences are responsible
XX CC for the folding and association of the NARs. The NARs (see AAR95965-
XX CC R95993) are selected from NF-kappa-B, SP1, TATA, human papillomavirus
XX CC (HPV) E2, HPV LTR, human immunodeficiency virus (HIV) LTR and Tat binding
XX CC units. The linker sequence is an oligopeptide, which does not interfere
XX CC with NAR function, but provides stability and control over the spacing of
XX CC the NAR from the rest of the TBA. The OSA is an attached support or
XX CC indicator, or other means of localisation of the probe. The probe can be
XX CC used in a method for detecting or localising a specific target nucleic
XX CC acid sequence (TNA). The method is highly sensitive, and has a high
XX CC degree of specificity. The method can be used for detecting specific
XX CC nucleic acid sequences, including those found in human cells, in HIV,
XX CC HPV, and other nucleic acid containing systems, including bacteria and
XX CC viruses
XX SQ Sequence 44 BP; 6 A; 12 C; 17 G; 9 T; 0 U; 0 Other;

Query Match 71.6%; Score 27.2; DB 2; Length 44;
Best Local Similarity 90.6%; Pred. No. 0.39;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGAC 33
    |||||
Db 7 GGGACTTTCGGCTGGGACTTTCGGGGAGGC 38

RESULT 50
AAA99615
ID AAA99615 standard; DNA; 35 BP.
XX AC AAA99615;
XX
```

```
DT 22-JAN-2001 (first entry)
XX DE NF-kB oligonucleotide #1.
XX KW NF-kB; alpha-melanocyte stimulating hormone; alpha-MSH; antibacterial;
XX KW fungicide; virucide; antiinflammatory; vaginitis; cystitis; urethritis;
XX KW balanoposthitis; toxic shock syndrome; sexually transmitted disease;
XX KW probe; ss.
XX OS Homo sapiens.
XX PN W0200056353-A2.
XX PD 28-SEP-2000.
XX PF 23-MAR-2000; 2000WO-US007846.
XX PR 24-MAR-1999; 99US-0126233P.
XX PA (ZENG-) ZENGEN INC.
XX PI Lipton J, Catania A;
XX DR WPI; 2000-628219/60.
XX PT Treating uro-genital conditions, such as vaginitis, cystitis, urethritis,
XX PT or balanoposthitis comprises using alpha-melanocyte stimulating hormone
XX PT or a derivative of it.
XX PS Example 9; Page 15; 37pp; English.
XX CC The present sequence is an oligonucleotide used to determine the level of
XX CC NF-kB activity in human UI cells treated with alpha-melanocyte
XX CC stimulating hormone (alpha-MSH). Alpha-MSH and its derivatives were shown
XX CC to inhibit TNF-alpha induced NF-kB activation and binding. Alpha-MSH and
XX CC its derivatives have potent antipyretic and antiinflammatory properties,
XX CC yet they have extremely low toxicity. A uro-genital condition treatment
XX CC system has been developed that comprises a carrier and a polypeptide
XX CC including a sequence derived from alpha-MSH. The system may be used to
XX CC treat a uro-genital condition such as vaginitis, cystitis, urethritis, or
XX CC balanoposthitis. It may also be used to prevent toxic shock syndrome and
XX CC infection from sexually transmitted diseases, and to treat an antibiotic
XX CC resistant microorganism. The polypeptides used in the treatment system
XX CC can reduce the viability of microbes, reduce the germination of yeast,
XX CC kill microbes, treat inflammation associated with microbial infection, and
XX CC increase the accumulation of cAMP in microbes and inhibit replication and
XX CC expression of viral pathogens
XX SQ Sequence 35 BP; 6 A; 9 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 69.5%; Score 26.4; DB 3; Length 35;
Best Local Similarity 96.4%; Pred. No. 0.79;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGACTTTCAGG 28
    |||||
Db 8 GGGGACTTTCGGCTGGGACTTTCATG 35

Search completed: February 15, 2006, 18:07:16
Job time : 297.413 secs
```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:56:18 ; Search time 85.4215 Seconds  
(without alignments)  
790.754 Million cell updates/sec

Title: US-09-669-187A-148

Perfect score: 38

Sequence: 1 999gacttccgctgggactttccaggggactttcc 38

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/ina/1 COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	38	2	US-08-607-519-2
2	30.8	81.1	43	2	US-08-353-476-29
3	30.2	79.5	46	2	US-08-353-476-28
4	30	78.9	39	2	US-08-450-257-43
C 5	30	78.9	39	2	US-08-450-257-44
6	30	78.9	39	2	US-08-450-246-43
C 7	30	78.9	39	2	US-08-450-246-44
8	30	78.9	39	2	US-08-450-098-43
C 9	30	78.9	39	2	US-08-450-098-44
10	30	78.9	39	2	US-08-451-233-43
C 11	30	78.9	39	2	US-08-451-233-44
12	30	78.9	39	2	US-08-450-236-43
C 13	30	78.9	39	2	US-08-450-236-44
14	30	78.9	39	3	US-08-235-403-43
C 15	30	78.9	39	3	US-08-235-403-44
16	29.8	78.4	44	3	US-09-314-691-9
17	29.8	78.4	44	3	US-09-999-495-9
18	29.8	78.4	44	3	US-09-992-837-9
19	29.8	78.4	44	3	US-10-000-720-9
20	29.2	76.8	45	2	US-08-580-988A-12
21	29.2	76.8	45	2	US-08-353-476-19
22	29.2	76.8	45	2	US-08-353-476-23
23	29	76.3	46	2	US-08-353-476-20
24	29	76.3	46	2	US-08-353-476-21

25	29	76.3	46	2	US-08-353-476-22	Sequence 22, Appl
26	29	76.3	46	2	US-08-353-476-27	Sequence 27, Appl
27	28.8	75.8	36	2	US-08-465-590-142	Sequence 142, App
28	28.8	75.8	36	3	US-08-711-417C-142	Sequence 142, App
29	28.8	75.8	36	3	US-09-723-909-142	Sequence 142, App
30	28.8	75.8	36	6	PCT-US93-08743-142	Sequence 142, App
31	28.4	74.7	37	2	US-08-353-476-38	Sequence 38, Appl
32	28	73.7	32	3	US-09-522-775A-9	Sequence 9, Appl
33	28	73.7	32	3	US-09-522-775A-11	Sequence 11, Appl
34	28	73.7	35	3	US-09-440-967-4	Sequence 4, Appl
35	27.6	72.6	45	3	US-08-353-476-26	Sequence 26, Appl
36	27.4	72.1	45	3	US-09-533-341-6	Sequence 6, Appl
C 37	27.4	72.1	44	2	US-08-353-476-24	Sequence 24, Appl
38	27.2	71.6	44	2	US-08-353-476-25	Sequence 25, Appl
39	26.4	69.5	35	3	US-09-535-066F-9	Sequence 9, Appl
40	26.4	69.5	35	3	US-09-533-341-5	Sequence 5, Appl
41	26	68.4	32	3	US-09-031-629A-5	Sequence 5, Appl
42	26	68.4	32	3	US-09-258-682-1	Sequence 1, Appl
43	26	68.4	33	2	US-08-484-397A-25	Sequence 25, Appl
C 44	26	68.4	33	2	US-08-484-397A-26	Sequence 26, Appl
C 45	25.8	67.9	35	3	US-09-535-066F-10	Sequence 10, Appl
46	25.2	66.3	48	2	US-08-353-476-30	Sequence 30, Appl
47	25	65.8	27	2	US-08-353-476-7	Sequence 7, Appl
48	24	63.2	25	3	US-09-844-915-1	Sequence 1, Appl
C 49	24	63.2	25	3	US-08-479-852-44	Sequence 44, Appl
50	24	63.2	27	2	US-08-479-852-44	Sequence 44, Appl
51	24	63.2	27	2	US-08-462-646-44	Sequence 44, Appl
52	24	63.2	27	2	US-08-462-646-124	Sequence 124, App
53	24	63.2	27	2	US-08-353-476-8	Sequence 8, Appl
54	24	63.2	27	3	US-09-013-406-44	Sequence 44, Appl
55	24	63.2	27	3	US-09-013-406-124	Sequence 124, App
56	24	63.2	27	3	US-09-168-947-17	Sequence 17, Appl
57	24	63.2	27	3	US-09-766-095-44	Sequence 44, Appl
58	24	63.2	27	3	US-09-766-095-124	Sequence 124, App
59	24	63.2	27	3	US-09-079-029-4	Sequence 4, Appl
60	24	63.2	29	3	US-08-528-069-14	Sequence 14, Appl
61	24	63.2	29	3	US-08-828-683A-10	Sequence 10, Appl
62	24	63.2	30	3	US-09-635-027B-1	Sequence 1, Appl
63	24	63.2	30	3	US-08-876-078-3	Sequence 3, Appl
64	23	60.5	23	3	US-08-831-823-3	Sequence 3, Appl
65	23	60.5	23	3	US-08-122-433-8	Sequence 8, Appl
66	22.4	58.9	25	2	US-09-092-077-60	Sequence 60, Appl
C 67	22	57.9	22	3	US-08-580-988A-13	Sequence 13, Appl
68	21.4	56.3	45	2	US-09-138-277C-12	Sequence 12, Appl
69	21	55.3	25	3	US-08-353-765-1	Sequence 1, Appl
70	20.4	53.7	23	3	US-09-138-277C-13	Sequence 13, Appl
C 71	20.2	53.2	26	3	US-08-353-476-16	Sequence 16, Appl
72	19.8	52.1	26	2	PCT-US92-10792-7	Sequence 7, Appl
73	19.2	50.5	24	6	US-08-353-476-9	Sequence 9, Appl
74	19.2	50.5	26	2	US-08-353-476-15	Sequence 15, Appl
75	19.2	50.5	26	2	US-10-040-802-24	Sequence 24, Appl
C 76	19	50.0	24	3	US-08-353-476-10	Sequence 10, Appl
77	19	50.0	26	2	US-08-353-476-14	Sequence 14, Appl
78	19	50.0	26	2	US-08-450-257-45	Sequence 45, Appl
79	18.6	48.9	39	2	US-08-450-257-46	Sequence 46, Appl
C 80	18.6	48.9	39	2	US-08-450-246-45	Sequence 45, Appl
81	18.6	48.9	39	2	US-08-450-246-46	Sequence 46, Appl
C 82	18.6	48.9	39	2	US-08-450-098-45	Sequence 45, Appl
83	18.6	48.9	39	2	US-08-450-098-46	Sequence 46, Appl
C 84	18.6	48.9	39	2	US-08-451-233-45	Sequence 45, Appl
C 85	18.6	48.9	39	2	US-08-451-233-46	Sequence 46, Appl
C 86	18.6	48.9	39	2	US-08-450-236-45	Sequence 45, Appl
C 87	18.6	48.9	39	2	US-08-450-236-46	Sequence 46, Appl
C 88	18.6	48.9	39	2	US-08-607-519-3	Sequence 3, Appl
89	18.6	48.9	39	3	US-08-235-403-45	Sequence 45, Appl
90	18.6	48.9	39	3	US-08-235-403-46	Sequence 46, Appl
C 91	18.6	48.9	39	3	US-08-386-141-22	Sequence 22, Appl
92	18.2	47.9	26	2	US-08-386-141-23	Sequence 23, Appl
C 93	17.6	46.3	26	2	US-08-353-476-13	Sequence 13, Appl
94	17.6	46.3	26	2	US-08-353-476-12	Sequence 12, Appl
95	17.2	45.3	26	2	US-09-522-775A-10	Sequence 10, Appl
C 96	17	44.7	17	3	US-08-353-476-11	Sequence 11, Appl
97	16.8	44.2	26	2	US-08-353-476-11	Sequence 11, Appl

C 98	16.6	43.7	47	3	US-09-641-638-1046	Sequence 1046, Ap	C 171	14	36.8	30	3	US-09-052-689-1	Sequence 1, Appli
C 99	16.6	43.7	47	3	US-10-170-097-1046	Sequence 1046, Ap	C 172	14	36.8	32	2	US-08-174-672D-49	Sequence 49, Appl
C 100	16.4	43.2	38	2	US-08-120-607A-12	Sequence 12, Appl	C 173	14	36.8	33	2	US-08-741-881-47	Sequence 47, Appl
C 101	16.4	43.2	38	2	US-08-453-848-27	Sequence 27, Appl	C 174	14	36.8	33	2	US-08-739-158-47	Sequence 47, Appl
C 102	16.4	43.2	38	2	US-09-169-027-27	Sequence 27, Appl	C 175	14	36.8	33	2	US-08-739-167-47	Sequence 47, Appl
C 103	16.2	42.6	40	2	US-08-682-212-23	Sequence 23, Appl	C 176	14	36.8	33	3	US-08-404-796-47	Sequence 47, Appl
C 104	16.2	42.6	46	2	US-08-734-925-5	Sequence 5, Appli	C 177	14	36.8	33	3	US-08-931-869-47	Sequence 47, Appl
C 105	15.8	41.6	47	3	US-09-386-642-36	Sequence 36, Appl	C 178	14	36.8	33	3	US-09-350-399-47	Sequence 47, Appl
C 106	15.4	40.5	25	3	US-09-388-349-4	Sequence 4, Appli	C 179	14	36.8	33	3	US-09-236-140A-47	Sequence 47, Appl
C 107	15.4	40.5	25	3	US-09-396-196G-74122	Sequence 74122, A	C 180	14	36.8	34	3	US-08-646-789A-35	Sequence 35, Appl
C 108	15.4	40.5	25	3	US-09-396-196G-110222	Sequence 110222, A	C 181	14	36.8	34	3	US-08-646-789A-93	Sequence 93, Appl
C 109	15.2	40.0	23	3	US-07-808-452-9	Sequence 9, Appli	C 182	14	36.8	38	2	US-08-663-769-5	Sequence 5, Appli
C 110	15.2	40.0	23	6	PCT-US92-10770-9	Sequence 9, Appli	C 183	14	36.8	38	2	US-08-425-684-92	Sequence 92, Appl
C 111	15.2	40.0	50	3	US-10-131-827-5964	Sequence 5964, Ap	C 184	14	36.8	40	2	US-08-675-502-92	Sequence 92, Appl
C 112	15	39.5	15	2	US-08-353-476-4	Sequence 4, Appli	C 185	14	36.8	40	2	US-09-245-802-92	Sequence 92, Appl
C 113	15	39.5	33	2	US-08-435-350-30	Sequence 30, Appl	C 186	14	36.8	40	9	5281520-28	Patent No. 5281520
C 114	15	39.5	45	2	US-08-528-057-17	Sequence 17, Appl	C 187	14	36.8	45	2	US-08-882-756-1	Sequence 1, Appli
C 115	14.8	38.9	31	2	US-08-390-850-254	Sequence 254, App	C 188	14	36.8	45	2	US-08-882-756-2	Sequence 2, Appli
C 116	14.8	38.9	31	2	US-08-390-850-255	Sequence 255, App	C 189	14	36.8	45	2	US-08-882-756-5	Sequence 5, Appli
C 117	14.8	38.9	31	2	US-08-390-850-256	Sequence 256, App	C 190	14	36.8	45	3	US-09-301-153-1	Sequence 1, Appli
C 118	14.8	38.9	31	2	US-08-435-634-254	Sequence 254, App	C 191	14	36.8	45	3	US-09-301-153-2	Sequence 2, Appli
C 119	14.8	38.9	31	2	US-08-435-634-255	Sequence 255, App	C 192	14	36.8	47	3	US-09-422-978-114	Sequence 114, App
C 120	14.8	38.9	31	2	US-08-435-634-256	Sequence 256, App	C 193	14	36.8	47	3	US-09-422-978-1280	Sequence 1280, Ap
C 121	14.6	38.4	25	3	US-09-396-196G-50814	Sequence 50814, A	C 194	14	36.8	47	3	US-09-422-978-2397	Sequence 2397, Ap
C 122	14.6	38.4	25	3	US-09-396-196G-89802	Sequence 89802, A	C 195	14	36.8	50	3	US-09-380-190A-40	Sequence 40, Appl
C 123	14.6	38.4	25	3	US-09-396-196G-124375	Sequence 124375, A	C 196	14	36.8	50	3	US-09-554-929-99	Sequence 99, Appl
C 124	14.6	38.4	47	3	US-09-671-317-664	Sequence 664, App	C 197	14	36.8	50	3	US-10-131-827-6644	Sequence 6644, Ap
C 125	14.6	38.4	50	3	US-08-832-571-5	Sequence 5, Appli	C 198	14	36.8	50	3	US-10-131-827-7034	Sequence 7034, Ap
C 126	14.4	37.9	25	3	US-09-396-196G-18395	Sequence 18395, A	C 199	13.8	36.3	20	3	US-09-198-452A-5896	Sequence 5896, Ap
C 127	14.4	37.9	25	3	US-09-396-196G-50815	Sequence 50815, A	C 200	13.8	36.3	25	3	US-09-396-196G-45915	Sequence 45915, A
C 128	14.4	37.9	37	2	US-08-426-236-8	Sequence 8, Appli	C 201	13.8	36.3	25	3	US-09-396-196G-89803	Sequence 89803, A
C 129	14.4	37.9	38	3	US-09-770-158-11	Sequence 11, Appl	C 202	13.8	36.3	25	3	US-09-396-196G-122080	Sequence 122080, A
C 130	14.4	37.9	46	3	US-09-372-934-25	Sequence 25, Appl	C 203	13.8	36.3	26	3	US-09-538-709-903	Sequence 903, App
C 131	14.4	37.9	46	3	US-09-766-916-25	Sequence 25, Appl	C 204	13.8	36.3	27	2	US-08-859-998-1252	Sequence 1252, Ap
C 132	14.4	37.9	46	3	US-09-766-898-25	Sequence 25, Appl	C 205	13.8	36.3	27	3	US-09-225-928-1252	Sequence 1252, Ap
C 133	14.4	37.9	46	3	US-09-637-040C-25	Sequence 25, Appl	C 206	13.8	36.3	27	3	US-09-225-928-1252	Sequence 1252, Ap
C 134	14.4	37.9	46	3	US-10-306-249-25	Sequence 25, Appl	C 207	13.8	36.3	27	3	US-09-225-928-1252	Sequence 1252, Ap
C 135	14.4	37.9	50	3	US-10-131-827-434	Sequence 434, App	C 208	13.8	36.3	36	2	US-08-221-816B-5	Sequence 5, Appli
C 136	14.4	37.9	50	3	US-10-131-827-2647	Sequence 2647, Ap	C 209	13.8	36.3	36	2	US-10-112-547-5	Sequence 5, Appli
C 137	14.2	37.4	25	3	US-09-396-196G-2950	Sequence 2950, Ap	C 210	13.8	36.3	36	3	US-10-112-241-5	Sequence 5, Appli
C 138	14.2	37.4	25	3	US-09-396-196G-67905	Sequence 67905, A	C 211	13.8	36.3	36	3	US-10-104-611-5	Sequence 5, Appli
C 139	14.2	37.4	40	2	US-08-503-964-3	Sequence 3, Appli	C 212	13.8	36.3	36	3	US-10-109-368-5	Sequence 5, Appli
C 140	14.2	37.4	40	2	US-08-766-014-19	Sequence 19, Appl	C 213	13.8	36.3	36	3	US-09-724-380-5	Sequence 5, Appli
C 141	14.2	37.4	40	2	US-08-640-378-19	Sequence 19, Appl	C 214	13.8	36.3	38	2	US-08-616-398-8	Sequence 8, Appli
C 142	14.2	37.4	40	2	US-08-679-522D-8	Sequence 8, Appli	C 215	13.8	36.3	38	2	US-08-963-946-22	Sequence 22, Appl
C 143	14.2	37.4	40	2	US-08-664-863B-12	Sequence 12, Appli	C 216	13.8	36.3	38	3	US-09-474-432B-1400	Sequence 1400, Ap
C 144	14.2	37.4	40	3	US-09-141-401-8	Sequence 8, Appli	C 217	13.8	36.3	38	3	US-09-476-387-1399	Sequence 1399, Ap
C 145	14.2	37.4	40	3	US-09-290-577-40	Sequence 40, Appl	C 218	13.8	36.3	38	3	US-09-685-664B-5689	Sequence 5689, Ap
C 146	14.2	37.4	40	3	US-09-061-757B-7	Sequence 7, Appli	C 219	13.8	36.3	39	2	US-08-634-060-55	Sequence 55, Appl
C 147	14.2	37.4	40	3	US-09-290-452-40	Sequence 40, Appl	C 220	13.8	36.3	39	2	US-08-634-060-56	Sequence 56, Appl
C 148	14.2	37.4	40	3	US-09-290-338-40	Sequence 40, Appl	C 221	13.8	36.3	41	3	US-08-327-874A-32	Sequence 32, Appl
C 149	14.2	37.4	40	3	US-09-686-179A-7	Sequence 7, Appli	C 222	13.8	36.3	41	3	US-10-008-960-32	Sequence 32, Appl
C 150	14.2	37.4	40	3	US-09-290-000-40	Sequence 40, Appl	C 223	13.8	36.3	41	6	PCT-US94-09700-32	Sequence 32, Appl
C 151	14.2	37.4	40	3	US-09-354-594A-40	Sequence 40, Appl	C 224	13.8	36.3	42	2	US-08-634-060-43	Sequence 43, Appl
C 152	14.2	37.4	40	3	US-09-981-621-7	Sequence 7, Appli	C 225	13.8	36.3	42	2	US-08-634-060-44	Sequence 44, Appl
C 153	14.2	37.4	40	3	US-09-705-043A-8	Sequence 8, Appli	C 226	13.8	36.3	47	3	US-09-422-978-3517	Sequence 3517, Ap
C 154	14.2	37.4	40	3	US-09-865-807-40	Sequence 40, Appl	C 227	13.8	36.3	50	3	US-10-131-827-3550	Sequence 3550, Ap
C 155	14.2	37.4	40	3	US-09-944-604-7	Sequence 7, Appli	C 228	13.8	36.3	50	3	US-10-131-827-5063	Sequence 5063, Ap
C 156	14.2	37.4	44	3	US-09-339-913B-100	Sequence 100, App	C 229	13.6	35.8	21	3	US-08-755-587-171	Sequence 171, App
C 157	14.2	37.4	44	3	US-09-339-904A-100	Sequence 100, App	C 230	13.6	35.8	25	3	US-09-396-196G-44164	Sequence 44164, A
C 158	14.2	37.4	44	3	US-08-769-062B-100	Sequence 100, App	C 231	13.6	35.8	25	3	US-09-396-196G-50788	Sequence 50788, A
C 159	14.2	37.4	44	3	US-09-344-002C-100	Sequence 100, App	C 232	13.6	35.8	25	3	US-09-396-196G-94631	Sequence 94631, A
C 160	14.2	37.4	44	3	US-09-559-565C-100	Sequence 100, App	C 233	13.6	35.8	25	3	US-09-396-196G-106551	Sequence 106551, A
C 161	14.2	37.4	44	3	US-09-693-350-100	Sequence 100, App	C 234	13.6	35.8	25	3	US-09-396-196G-106551	Sequence 106551, A
C 162	14.2	37.4	44	3	US-09-693-389-100	Sequence 100, App	C 235	13.6	35.8	29	3	US-09-810-506-5	Sequence 5, Appli
C 163	14.2	37.4	44	3	US-09-559-671A-100	Sequence 100, App	C 236	13.6	35.8	37	2	US-08-468-700-17	Sequence 17, Appl
C 164	14.2	37.4	44	3	US-09-339-926A-100	Sequence 100, App	C 237	13.6	35.8	37	2	US-08-704-706A-17	Sequence 17, Appl
C 165	14.2	37.4	44	3	US-09-954-692-100	Sequence 100, App	C 238	13.6	35.8	37	2	US-08-985-659-17	Sequence 17, Appl
C 166	14.2	37.4	47	3	US-09-422-978-1819	Sequence 1819, Ap	C 239	13.6	35.8	40	3	US-09-626-354-2	Sequence 2, Appli
C 167	14.2	37.4	50	2	US-08-832-468-5	Sequence 5, Appli	C 240	13.6	35.8	47	3	US-09-422-978-2935	Sequence 2935, Ap
C 168	14	36.8	21	3	US-09-021-247-6	Sequence 6, Appli	C 241	13.6	35.8	49	3	US-10-012-231A-82	Sequence 82, Appl
C 169	14	36.8	21	3	US-09-810-863-6	Sequence 6, Appli	C 242	13.6	35.8	49	3	US-10-015-389A-82	Sequence 82, Appl
C 170	14	36.8	25	3	US-09-396-196G-108554	Sequence 108554, A	C 243	13.6	35.8	49	3	US-10-006-768A-82	Sequence 82, Appl



244	13.6	35.8	49	3	US-10-015-671A-82	Sequence 82, Appl
245	13.6	35.8	49	3	US-10-015-393A-82	Sequence 82, Appl
246	13.6	35.8	49	3	US-10-011-833A-82	Sequence 82, Appl
247	13.6	35.8	49	3	US-10-006-041A-82	Sequence 82, Appl
248	13.6	35.8	49	3	US-10-012-064A-82	Sequence 82, Appl
249	13.6	35.8	50	3	US-10-131-827-3363	Sequence 3363, Ap
c 250	13.4	35.3	25	3	US-09-396-196G-4564	Sequence 4564, Ap
c 251	13.4	35.3	25	3	US-09-396-196G-63468	Sequence 63468, A
c 252	13.4	35.3	25	3	US-09-396-196G-72208	Sequence 72208, A
c 253	13.4	35.3	25	3	US-09-396-196G-30859	Sequence 90859, A
c 254	13.4	35.3	25	3	US-09-396-196G-50859	Sequence 90860, A
c 255	13.4	35.3	25	3	US-09-396-196G-95301	Sequence 95301, A
c 256	13.4	35.3	25	3	US-09-396-196G-106418	Sequence 106418,
c 257	13.4	35.3	25	3	US-09-396-196G-112751	Sequence 112751,
c 258	13.4	35.3	27	2	US-08-758-306-348	Sequence 348, App
259	13.4	35.3	27	3	US-09-253-396A-7	Sequence 7, Appli
260	13.4	35.3	29	2	US-07-642-734C-19	Sequence 19, Appl
261	13.4	35.3	30	3	US-08-439-009A-19	Sequence 19, Appl
c 262	13.4	35.3	30	3	US-09-341-007B-30	Sequence 30, Appl
c 263	13.4	35.3	32	2	US-08-942-423-59	Sequence 59, Appl
264	13.4	35.3	32	2	US-08-942-423-62	Sequence 62, Appl
265	13.4	35.3	32	3	US-09-595-684B-65	Sequence 65, Appl
c 266	13.4	35.3	35	9	5171670-3	Patent No. 5171670
267	13.4	35.3	37	2	US-08-616-398-7	Sequence 7, Appli
268	13.4	35.3	37	3	US-09-600-747-4	Sequence 4, Appli
269	13.4	35.3	38	2	US-08-963-946-33	Sequence 33, Appl
c 270	13.4	35.3	40	3	US-08-322-874A-33	Sequence 33, Appl
c 271	13.4	35.3	40	3	US-10-008-960-33	Sequence 33, Appl
c 272	13.4	35.3	40	6	PCR-US894-09700-33	Sequence 33, Appl
c 273	13.4	35.3	42	3	US-09-425-804-18	Sequence 18, Appl
c 274	13.4	35.3	42	6	PCR-US95-13975-36	Sequence 36, Appl
275	13.4	35.3	45	2	US-08-661-507-5	Sequence 5, Appli
276	13.2	34.7	45	2	US-09-396-196G-96047	Sequence 96047, A
277	13.2	34.7	25	3	US-09-396-196G-96048	Sequence 96048, A
278	13.2	34.7	25	3	US-09-396-196G-96049	Sequence 96049, A
279	13.2	34.7	25	3	US-09-396-196G-106466	Sequence 106466,
c 280	13.2	34.7	25	3	US-09-396-196G-108555	Sequence 108555,
c 281	13.2	34.7	25	3	US-09-396-196G-119899	Sequence 119899,
c 282	13.2	34.7	25	3	US-09-396-196G-119900	Sequence 119900,
c 283	13.2	34.7	25	3	US-09-396-196G-119901	Sequence 119901,
c 284	13.2	34.7	28	2	US-09-396-196G-119902	Sequence 119902,
c 285	13.2	34.7	28	2	US-08-859-998-924	Sequence 924, App
c 286	13.2	34.7	28	3	US-09-225-928-924	Sequence 924, App
c 287	13.2	34.7	28	3	US-09-225-201B-924	Sequence 13, Appl
c 288	13.2	34.7	29	2	US-08-846-012A-13	Sequence 13, Appl
c 289	13.2	34.7	29	2	US-09-100-297-13	Sequence 13, Appl
c 290	13.2	34.7	29	3	US-09-084-120-6	Sequence 6, Appli
c 291	13.2	34.7	29	3	US-09-724-678D-10	Sequence 10, Appl
c 292	13.2	34.7	33	3	US-09-277-431A-19	Sequence 19, Appl
c 293	13.2	34.7	38	2	US-08-663-769-3	Sequence 3, Appli
c 294	13.2	34.7	41	3	US-08-813-507-76	Sequence 76, Appl
c 295	13.2	34.7	41	3	US-09-351-814-55	Sequence 55, Appl
c 296	13.2	34.7	41	3	US-09-464-453-76	Sequence 76, Appl
c						

## ALIGNMENTS

```

RESULT 1
US-08-607-510-2
; Sequence 2, Application US/08607519
; Patent No. 5930090
; GENERAL INFORMATION:
; APPLICANT: Nabel, Gary J.
; TITLE OF INVENTION: METHODS AND
; TITLE OF INVENTION: OF DISEASES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCC.

```

```

1  ADDRESSEE:  P.C.
2  STREET:  1755 S. Jefferson Davis Highway, Suite 400
3  CITY:  Arlington
4  STATE:  Virginia
5  COUNTRY:  U.S.A.
6  ZIP:  22202
7
8  COMPUTER READABLE FORM:
9  MEDIUM TYPE:  Floppy disk
10 COMPUTER:  IBM PC compatible
11 OPERATING SYSTEM:  PC-DOS/MS-DOS
12 SOFTWARE:  PatentIn Release #1.0, Version #1.25
13
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER:  US/08/607,519
16 FILING DATE:  27-FEB-1996
17 CLASSIFICATION:  514
18
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER:  US 08/123,188
21 FILING DATE:  20-SEP-1993
22 ATTORNEY/AGENT INFORMATION:
23 NAME:  Abdon, No. 5990090man P.
24 REGISTRATION NUMBER:  24,618
25 REFERENCE/DOCKET NUMBER:  6042-001-68
26
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE:  (703) 413-3000
29 TELEFAX:  (703) 413-2220
30 TELEX:  248855 OPAT UR
31
32 INFORMATION FOR SEQ ID NO:  2:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH:  38 base pairs
35 TYPE:  nucleic acid
36 STRANDEDNESS:  both
37 TOPOLOGY:  linear
38
39 MOLECULE TYPE:  Other nucleic acid;
40 DESCRIPTION:  SYNTHETIC DNA
41 FEATURE:
42
43 NAME/KEY:  misc difference
44 LOCATION:  replace(1..38, "")
45
46 OTHER INFORMATION:  /note= "ANY OF THE PHOSPHATE GROUPS
47 OTHER INFORMATION:  LINKING ANY OF THE NUCLEOSIDES MAY BE REPLACED
48 OTHER INFORMATION:  WITH PHOSPHOROTHIOATE GROUPS, METHYL ESTER
49
50 US-08-607-519-2
51
52 Query Match          100.0%; Score 38; DB 2; Length 38;
53 Best Local Similarity 100.0%; Pred. No. 3.le-06;
54 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps
55
56 Qy  1  GGGGACTTTCGGTGGGGACTTTCACGGGGGACTTTC 38
57      |||||
58 Db  1  GGGGACTTTCGGTGGGGACTTTCACGGGGGACTTTC 38
59
60 RESULT 2
61 US-08-353-476-29
62 ; Sequence 29, Application US/08353476
63 ; Patent No. 5871902
64 ; GENERAL INFORMATION:
65 ; APPLICANT:  Weininger, Susan
66 ; APPLICANT:  Weininger, Arthur M
67 ; TITLE OF INVENTION:  METHOD OF DETECTION OF DNA WITH A
68 ; TITLE OF INVENTION:  SPECIFIC SEQUENCE COMPOSITION
69 ; NUMBER OF SEQUENCES:  117
70 ; CORRESPONDENCE ADDRESS:
71 ; ADDRESSEE:  Saliwanchik & Saliwanchik
72 ; STREET:  2421 N.W. 41st St., Suite A-1
73 ; CITY:  Gainesville
74 ; STATE:  Florida
75 ; COUNTRY:  USA
76 ; ZIP:  32606
77
78 COMPUTER READABLE FORM:
79 MEDIUM TYPE:  Floppy disk
80 COMPUTER:  IBM PC compatible
81 OPERATING SYSTEM:  PC-DOS/MS-DOS
82 SOFTWARE:  PatentIn Release #1.0, Version #1.25

```



Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTCC 38  
|||||  
Db 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTTC 38  
|||||

RESULT 5  
US-08-450-257-44/c  
; Sequence 44, Application US/08450257  
; Patent No. 5652122  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,257  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,403  
; FILING DATE: 28-APR-1994  
; APPLICATION NUMBER: US 07/934,375  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/098,766  
; FILING DATE: 28-JUL-1993  
; APPLICATION NUMBER: PCT/US93/07833  
; FILING DATE: 19-AUG-1993  
; APPLICATION NUMBER: US 07/454,450  
; FILING DATE: 21-DEC-1989  
; APPLICATION NUMBER: US 07/636,662  
; FILING DATE: 02-JAN-1991  
; APPLICATION NUMBER: US 08/158,015  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B170 CIP 2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-450-257-44

Query Match 78.9%; Score 30; DB 2; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.0052;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTCC 38  
|||||  
Db 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTTC 38  
|||||

RESULT 6  
US-08-450-246-43  
; Sequence 43, Application US/08450246  
; Patent No. 5670617  
; GENERAL INFORMATION:  
; APPLICANT: FRANKEL, Alan  
; APPLICANT: PABO, Carl  
; APPLICANT: BARSOUM, James G.  
; APPLICANT: FAWELL, Stephen E.  
; APPLICANT: PEPINSKY, R. B.  
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,246  
; FILING DATE: 25-MAY-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/235,403  
; FILING DATE: 28-APR-1994  
; APPLICATION NUMBER: US 07/934,375  
; FILING DATE: 21-AUG-1992  
; APPLICATION NUMBER: US 07/098,766  
; FILING DATE: 28-JUL-1993  
; APPLICATION NUMBER: PCT/US93/07833  
; FILING DATE: 19-AUG-1993  
; APPLICATION NUMBER: US 07/454,450  
; FILING DATE: 21-DEC-1989  
; APPLICATION NUMBER: US 07/636,662  
; FILING DATE: 02-JAN-1991  
; APPLICATION NUMBER: US 08/158,015  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B170 CIP 2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-450-246-43

Query Match 78.9%; Score 30; DB 2; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.0052;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTCC 38  
|||||  
Db 1 GGGGACTTTCGGCTGGGGACTTTCCAGGGGGACTTTTC 38  
|||||

RESULT 7

```

US-08-450-246-44/c
; Sequence No. 44, Application US/08450246
; Patent No. 5670617
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,246
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-450-246-44

```

Query Match 78.9%; Score 30; DB 2; Length 39;  
Best Local Similarity 86.8%;  
Matches 33; Conservative 0; Mismatches 5; Indels  
Pred. No. 0.0052;

Qy 1 GGGGACTTTCGGCTGGGGACTTTCAGGGGGACTTTCC 38  
Db 39 GGGGACTTTCGGCTGGGGACTTTCACGGGGGACTTTC 2

RESULT 8  
US-08-450-098-43  
; Sequence 43, Application US/08450098  
; Patent No. 567980  
; GENERAL INFORMATION:

```

1 APPLICANT: FRANKEL, Alan
2 APPLICANT: PABO, Carl
3 APPLICANT: BARSOUM, James G.
4 APPLICANT: FAWELL, Stephen E.
5 APPLICANT: PEPINSKY, R. B.
6 TITLE OF INVENTION: FAT-DERIVED TRANSPORT POLYPEPTIDES
7 NUMBER OF SEQUENCES: 69
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: FISH & NEAVE
10 STREET: 1251 Avenue of the Americas
11 CITY: New York
12 STATE: New York
13 COUNTRY: USA
14 ZIP: 10020
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent In Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/450,098
22 FILING DATE: 25-MAY-1995
23 CLASSIFICATION: 514
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/235,403
26 FILING DATE: 28-APR-1994
27 APPLICATION NUMBER: US 07/934,375
28 FILING DATE: 21-AUG-1992
29 APPLICATION NUMBER: US 07/098,766
30 FILING DATE: 28-JUL-1993
31 APPLICATION NUMBER: PCT/US93/07833
32 FILING DATE: 19-AUG-1993
33 APPLICATION NUMBER: US 07/454,450
34 FILING DATE: 21-DEC-1989
35 APPLICATION NUMBER: US 07/636,662
36 FILING DATE: 02-JAN-1991
37 APPLICATION NUMBER: US 08/158,015
38 FILING DATE: 24-NOV-1993
39 ATTORNEY/AGENT INFORMATION:
40 NAME: Haley Jr., James F.
41 REGISTRATION NUMBER: 27,794
42 REFERENCE/DOCKET NUMBER: 5170 CIP 2
43 TELECOMMUNICATION INFORMATION:
44 TELEPHONE: (212) 596-9000
45 TELEFAX: (212) 596-9090
46 TELEX: 14-8367
47 INFORMATION FOR SEQ ID NO: 43:
48 SEQUENCE CHARACTERISTICS:
49 LENGTH: 39 base pairs
50 TYPE: nucleic acid
51 STRANDEDNESS: single
52 TOPOLOGY: linear
53 MOLECULE TYPE: DNA (genomic)
54 US-08-450-098-43
55
56 Query Match 79.9%; Score 30; DB 2; Length 39;
57 Best Local Similarity 86.8%; Pred. No. 0.0052;
58 Matches 33; Conservative 0; Mismatches 5; Indels
59
60 QY 1 GGGGACATTTCCGCTGGGGACATTTTCCAGGGGGACATTTCC 38
61
62 Db 1 GGGGACATTTCCGCTGGGGACATTTTCCAGGGGGACATTTTC 38
63
64 RESULT 9
65 US-08-450-098-44/c
66 Sequence 44. Application US/08450098
67 Patent No. 5674980
68 GENERAL INFORMATION:
69 APPLICANT: FRANKEL, Alan
70 APPLICANT: PABO, Carl
71 APPLICANT: BARSOUM, James G.
72 APPLICANT: FAWELL, Stephen E.

```

```
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,098
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9090
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-450-098-44

Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.0052;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGGACTTTCACGGGGGACTTTCC 38
   |||||
Db 39 GGGGACTTCCGCTGGGGACTTTCACGGGGGACTTTC 2

RESULT 10
US-08-451-233-43
; Sequence 43, Application US/08451233
; Patent No. 5747641
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,233
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
; APPLICATION NUMBER: US 07/098,766
; FILING DATE: 28-JUL-1993
; APPLICATION NUMBER: PCT/US93/07833
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 07/454,450
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: US 07/636,662
; FILING DATE: 02-JAN-1991
; APPLICATION NUMBER: US 08/158,015
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B170 CIP 2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9090
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-451-233-43

Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.0052;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGGACTTTCACGGGGGACTTTCC 38
   |||||
Db 1 GGGGACTTCCGCTGGGGACTTTCACGGGGGACTTTC 38

RESULT 11
US-08-451-233-44/c
; Sequence 44, Application US/08451233
; Patent No. 5747641
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
```

```
/ COUNTRY: USA
/ ZIP: 10020
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/451,233
/ FILING DATE: 25-MAY-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION NUMBER: US 08/235,403
/ FILING DATE: 28-APR-1994
/ APPLICATION NUMBER: US 07/934,375
/ FILING DATE: 21-AUG-1992
/ APPLICATION NUMBER: US 07/934,375
/ FILING DATE: 21-AUG-1992
/ APPLICATION NUMBER: US 07/098,766
/ FILING DATE: 28-JUL-1993
/ APPLICATION NUMBER: PCT/US93/07833
/ FILING DATE: 19-AUG-1993
/ APPLICATION NUMBER: US 07/454,450
/ FILING DATE: 21-DEC-1989
/ APPLICATION NUMBER: US 07/636,662
/ FILING DATE: 02-JAN-1991
/ APPLICATION NUMBER: US 08/158,015
/ FILING DATE: 24-NOV-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Haley Jr., James F.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: B170 CIP 2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 596-9000
/ TELEFAX: (212) 596-9090
/ TELEX: 14-8367
/ INFORMATION FOR SEQ ID NO: 44:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 39 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-451-233-44

Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.0052;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTC 38
Db 39 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTC 2

RESULT 12
US-08-450-236-43
; Sequence 43, Application US/08450236
; Patent No. 5804604
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM: disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

```
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/450,236
/ FILING DATE: 25-MAY-1995
/ CLASSIFICATION: 514
/ PRIOR APPLICATION NUMBER: US 08/235,403
/ FILING DATE: 28-APR-1994
/ APPLICATION NUMBER: US 07/934,375
/ FILING DATE: 21-AUG-1992
/ APPLICATION NUMBER: US 07/098,766
/ FILING DATE: 28-JUL-1993
/ APPLICATION NUMBER: PCT/US93/07833
/ FILING DATE: 19-AUG-1993
/ APPLICATION NUMBER: US 07/454,450
/ FILING DATE: 21-DEC-1989
/ APPLICATION NUMBER: US 07/636,662
/ FILING DATE: 02-JAN-1991
/ APPLICATION NUMBER: US 08/158,015
/ FILING DATE: 24-NOV-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Haley Jr., James F.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: B170 CIP 2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 596-9000
/ TELEFAX: (212) 596-9090
/ TELEX: 14-8367
/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 39 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-450-236-43

Query Match 78.9%; Score 30; DB 2; Length 39;
Best Local Similarity 86.8%; Pred. No. 0.0052;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTC 38
Db 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTC 38

RESULT 13
US-08-450-236-44/c
; Sequence 44, Application US/08450236
; Patent No. 5804604
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSOUM, James G.
; APPLICANT: FAWELL, Stephen E.
; APPLICANT: PEPINSKY, R. B.
; TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

/ APPLICATION NUMBER: US/08/450,236  
/ FILING DATE: 25-MAY-1995  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 08/235,403  
/ FILING DATE: 28-APR-1994  
/ APPLICATION NUMBER: US 07/934,375  
/ FILING DATE: 21-AUG-1992  
/ APPLICATION NUMBER: US 07/098,766  
/ FILING DATE: 28-JUL-1993  
/ APPLICATION NUMBER: PCT/US93/07833  
/ FILING DATE: 19-AUG-1993  
/ APPLICATION NUMBER: US 07/454,450  
/ FILING DATE: 21-DEC-1989  
/ APPLICATION NUMBER: US 07/636,662  
/ FILING DATE: 02-JAN-1991  
/ APPLICATION NUMBER: US 08/158,015  
/ FILING DATE: 24-NOV-1993  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Haley Jr., James F.  
/ REGISTRATION NUMBER: 27,794  
/ REFERENCE/DOCKET NUMBER: B170 CIP 2  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212) 596-9000  
/ TELEFAX: (212) 596-9090  
/ TELEX: 14-8367  
/ INFORMATION FOR SEQ ID NO: 44:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 39 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ US-08-450-236-44

Query Match 78.9%; Score 30; DB 2; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.0052;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38  
Db 39 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 2

RESULT 14  
US-08-235-403-43  
/ Sequence 43, Application US/08235403  
/ Patent No. 6316003  
/ GENERAL INFORMATION:  
/ APPLICANT: FRANKEL, Alan  
/ APPLICANT: PABO, Carl  
/ APPLICANT: BARSOUM, James G.  
/ APPLICANT: FAWELL, Stephen E.  
/ APPLICANT: PEPINSKY, R. B.  
/ TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
/ NUMBER OF SEQUENCES: 69  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: FISH & NEAVE  
/ STREET: 1251 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10020  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/235,403  
/ FILING DATE:  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 07/934,375  
/ FILING DATE: 21-AUG-1992  
/ APPLICATION NUMBER: US 07/098,766  
/ FILING DATE: 28-JUL-1993  
/ APPLICATION NUMBER: PCT/US93/07833  
/ FILING DATE: 19-AUG-1993  
/ APPLICATION NUMBER: US 07/454,450  
/ FILING DATE: 21-DEC-1989  
/ APPLICATION NUMBER: US 07/636,662  
/ FILING DATE: 02-JAN-1991  
/ APPLICATION NUMBER: US 08/158,015  
/ FILING DATE: 24-NOV-1993  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Haley Jr., James F.  
/ REGISTRATION NUMBER: 27,794  
/ REFERENCE/DOCKET NUMBER: B170 CIP 2  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212) 596-9000  
/ TELEFAX: (212) 596-9090  
/ TELEX: 14-8367  
/ INFORMATION FOR SEQ ID NO: 43:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 39 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ US-08-235-403-43

Query Match 78.9%; Score 30; DB 3; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.0052;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38  
Db 1 GGGGACTTTCGCTGGGGACTTTCACGGGGGACTTTC 38

RESULT 15  
US-08-235-403-44/c  
/ Sequence 44, Application US/08235403  
/ Patent No. 6316003  
/ GENERAL INFORMATION:  
/ APPLICANT: FRANKEL, Alan  
/ APPLICANT: PABO, Carl  
/ APPLICANT: BARSOUM, James G.  
/ APPLICANT: FAWELL, Stephen E.  
/ APPLICANT: PEPINSKY, R. B.  
/ TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES  
/ NUMBER OF SEQUENCES: 69  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: FISH & NEAVE  
/ STREET: 1251 Avenue of the Americas  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10020  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent In Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/235,403  
/ FILING DATE:  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 07/934,375  
/ FILING DATE: 21-AUG-1992  
/ APPLICATION NUMBER: US 07/098,766  
/ FILING DATE: 28-JUL-1993  
/ APPLICATION NUMBER: PCT/US93/07833  
/ FILING DATE: 19-AUG-1993

; APPLICATION NUMBER: US 07/454,450  
; FILING DATE: 21-DEC-1989  
; APPLICATION NUMBER: US 07/636,662  
; FILING DATE: 02-JAN-1991  
; APPLICATION NUMBER: US 08/158,015  
; FILING DATE: 24-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B170 CIP 2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-235-403-44

Query Match 78.9%; Score 30; DB 3; Length 39;  
Best Local Similarity 86.8%; Pred. No. 0.0052;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGACTTTCGGCTGGGACTTTCAGGGGACTTCC 38  
DB 39 GGGGACTTTCGGCTGGGACTTTCACGGGGGACTTTC 2

## RESULT 16

US-09-314-691-9

; Sequence 9, Application US/09314691  
; Patent No. 6444233  
; GENERAL INFORMATION:  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: BLAKE, MARY E.  
; APPLICANT: GUTTERMAN, JORDAN U.  
; APPLICANT: HOFFMANN, JOSEPH J.  
; APPLICANT: BAILEY, DAVID T.  
; APPLICANT: JAYATILAKE, GAMINI S.  
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: CLFR:006  
; CURRENT APPLICATION NUMBER: US/09/314,691  
; CURRENT FILING DATE: 1999-05-19  
; EARLIER APPLICATION NUMBER: 60/099,066  
; EARLIER FILING DATE: 1998-09-03  
; EARLIER APPLICATION NUMBER: 60/085,997  
; EARLIER FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
; US-09-314-691-9

Query Match 78.4%; Score 29.8; DB 3; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.0065;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGACT 34  
DB 10 GGGACTTTCGGCTGGGACTTTCACGGGGAGCT 42

## RESULT 17

US-09-999-495-9

; Sequence 9, Application US/09999495  
; Patent No. 6889398  
; GENERAL INFORMATION:  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: BLAKE, MARY E.  
; APPLICANT: GUTTERMAN, JORDAN U.  
; APPLICANT: HOFFMANN, JOSEPH J.  
; APPLICANT: BAILEY, DAVID T.  
; APPLICANT: JAYATILAKE, GAMINI S.  
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: CLFR:006  
; CURRENT APPLICATION NUMBER: US/09/999,495  
; CURRENT FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 09/314,691  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/099,066  
; PRIOR FILING DATE: 1998-09-03  
; PRIOR APPLICATION NUMBER: 60/085,997  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
; US-09-999-495-9

Query Match 78.4%; Score 29.8; DB 3; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.0065;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGACT 34  
DB 10 GGGACTTTCGGCTGGGACTTTCACGGGGAGCT 42

## RESULT 18

US-09-992-837-9

; Sequence 9, Application US/09992837  
; Patent No. 6746696  
; GENERAL INFORMATION:  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: BLAKE, MARY E.  
; APPLICANT: GUTTERMAN, JORDAN U.  
; APPLICANT: HOFFMANN, JOSEPH J.  
; APPLICANT: BAILEY, DAVID T.  
; APPLICANT: JAYATILAKE, GAMINI S.  
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: CLFR:006  
; CURRENT APPLICATION NUMBER: US/09/992,837  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/314,691  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/085,997  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
; US-09-992-837-9

Query Match 78.4%; Score 29.8; DB 3; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.0065;  
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



```
Qy 2 GGGACTTCCGCTGGGAGCTTTCAGGGGACT 34
Db 10 GGGACTTCCGCTGGGAGCTTTCAGGGGACT 42

RESULT 19
US-10-000-720-9
; Sequence 9, Application US/10000720
; Patent No. 6962720
; GENERAL INFORMATION:
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: BLAKE, MARY E.
; APPLICANT: GUTTERMAN, JORDAN U.
; APPLICANT: HOFFMANN, JOSEPH J.
; APPLICANT: BAILEY, DAVID T.
; APPLICANT: JAYATILAKE, GAMINI S.
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: CLFR-006
; CURRENT APPLICATION NUMBER: US/10/000,720
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/314,691
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,066
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/085,997
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-000-720-9

Query Match 78.4%; Score 29.8; DB 3; Length 44;
Best Local Similarity 93.9%; Pred. No. 0.0065;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGACTTCCGCTGGGAGCTTTCAGGGGACT 34
Db 10 GGGACTTCCGCTGGGAGCTTTCAGGGGACT 42

RESULT 20
US-580-988A-12
; Sequence 12, Application US/08580988A
; Patent No. 5856161
; GENERAL INFORMATION:
; APPLICANT: Aggarwal et al.
; TITLE OF INVENTION: Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
; TITLE OF INVENTION: For Its Use
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,988A
; FILING DATE: January 3, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D., J.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5721CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-6908
; TELEFAX: 713-777-2321
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 bp
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: other nucleic acid
; HYPOTHEICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; US-08-580-988A-12

Query Match 76.8%; Score 29.2; DB 2; Length 45;
Best Local Similarity 91.2%; Pred. No. 0.011;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGACTTCCGCTGGGAGCTTTCAGGGGACTT 35
Db 10 GGGACTTCCGCTGGGAGCTTTCAGGGGACT 43

RESULT 21
US-08-353-476-19
; Sequence 19, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
```

US-08-353-476-19

Query Match 76.8%; Score 29.2; DB 2; Length 45;  
Best Local Similarity 91.2%; Pred. No. 0.011;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGACTTTCAGGGGACTT 35  
|||||  
Db 7 GGGACTTCCGCTGGGACTTTCAGGGGAGCGT 40

RESULT 22

US-08-353-476-23

; Sequence 23, Application US/08353476

; Patent No. 5871902

; GENERAL INFORMATION:

; APPLICANT: Weininger, Susan

; APPLICANT: Weininger, Arthur M

; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A

; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

; NUMBER OF SEQUENCES: 117

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik &amp; Saliwanchik

; STREET: 2421 N.W. 41st St., Suite A-1

; CITY: Gainesville

; STATE: Florida

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/353,476

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Bencen, Gerard H

; REGISTRATION NUMBER: 35,746

; REFERENCE/DOCKET NUMBER: GP-100

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (904) 375-8100

; TELEFAX: (904) 372-5800

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 45 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-353-476-23

Query Match 76.8%; Score 29.2; DB 2; Length 45;  
Best Local Similarity 91.2%; Pred. No. 0.011;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGACTTTCAGGGGACTT 35  
|||||  
Db 7 GGGACTTCCGCTGGGACTTTCAGGGGAGCGT 40

RESULT 23

US-08-353-476-20

; Sequence 20, Application US/08353476

; Patent No. 5871902

; GENERAL INFORMATION:

; APPLICANT: Weininger, Susan

; APPLICANT: Weininger, Arthur M

; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A

; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/353,476  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bencen, Gerard H  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 46 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-353-476-20

Query Match 76.3%; Score 29; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGACTTTCAGGGG 30  
|||||  
Db 7 GGGACTTCCGCTGGGACTTTCAGGGG 35

RESULT 24

US-08-353-476-21

; Sequence 21, Application US/08353476

; Patent No. 5871902

; GENERAL INFORMATION:

; APPLICANT: Weininger, Susan

; APPLICANT: Weininger, Arthur M

; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A

; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

; NUMBER OF SEQUENCES: 117

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik &amp; Saliwanchik

; STREET: 2421 N.W. 41st St., Suite A-1

; CITY: Gainesville

; STATE: Florida

; COUNTRY: USA

; ZIP: 32606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/353,476

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Bencen, Gerard H

; REGISTRATION NUMBER: 35,746

REFERENCE/DOCKET NUMBER: GP-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-353-476-21

Query Match 76.3%; Score 29; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACTTTCAGGGG 30  
|||||  
DB 7 GGGACTTTCGCTGGGGACTTTCAGGGG 35

RESULT 25  
US-08-353-476-22  
Sequence 22, Application US/08353476  
Patent No. 5871902  
GENERAL INFORMATION:  
APPLICANT: Weininger, Susan  
APPLICANT: Weininger, Arthur M  
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A  
REFERENCE/DOCKET NUMBER: GP-100  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st St., Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bencen, Gerard H  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-353-476-22

Query Match 76.3%; Score 29; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACTTTCAGGGG 30

Db 7 GGGACTTTCGCTGGGGACTTTCAGGGG 35  
|||||

RESULT 26  
US-08-353-476-27  
Sequence 27, Application US/08353476  
Patent No. 5871902  
GENERAL INFORMATION:  
APPLICANT: Weininger, Susan  
APPLICANT: Weininger, Arthur M  
TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A  
REFERENCE/DOCKET NUMBER: GP-100  
NUMBER OF SEQUENCES: 117  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st St., Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bencen, Gerard H  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-353-476-27

Query Match 76.3%; Score 29; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACTTTCAGGGG 30  
|||||  
DB 7 GGGACTTTCGCTGGGGACTTTCAGGGG 35

RESULT 27  
US-08-465-590-142  
Sequence 142, Application US/08465590  
Patent No. 5824770  
GENERAL INFORMATION:  
APPLICANT: Georgopoulos, Katia A.  
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE  
NUMBER OF SEQUENCES: 164  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 STATE STREET, Suite 510  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,590
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/238,212
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,438
; FILING DATE: 14-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,695
; REFERENCE/DOCKET NUMBER: MPG-006C2DV
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-465-590-142

Query Match 75.8%; Score 28.8; DB 2; Length 36;
Best Local Similarity 93.8%; Pred. No. 0.016;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGGACTTTCAGGGGAC 33
Db 4 GGGACTTTCGGCTGGGGACTTTCAGGGAGGC 35

RESULT 28
US-08-711-417C-142
; Sequence 142, Application US/08/711417C
; Patent No. 6228611
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417C
; FILING DATE: 05-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```

```

; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-08-711-417C-142

Query Match 75.8%; Score 28.8; DB 3; Length 36;
Best Local Similarity 93.8%; Pred. No. 0.016;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGGACTTTCAGGGGAC 33
Db 4 GGGACTTTCGGCTGGGGACTTTCAGGGAGGC 35

RESULT 29
US-09-723-909-142
; Sequence 142, Application US/09/723909
; Patent No. 6630141
; GENERAL INFORMATION:
; APPLICANT: Georgopoulos, Katia A.
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
; NUMBER OF SEQUENCES: 202
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/723,909
; FILING DATE: 28-NOV-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/711,417
; FILING DATE: 05-SEP-1996
; APPLICATION NUMBER: 08/238,212
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 08/121,438
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: 07/946,233
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis P.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10287/007001
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```

## US-09-723-909-142

Query Match 75.8%; Score 28.8; DB 3; Length 36;  
Best Local Similarity 93.8%; Pred. No. 0.016;  
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGAC 33  
|||||  
Db 4 GGGACTTTCGGCTGGGACTTTCAGGGAGGC 35

## RESULT 30

PCT-US93-08743-142  
; Sequence 142, Application PC/TUS9308743  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE  
; NUMBER OF SEQUENCES: 152  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08743  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 946,233  
; FILING DATE: 14-SEP-1992  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 142:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
PCT-US93-08743-142

Query Match 75.8%; Score 28.8; DB 6; Length 36;  
Best Local Similarity 93.8%; Pred. No. 0.016;  
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGAC 33  
|||||  
Db 4 GGGACTTTCGGCTGGGACTTTCAGGGAGGC 35

## RESULT 31

US-08-353-476-38  
; Sequence 38, Application US/08353476  
; Patent No. 5871902  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A  
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/353,476

; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bencen, Gerard H  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-353-476-38

Query Match 74.7%; Score 28.4; DB 2; Length 37;  
Best Local Similarity 96.7%; Pred. No. 0.023;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGG 31  
|||||  
Db 7 GGGACTTTCGGCTGGGACTTTCAGGGAG 36

## RESULT 32

US-09-522-775A-9  
; Sequence 9, Application US/09522775A  
; Patent No. 6660906  
; GENERAL INFORMATION:  
; APPLICANT: Tsichlis, Philip N.  
; TITLE OF INVENTION: Inhibition of Tpl2 To Treat inflammatory Diseases  
; FILE REFERENCE: OTT-3202  
; CURRENT APPLICATION NUMBER: US/09/522,775A  
; CURRENT FILING DATE: 2000-03-08  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-09-522-775A-9

Query Match 73.7%; Score 28; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.032;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGG 29  
|||||  
Db 5 GGGACTTTCGGCTGGGACTTTCAGGG 32

## RESULT 33

US-09-522-775A-11  
; Sequence 11, Application US/09522775A  
; Patent No. 6660906  
; GENERAL INFORMATION:  
; APPLICANT: Tsichlis, Philip N.  
; TITLE OF INVENTION: Inhibition of Tpl2 To Treat inflammatory Diseases  
; FILE REFERENCE: OTT-3202  
; CURRENT APPLICATION NUMBER: US/09/522,775A  
; CURRENT FILING DATE: 2000-03-08  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 32  
; TYPE: DNA

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-522-775A-11

Query Match      73.7%; Score 28; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GGGACTTTCGCTGGGGGACTTTCAGG 29
    |||||
Db   5 GGGACTTTCGCTGGGGGACTTTCAGG 32
    |||||

RESULT 34
US-09-440-967-4
; Sequence 4, Application US/09440967
; Patent No. 6730302
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: INTRACELLULAR TARGETED DELIVERY OF COMPOUNDS BY 70 KD HEAT SHOCK
; FILE REFERENCE: DB8
; CURRENT APPLICATION NUMBER: US/09/440,967
; CURRENT FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/109,872
; PRIOR FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-440-967-4

Query Match      73.7%; Score 28; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGGACTTTCGCTGGGGGACTTTCAGG 28
    |||||
Db   8 GGGACTTTCGCTGGGGGACTTTCAGG 35
    |||||

RESULT 35
US-08-353-476-26
; Sequence 26, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-522-775A-11

Query Match      72.6%; Score 27.6; DB 2; Length 45;
Best Local Similarity 88.2%; Pred. No. 0.05;
Matches 30; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY  2 GGGACTTTCGCTGGGGGACTTTCAGGGGACTT 35
    |||||
Db   7 GGGACTTTCGCTGGGGGACTTTCAGAGAGCGGT 40
    |||||

RESULT 36
US-09-533-341-6/c
; Sequence 6, Application US/09533341
; Patent No. 6803044
; GENERAL INFORMATION:
; APPLICANT: Zengen, Inc.
; APPLICANT: Lipton, James M.
; APPLICANT: Catania, Anna P.
; TITLE OF INVENTION: ANTIMICROBIAL AND ANTI-INFLAMMATORY PEPTIDES FOR USE IN HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 54275.8004.US00
; CURRENT APPLICATION NUMBER: US/09/533,341
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 60/126,233
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-533-341-6

Query Match      72.1%; Score 27.4; DB 3; Length 35;
Best Local Similarity 96.6%; Pred. No. 0.057;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 GGGACTTTCGCTGGGGGACTTTCAGGG 29
    |||||
Db   32 GGGACTTTCGCTGGGGGACTTTCATGG 4
    |||||

RESULT 37
US-08-353-476-24
; Sequence 24, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
```

; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; APPLICATION NUMBER: US/08/353,476  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bencen, Gerard H  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-353-476-24

Query Match 72.1%; Score 27.4; DB 2; Length 44;  
Best Local Similarity 83.8%; Pred. No. 0.06; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 6;

QY 2 GGGACTTTCCGCTGGGACTTTCAGGGGACTTTC 38  
DB 7 GGGACTTTCGCTGGGACTTTCGGGGAGGTGGCC 43

RESULT 38  
US-08-353-476-25  
; Sequence 25, Application US/08353476  
; Patent No. 5871902  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A  
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
; NUMBER OF SEQUENCES: 117  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; APPLICATION NUMBER: US/08/353,476  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bencen, Gerard H  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: (904) 372-5800  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-353-476-25

Query Match 71.6%; Score 27.2; DB 2; Length 44;  
Best Local Similarity 90.6%; Pred. No. 0.072; Indels 0; Gaps 0;  
Matches 29; Conservative 0; Mismatches 3;

QY 2 GGGACTTTCGCTGGGACTTTCAGGGGAC 33  
DB 7 GGGACTTTCGCTGGGACTTTCGGGGAGGC 38

RESULT 39  
US-09-535-066F-9  
; Sequence 9, Application US/09535066F  
; Patent No. 6800291  
; GENERAL INFORMATION:  
; APPLICANT: ZENGEN, INC.  
; APPLICANT: Lipton, M.J.  
; APPLICANT: Catania, A.P.  
; TITLE OF INVENTION: A LYS-PRO-VAL DIMER, FORMULATIONS AND APPLICATIONS  
; FILE REFERENCE: 54275.8005.US00  
; CURRENT APPLICATION NUMBER: US/09/535,066F  
; CURRENT FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: US 60/126,233  
; PRIOR FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide probes for NF-kB.  
US-09-535-066F-9

Query Match 69.5%; Score 26.4; DB 3; Length 35;  
Best Local Similarity 96.4%; Pred. No. 0.14; Indels 0; Gaps 0;  
Matches 27; Conservative 0; Mismatches 1;

QY 1 GGGGACTTTCGCTGGGGACTTTCAGG 28  
DB 8 GGGGACTTTCGCTGGGGACTTTCATG 35

RESULT 40  
US-09-533-341-5  
; Sequence 5, Application US/09533341  
; Patent No. 6803044  
; GENERAL INFORMATION:  
; APPLICANT: Zengen, Inc.  
; APPLICANT: Lipton, James M.  
; APPLICANT: Catania, Anna P.  
; TITLE OF INVENTION: ANTIMICROBIAL AND ANTI-INFLAMMATORY PEPTIDES FOR USE IN HUMAN  
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS  
; FILE REFERENCE: 54275.8004.US00  
; CURRENT APPLICATION NUMBER: US/09/533,341  
; CURRENT FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: US 60/126,233  
; PRIOR FILING DATE: 1999-03-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide

## US-09-533-341-5

Query Match 69.5%; Score 26.4; DB 3; Length 35;  
Best Local Similarity 96.4%; Pred. No. 0.14;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGGCTGGGGACTTTCCAGG 28  
|||||  
Db 8 GGGGACTTTCGGCTGGGGACTTTCCATG 35

## RESULT 41

US-09-031-629A-5  
; Sequence 5, Application US/09031629A  
; Patent No. 6617171  
; GENERAL INFORMATION:  
; APPLICANT: Faustman  
; APPLICANT: Hayaashi  
; TITLE OF INVENTION: Methods for Treating and Diagnosing Autoimmune Disease  
; FILE REFERENCE: MGH/Faustman 17633/1030  
; CURRENT APPLICATION NUMBER: US/09/031,629A  
; CURRENT FILING DATE: 1998-02-21  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Probe for  
; OTHER INFORMATION: wild-type kappa B1 sequence  
US-09-031-629A-5

Query Match 68.4%; Score 26; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGGACTTTCCAG 27  
|||||  
Db 7 GGGACTTTCGGCTGGGGACTTTCCAG 32

## RESULT 42

US-09-258-682-1  
; Sequence 1, Application US/09258682  
; Patent No. 6773705  
; GENERAL INFORMATION:  
; APPLICANT: Faustman et al., Denise L.  
; TITLE OF INVENTION: Methods for diagnosing and treating autoimmune disease  
; FILE REFERENCE: 17633-1120 Kathleen M. Williams  
; CURRENT APPLICATION NUMBER: US/09/258,682  
; CURRENT FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-258-682-1

Query Match 68.4%; Score 26; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGGACTTTCCAG 27  
|||||  
Db 7 GGGACTTTCGGCTGGGGACTTTCCAG 32

## RESULT 43

US-08-484-397A-25  
; Sequence 25, Application US/08484397A  
; Patent No. 5869055

## GENERAL INFORMATION:

; APPLICANT: Juan, Shao-Chieh  
; APPLICANT: Lichenstein, Henri S.  
; APPLICANT: Wright, Samuel D.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: AMGEN INC  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: CA  
; COUNTRY: US  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,397A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Curry, Daniel R.  
; REGISTRATION NUMBER: 32,727  
; REFERENCE/DOCKET NUMBER: A-324A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 805/447-1000  
; TELEFAX: 805/447-1090  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-484-397A-25

Query Match 68.4%; Score 26; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGGCTGGGGACTTTCCAG 27  
|||||  
Db 7 GGGACTTTCGGCTGGGGACTTTCCAG 32

## RESULT 44

US-08-484-397A-26/c  
; Sequence 26, Application US/08484397A  
; Patent No. 5869055  
; GENERAL INFORMATION:  
; APPLICANT: Juan, Shao-Chieh  
; APPLICANT: Lichenstein, Henri S.  
; APPLICANT: Wright, Samuel D.  
; TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: AMGEN INC  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: CA  
; COUNTRY: US  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,397A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424



```
; ATTORNEY/AGENT INFORMATION:
; NAME: Curry, Daniel R.
; REGISTRATION NUMBER: 32,727
; REFERENCE/DOCKET NUMBER: A-324A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/447-1000
; TELEFAX: 805/447-1090
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-484-397A-26

Query Match 68.4%; Score 26; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGACTTTCAG 27
Db 31 GGGACTTTCGGCTGGGACTTTCAG 6

RESULT 45
US-09-535-066F-10/c
; Sequence 10, Application US/09535066F
; Patent No. 6800291
; GENERAL INFORMATION:
; APPLICANT: ZENGEN, INC.
; APPLICANT: Lipton, M.J.
; APPLICANT: Catania, A.P.
; TITLE OF INVENTION: A LYS-PRO-VAL DIMER, FORMULATIONS AND APPLICATIONS
; FILE REFERENCE: 54275.8005.US00
; CURRENT APPLICATION NUMBER: US/09/535,066F
; CURRENT FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 60/126,233
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probes for NF-kB.
US-09-535-066F-10

Query Match 67.9%; Score 25.8; DB 3; Length 35;
Best Local Similarity 93.1%; Pred. No. 0.25;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGACTTTCGGCTGGGACTTTCAGG 29
Db 32 GGGAGTTTCGGCTGGGACTTTCARG 4

RESULT 46
US-08-353-476-30
; Sequence 30, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; REFERENCE/DOCKET NUMBER: 35,746
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
```

```
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-353-476-30

Query Match 66.3%; Score 25.2; DB 2; Length 48;
Best Local Similarity 90.0%; Pred. No. 0.47;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CTTTCGCTGGGACTTTCAGGGGACTT 35
Db 1 CTTTCGCTGGGACTTTCAGGGGAGCGT 30

RESULT 47
US-08-353-476-7
; Sequence 7, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,476
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (904) 375-8100
; TELEFAX: (904) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
```

```

; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-353-476-7

Query Match          65.8%; Score 25; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCCA 26
Db 3 GGGACTTTCGCTGGGACTTTCCA 27

RESULT 48
US-09-844-915-1
; Sequence 1, Application US/09844915
; Patent No. 6936468
; GENERAL INFORMATION:
; APPLICANT: Robbins, Paul D.
; APPLICANT: Lu, Lina
; APPLICANT: Giannoukakis, Nick
; TITLE OF INVENTION: THE USE OF TOLEROGENIC DENDRITIC CELLS
; TITLE OF INVENTION: FOR ENHANCING TOLEROGENICITY IN A HOST AND METHODS FOR
; TITLE OF INVENTION: MAKING THE SAME
; FILE REFERENCE: AP32737 / 072396.0225
; CURRENT APPLICATION NUMBER: US/09/844,915
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,479
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleotide sequence
US-09-844-915-1

Query Match          63.2%; Score 24; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCC 25
Db 2 GGGACTTTCGCTGGGACTTTCC 25

RESULT 49
US-09-844-915-2/c
; Sequence 2, Application US/09844915
; Patent No. 6936468
; GENERAL INFORMATION:
; APPLICANT: Robbins, Paul D.
; APPLICANT: Lu, Lina
; APPLICANT: Giannoukakis, Nick
; TITLE OF INVENTION: THE USE OF TOLEROGENIC DENDRITIC CELLS
; TITLE OF INVENTION: FOR ENHANCING TOLEROGENICITY IN A HOST AND METHODS FOR
; TITLE OF INVENTION: MAKING THE SAME
; FILE REFERENCE: AP32737 / 072396.0225
; CURRENT APPLICATION NUMBER: US/09/844,915
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,479
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleotide sequence
US-09-844-915-2

Query Match          63.2%; Score 24; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCC 25
Db 2 GGGACTTTCGCTGGGACTTTCC 25

RESULT 50
US-08-479-852-44
; Sequence 44, Application US/08479852
; Patent No. 5712385
; GENERAL INFORMATION:
; APPLICANT: Sherrol H. McDonough, Thomas B. Ryder,
; APPLICANT: Yeasing Yang
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND PROBES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,852
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/040,745
; FILING DATE:
; APPLICATION NUMBER: U.S. Serial No. 5712385 07/550,837
; FILING DATE: 7/10/90
; APPLICATION NUMBER: U.S. Serial No. 5712385 07/379,501
; FILING DATE: 7/11/89
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 196/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-479-852-44

Query Match          63.2%; Score 24; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCC 25
Db 4 GGGACTTTCGCTGGGACTTTCC 27
```

Search completed: February 15, 2006, 21:14:22  
Job time : 89.4215 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 01:43:22 ; Search time 551.471 Seconds  
(without alignments)  
569.815 Million cell updates/sec

Title: US-09-669-187A-148

Perfect score: 38

Sequence: 1 ggggaatttcctgctgggactttccagggggactttcc 38

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 11091250

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications NA\_Main:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	38	100.0	38	3	US-09-888-326-417 Sequence 417, App
2	38	100.0	38	3	US-09-776-479-148 Sequence 148, App
3	38	100.0	38	3	US-09-776-479-148 Sequence 148, App
4	38	100.0	38	5	US-10-112-653-141 Sequence 141, App
5	38	100.0	38	5	US-10-017-995-148 Sequence 148, App
6	38	100.0	38	6	US-10-314-578-148 Sequence 148, App
7	38	100.0	38	8	US-10-831-778-148 Sequence 148, App
8	30.8	81.1	43	2	US-08-860-844-29 Sequence 29, App
9	30.8	81.1	43	6	US-10-407-543-29 Sequence 29, App
10	30.2	79.5	46	2	US-08-860-844-28 Sequence 28, App
11	30.2	79.5	46	6	US-10-407-543-28 Sequence 28, App
12	29.8	78.4	44	3	US-09-992-837-9 Sequence 9, Appli
13	29.8	78.4	44	3	US-09-999-495-9 Sequence 9, Appli
14	29.8	78.4	44	5	US-10-000-720-9 Sequence 9, Appli
15	29.8	78.4	44	6	US-10-238-647-9 Sequence 9, Appli
16	29.2	76.8	45	2	US-08-860-844-19 Sequence 19, Appl
17	29.2	76.8	45	6	US-08-860-844-23 Sequence 23, Appl
18	29.2	76.8	45	6	US-10-407-543-19 Sequence 19, Appl
19	29.2	76.8	45	6	US-10-407-543-23 Sequence 23, Appl
20	29.2	76.8	45	7	US-10-602-303-4 Sequence 4, Appli
21	29.2	76.8	45	9	US-10-925-608-1 Sequence 1, Appli
22	29.2	76.8	45	9	US-10-981-082-1 Sequence 1, Appli
23	29	76.3	46	2	US-08-860-844-20 Sequence 20, Appl

24	29	76.3	46	2	US-08-860-844-21 Sequence 21, Appl
25	29	76.3	46	2	US-08-860-844-22 Sequence 22, Appl
26	29	76.3	46	2	US-08-860-844-27 Sequence 27, Appl
27	29	76.3	46	6	US-10-407-543-20 Sequence 20, Appl
28	29	76.3	46	6	US-10-407-543-21 Sequence 21, Appl
29	29	76.3	46	6	US-10-407-543-22 Sequence 22, Appl
30	29	76.3	46	6	US-10-407-543-27 Sequence 27, Appl
31	28.4	74.7	37	6	US-08-860-844-38 Sequence 38, Appl
32	28.4	74.7	37	6	US-10-407-543-38 Sequence 38, Appl
33	28	73.7	34	8	US-10-037-341-53 Sequence 53, Appl
34	27.6	72.6	45	2	US-08-860-844-26 Sequence 26, Appl
35	27.6	72.6	45	6	US-10-407-543-26 Sequence 26, Appl
36	27.4	72.1	44	5	US-10-235-682-9 Sequence 9, Appli
37	27.4	72.1	44	6	US-08-860-844-24 Sequence 24, Appl
38	27.4	72.1	44	6	US-10-407-543-24 Sequence 24, Appl
39	27.2	71.6	44	2	US-08-860-844-25 Sequence 25, Appl
40	27.2	71.6	44	6	US-10-407-543-25 Sequence 25, Appl
41	26.4	69.5	35	5	US-10-235-682-8 Sequence 8, Appli
42	26.4	69.5	35	8	US-10-659-053-11 Sequence 11, Appl
43	26	68.4	32	3	US-09-031-629A-5 Sequence 5, Appli
44	26	68.4	32	9	US-10-775-487A-1 Sequence 1, Appli
45	25.8	67.9	35	8	US-10-659-053-12 Sequence 12, Appl
46	25.2	66.3	48	2	US-08-860-844-30 Sequence 30, Appl
47	25.2	66.3	48	6	US-10-407-543-30 Sequence 30, Appl
48	25	65.8	27	2	US-08-860-844-7 Sequence 7, Appli
49	25	65.8	27	6	US-10-407-543-7 Sequence 7, Appli
50	24	63.2	25	3	US-09-844-915-1 Sequence 1, Appli
51	24	63.2	25	3	US-09-844-915-2 Sequence 2, Appli
52	24	63.2	25	2	US-08-860-844-8 Sequence 8, Appli
53	24	63.2	27	3	US-09-766-095-44 Sequence 44, Appl
54	24	63.2	27	3	US-09-766-095-124 Sequence 124, App
55	24	63.2	27	6	US-10-244-490-17 Sequence 17, Appl
56	24	63.2	27	6	US-10-407-543-8 Sequence 8, Appli
57	24	63.2	29	3	US-09-747-552-1 Sequence 1, Appli
58	24	63.2	29	3	US-09-747-552-2 Sequence 2, Appli
59	24	63.2	29	3	US-09-887-879-12 Sequence 12, Appl
60	24	63.2	29	3	US-09-993-234-10 Sequence 10, Appl
61	24	63.2	29	3	US-09-992-964-12 Sequence 12, Appl
62	24	63.2	29	5	US-10-080-455-6 Sequence 6, Appli
63	24	63.2	29	5	US-10-052-798-4 Sequence 4, Appli
64	24	63.2	29	5	US-10-081-280-10 Sequence 10, Appl
65	24	63.2	29	5	US-10-112-793-10 Sequence 10, Appl
66	24	63.2	29	5	US-10-112-193-14 Sequence 14, Appl
67	24	63.2	29	5	US-10-207-295-4 Sequence 4, Appli
68	24	63.2	29	6	US-10-242-383-12 Sequence 12, Appl
69	24	63.2	29	6	US-10-288-917-4 Sequence 4, Appli
70	24	63.2	29	6	US-10-423-448-4 Sequence 4, Appli
71	24	63.2	29	8	US-10-713-391-6 Sequence 6, Appli
72	23	60.5	23	3	US-09-888-938-3 Sequence 3, Appli
73	23	60.5	23	3	US-09-852-238A-3 Sequence 3, Appli
74	22	57.9	22	8	US-10-862-363-60 Sequence 60, Appl
75	21.4	56.3	29	6	US-10-383-773-1 Sequence 1, Appli
76	21.4	56.3	29	9	US-10-981-082-2 Sequence 2, Appli
77	20.2	53.2	31	7	US-10-673-882-3 Sequence 3, Appli
78	20.2	53.2	31	9	US-10-926-749-3 Sequence 3, Appli
79	19.8	52.1	26	2	US-08-860-844-16 Sequence 16, Appl
80	19.8	52.1	26	6	US-10-407-543-16 Sequence 16, Appl
81	19.2	50.5	26	2	US-08-860-844-9 Sequence 9, Appli
82	19.2	50.5	26	2	US-08-860-844-15 Sequence 15, Appl
83	19.2	50.5	26	6	US-10-407-543-9 Sequence 9, Appli
84	19.2	50.5	26	6	US-10-407-543-15 Sequence 15, Appl
85	19	50.0	19	6	US-10-225-023-556 Sequence 556, App
86	19	50.0	19	6	US-10-225-023-576 Sequence 576, App
87	19	50.0	19	6	US-10-225-023-606 Sequence 606, App
88	19	50.0	19	6	US-10-225-023-617 Sequence 617, App
89	19	50.0	19	6	US-10-225-023-622 Sequence 622, App
90	19	50.0	19	6	US-10-225-023-661 Sequence 661, App
91	19	50.0	19	6	US-10-225-023-689 Sequence 689, App
92	19	50.0	19	6	US-10-225-023-1294 Sequence 1294, Ap
93	19	50.0	19	6	US-10-225-023-1314 Sequence 1314, Ap
94	19	50.0	19	6	US-10-225-023-1344 Sequence 1344, Ap
95	19	50.0	19	6	US-10-225-023-1355 Sequence 1355, Ap
96	19	50.0	19	6	US-10-225-023-1360 Sequence 1360, Ap

C 97	19	50.0	19	50.0	19	6	US-10-225-023-1399	Sequence 1399, Ap	170	15.4	40.5	25	7	US-10-719-956-467968	Sequence 467968,
C 98	19	50.0	19	50.0	19	6	US-10-225-023-1427	Sequence 1427, Ap	171	15.4	40.5	25	8	US-10-719-900-424043	Sequence 424043,
C 99	19	50.0	19	50.0	19	6	US-10-923-473-556	Sequence 556, App	C 172	15.4	40.5	25	8	US-10-719-900-877620	Sequence 877620,
100	19	50.0	19	50.0	19	9	US-10-923-473-576	Sequence 576, App	C 173	15.4	40.5	25	8	US-10-719-900-967003	Sequence 967003,
101	19	50.0	19	50.0	19	9	US-10-923-473-606	Sequence 606, App	C 174	15.4	40.5	25	9	US-10-809-189-74122	Sequence 74122, A
102	19	50.0	19	50.0	19	9	US-10-923-473-617	Sequence 617, App	C 175	15.4	40.5	25	9	US-10-809-189-110222	Sequence 110222,
103	19	50.0	19	50.0	19	9	US-10-923-473-622	Sequence 622, App	C 176	15.4	40.5	25	9	US-10-661-378-4	Sequence 4, Appli
104	19	50.0	19	50.0	19	9	US-10-923-473-661	Sequence 661, App	177	15.4	40.5	25	10	US-11-036-317-107187	Sequence 107187,
105	19	50.0	19	50.0	19	9	US-10-923-473-689	Sequence 689, App	178	15.4	40.5	25	10	US-11-036-317-330597	Sequence 330597,
C 106	19	50.0	19	50.0	19	9	US-10-923-473-1294	Sequence 1294, Ap	C 179	15.4	40.5	25	10	US-11-060-756-279032	Sequence 279032,
C 107	19	50.0	19	50.0	19	9	US-10-923-473-1344	Sequence 1314, Ap	C 180	15.2	40.0	25	7	US-10-681-773-62807	Sequence 62807, A
C 108	19	50.0	19	50.0	19	9	US-10-923-473-1344	Sequence 1344, Ap	C 181	15.2	40.0	25	7	US-10-681-773-62809	Sequence 62809, A
C 109	19	50.0	19	50.0	19	9	US-10-923-473-1355	Sequence 1355, Ap	C 182	15.2	40.0	25	7	US-10-681-773-114771	Sequence 114771,
C 110	19	50.0	19	50.0	19	9	US-10-923-473-1360	Sequence 1360, Ap	C 183	15.2	40.0	25	8	US-10-681-773-114772	Sequence 114772,
C 111	19	50.0	19	50.0	19	9	US-10-923-473-1399	Sequence 1399, Ap	C 184	15.2	40.0	25	8	US-10-719-900-147015	Sequence 147015,
C 112	19	50.0	19	50.0	19	9	US-10-923-473-1427	Sequence 1427, Ap	C 185	15.2	40.0	25	8	US-10-719-900-749313	Sequence 749313,
C 113	19	50.0	19	50.0	19	9	US-10-923-473-1427	Sequence 1427, Ap	C 186	15.2	40.0	25	8	US-10-719-900-834294	Sequence 834294,
C 114	19	50.0	19	50.0	19	9	US-10-923-473-1427	Sequence 1427, Ap	C 187	15.2	40.0	25	10	US-11-036-317-100981	Sequence 100981,
C 115	19	50.0	19	50.0	19	9	US-10-923-473-1427	Sequence 1427, Ap	C 188	15.2	40.0	32	7	US-10-296-085A-72	Sequence 72, Appl
C 116	19	50.0	19	50.0	19	9	US-10-923-473-1427	Sequence 1427, Ap	C 189	15.2	40.0	48	3	US-09-877-478-5923	Sequence 5923, Ap
C 117	17.6	46.3	26	6	US-10-407-543-10	Sequence 10, Appl	194	15	C 190	15.2	40.0	48	7	US-10-342-903-5923	Sequence 5923, Ap
C 118	17.6	46.3	26	6	US-10-407-543-10	Sequence 10, Appl	194	15	C 191	15.2	40.0	48	7	US-10-669-841-10814	Sequence 10814, A
C 119	17.6	46.3	26	6	US-10-407-543-10	Sequence 10, Appl	194	15	C 192	15.2	40.0	50	6	US-10-131-827-5964	Sequence 5964, Ap
C 120	17.6	46.3	26	6	US-10-407-543-10	Sequence 10, Appl	194	15	C 193	15	39.5	15	2	US-08-860-844-4	Sequence 4, Appli
C 121	17.6	46.3	26	6	US-10-407-543-10	Sequence 10, Appl	194	15	C 194	15	39.5	15	6	US-10-407-543-4	Sequence 4, Appli
C 122	17.6	46.3	26	6	US-10-407-543-10	Sequence 10, Appl	194	15	C 195	15	39.5	15	5	US-10-098-263B-89477	Sequence 89477, A
C 123	17.2	45.3	26	6	US-10-407-543-10	Sequence 10, Appl	194	15	C 196	15	39.5	25	5	US-10-098-263B-89478	Sequence 89478, A
C 124	16.8	44.2	26	6	US-10-407-543-10	Sequence 10, Appl	194	15	C 197	15	39.5	25	7	US-10-719-956-18936	Sequence 18936, A
C 125	16.8	44.2	26	6	US-10-407-543-10	Sequence 10, Appl	194	15	C 198	15	39.5	25	7	US-10-719-956-111676	Sequence 111676,
C 126	16.8	44.2	26	6	US-10-407-543-10	Sequence 10, Appl	194	15	C 199	15	39.5	25	7	US-10-719-956-154856	Sequence 154856,
C 127	16.8	44.2	26	6	US-10-407-543-10	Sequence 10, Appl	194	15	C 200	15	39.5	25	7	US-10-719-956-162253	Sequence 162253,
C 128	16.8	44.2	26	6	US-10-407-543-10	Sequence 10, Appl	194	15	C 201	15	39.5	25	7	US-10-719-956-162255	Sequence 162255,
C 129	16.6	43.7	25	8	US-10-942-561A-18	Sequence 18, Appl	202	15	C 202	15	39.5	25	7	US-10-719-956-395203	Sequence 395203,
C 130	16.6	43.7	25	8	US-10-942-561A-18	Sequence 18, Appl	202	15	C 203	15	39.5	25	8	US-10-719-900-410035	Sequence 410035,
C 131	16.6	43.7	25	8	US-10-942-561A-18	Sequence 18, Appl	202	15	C 204	15	39.5	25	8	US-10-719-900-427917	Sequence 427917,
C 132	16.6	43.7	25	8	US-10-942-561A-18	Sequence 18, Appl	202	15	C 205	15	39.5	25	8	US-10-719-900-595944	Sequence 595944,
C 133	16.6	43.7	25	8	US-10-942-561A-18	Sequence 18, Appl	202	15	C 206	15	39.5	25	8	US-10-719-900-687512	Sequence 687512,
C 134	16.4	43.2	41	7	US-10-035-833A-410	Sequence 410, App	207	15	C 207	15	39.5	25	10	US-11-036-317-98328	Sequence 98328, A
C 135	16.4	43.2	41	7	US-10-035-833A-410	Sequence 410, App	207	15	C 208	15	39.5	25	10	US-11-036-317-98328	Sequence 98328, A
C 136	16.2	42.6	25	7	US-10-681-773-42889	Sequence 42889, A	209	15	C 209	15	39.5	25	10	US-11-036-317-167249	Sequence 167249,
C 137	16.2	42.6	25	7	US-10-681-773-42890	Sequence 42890, A	210	15	C 210	15	39.5	25	10	US-11-036-317-219733	Sequence 219733,
C 138	16.2	42.6	25	7	US-10-681-773-42890	Sequence 42890, A	210	15	C 211	15	39.5	25	10	US-11-036-317-345805	Sequence 345805,
C 139	16.2	42.6	25	7	US-10-681-773-42890	Sequence 42890, A	210	15	C 212	15	39.5	25	10	US-11-036-317-354890	Sequence 354890,
C 140	16.2	42.6	25	7	US-10-681-773-42890	Sequence 42890, A	210	15	C 213	15	39.5	25	10	US-11-036-317-356160	Sequence 356160,
C 141	16.2	42.6	25	7	US-10-681-773-42890	Sequence 42890, A	210	15	C 214	15	39.5	25	10	US-11-036-317-426282	Sequence 426282,
C 142	16.2	42.6	25	7	US-10-681-773-42890	Sequence 42890, A	210	15	C 215	15	39.5	25	10	US-11-036-317-426282	Sequence 426282,
C 143	16.2	42.6	25	7	US-10-681-773-42890	Sequence 42890, A	210	15	C 216	15	39.5	25	10	US-11-036-317-474393	Sequence 474393,
C 144	16.2	42.6	25	7	US-10-681-773-42890	Sequence 42890, A	210	15	C 217	15	39.5	25	10	US-11-036-317-705651	Sequence 705651,
C 145	16.2	42.6	25	7	US-10-681-773-42890	Sequence 42890, A	210	15	C 218	15	39.5	25	10	US-11-036-317-777918	Sequence 777918,
C 146	16.2	42.6	25	7	US-10-681-773-42890	Sequence 42890, A	210	15	C 219	15	39.5	25	10	US-11-036-317-777918	Sequence 777918,
C 147	16.2	42.6	25	7	US-10-681-773-42890	Sequence 42890, A	210	15	C 220	15	39.5	25	10	US-11-060-756-274270	Sequence 274270,
C 148	15.8	41.6	21	8	US-10-751-736-10156	Sequence 10156, A	221	15	C 221	15	39.5	31	3	US-09-801-274-11427	Sequence 1127, Ap
C 149	15.8	41.6	21	8	US-10-751-736-10156	Sequence 10156, A	221	15	C 222	15	39.5	31	3	US-10-187-975-130	Sequence 130, App
C 150	15.8	41.6	21	8	US-10-751-736-10156	Sequence 10156, A	221	15	C 223	15	39.5	31	3	US-10-214-417A-75	Sequence 75, Appl
C 151	15.8	41.6	21	8	US-10-751-736-10156	Sequence 10156, A	221	15	C 224	15	39.5	31	3	US-10-214-417A-75	Sequence 75, Appl
C 152	15.8	41.6	21	8	US-10-751-736-10156	Sequence 10156, A	221	15	C 225	15	39.5	31	3	US-10-214-417A-75	Sequence 75, Appl
C 153	15.6	41.1	25	5	US-10-098-263B-53836	Sequence 53836, A	226	14.8	C 226	14.8	38.9	25	7	US-10-681-773-37365	Sequence 37365, Ap
C 154	15.6	41.1	25	7	US-10-719-956-287898	Sequence 287898, A	227	14.8	C 227	14.8	38.9	25	7	US-10-681-773-40488	Sequence 40488, A
C 155	15.6	41.1	25	7	US-10-719-956-287898	Sequence 287898, A	227	14.8	C 228	14.8	38.9	25	7	US-10-681-773-46450	Sequence 46450, A
C 156	15.6	41.1	25	7	US-10-719-956-287898	Sequence 287898, A	227	14.8	C 229	14.8	38.9	25	7	US-10-719-956-46281	Sequence 46281, A
C 157	15.6	41.1	25	7	US-10-719-956-287898	Sequence 287898, A	227	14.8	C 230	14.8	38.9	25	7	US-10-719-956-46281	Sequence 46281, A
C 158	15.6	41.1	25	7	US-10-719-956-287898	Sequence 287898, A	227	14.8	C 231	14.8	38.9	25	7	US-10-719-956-46281	Sequence 46281, A
C 159	15.6	41.1	25	7	US-10-719-956-287898	Sequence 287898, A	227	14.8	C 232	14.8	38.9	25	7	US-10-719-956-46281	Sequence 46281, A
C 160	15.6	41.1	25	7	US-10-719-956-287898	Sequence 287898, A	227	14.8	C 233	14.8	38.9	25	7	US-10-719-956-46281	Sequence 46281, A
C 161	15.4	40.5	21	8	US-10-751-736-10039	Sequence 10039, A	234	14.8	C 234	14.8	38.9	34	6	US-10-292-896-85	Sequence 190043,
C 162	16.2	44.2	26	6	US-10-407-543-10	Sequence 10, Appl	235	14.8	C 235	14.8	38.9	34	6	US-10-292-896-85	Sequence 85, Appl
C 163	15.4	40.5	21	8	US-10-751-736-10040	Sequence 10040, A	234	14.8	C 236	14.8	38.9	34	6	US-10-292-896-85	Sequence 85, Appl
C 164	15.4	40.5	21	8	US-10-751-736-10040	Sequence 10040, A	234	14.8	C 237	14.8	38.9	34	6	US-10-292-896-85	Sequence 85, Appl
C 165	15.4	40.5	21	8	US-10-751-736-10040	Sequence 10040, A	234	14.8	C 238	14.8	38.9	34	6	US-10-292-896-85	Sequence 85, Appl
C 166	15.4	40.5	21	8	US-10-751-736-10040	Sequence 10040, A	234	14.8	C 239	14.8	38.9	34	6	US-10-292-896-85	Sequence 85, Appl
C 167	15.4	40.5	21	8	US-10-751-736-10040	Sequence 10040, A	234	14.8	C 240	14.6	38.4	24	3	US-10-940-185-403	Sequence 182, App
C 168	15.4	40.5	21	8	US-10-751-736-10040	Sequence 10040, A	234	14.8	C 241	14.6	38.4	24	3	US-10-940-185-403	Sequence 403, App
C 169	15.4	40.5	21	8	US-10-751-736-										



```
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-148

Query Match      100.0%; Score 38; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38
Db 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38

RESULT 4
US-10-112-653-141
; Sequence 141, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060 (AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 141
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-141

Query Match      100.0%; Score 38; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38
Db 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38

RESULT 5
US-10-017-995-148
; Sequence 148, Application US/10017995
; Publication No. US2003005014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; FILE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-148

Query Match      100.0%; Score 38; DB 5; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38
Db 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38

RESULT 6
US-10-314-578-148
; Sequence 148, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-148

Query Match      100.0%; Score 38; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38
Db 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTTCC 38

RESULT 7
US-10-831-778-148
; Sequence 148, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fourton, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 148
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-148
```



## US-10-831-778-148

Query Match 100.0%; Score 38; DB 8; Length 38;  
Best Local Similarity 100.0%; Pred. No. 2.7e-05;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGGACTTTCAGGGGGACTTCC 38  
|||||  
Db 1 GGGGACTTCCGCTGGGGACTTTCAGGGGGACTTCC 38

## RESULT 8

US-08-860-844-29  
; Sequence 29, Application US/08860844  
; Publication No. US20030104361A1  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,844  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/353,476  
; FILING DATE: 09-DEC-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 43 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

US-08-860-844-29

Query Match 81.1%; Score 30.8; DB 2; Length 43;  
Best Local Similarity 94.1%; Pred. No. 0.019;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGGACTTTCAGGGGGACT 34  
|||||  
Db 6 GGGGACTTCCGCTGGGGACTTTCAGGGGGACT 39

## RESULT 9

US-10-407-543-29  
; Sequence 29, Application US/10407543  
; Publication No. US20030175789A1  
; GENERAL INFORMATION:

APPLICANT: Weininger, Susan  
Weininger, Arthur M  
TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
SPECIFIC SEQUENCE COMPOSITION  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st St., Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/407,543  
FILING DATE: 03-Apr-2003  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,844  
FILING DATE: 09-JUN-1997  
APPLICATION NUMBER: 08/353,476  
FILING DATE: 09-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-10-407-543-29  
Query Match 81.1%; Score 30.8; DB 6; Length 43;  
Best Local Similarity 94.1%; Pred. No. 0.019;  
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGGACTTTCAGGGGGACT 34  
|||||  
Db 6 GGGGACTTCCGCTGGGGACTTTCAGGGGGACT 39

RESULT 10  
US-08-860-844-28  
; Sequence 28, Application US/08860844  
; Publication No. US20030104361A1  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

US-08-860-844-29

```
/
/
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/860,844
/ FILING DATE: 09-JUN-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/353,476
/ FILING DATE: 09-DEC-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 35,746
/ REFERENCE/DOCKET NUMBER: GP-100C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 28:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ US-08-860-844-28

Query Match 79.5%; Score 30.2; DB 2; Length 46;
Best Local Similarity 91.4%; Pred. No. 0.032;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGGACTTCCAGGGGGACTT 35
| | | | | | | | | | | | | | | | | | | |
Db 6 GGGGACTTCCGCTGGGGACTTCCAGGGGGGGT 40
| | | | | | | | | | | | | | | | | | | |

RESULT 11
US-10-407-543-28
/ Sequence 28, Application US/10407543
/ Publication No. US20030175789A1
/ GENERAL INFORMATION:
/ APPLICANT: Weininger, Susan
/ TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
/ SPECIFIC SEQUENCE COMPOSITION
/ NUMBER OF SEQUENCES: 118
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st St., Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/407,543
/ FILING DATE: 03-APR-2003
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/860,844
/ FILING DATE: 09-JUN-1997
/ APPLICATION NUMBER: 08/353,476
/ FILING DATE: 09-DEC-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 35,746
/ REFERENCE/DOCKET NUMBER: GP-100C1
/

/
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 28:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 46 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ US-10-407-543-28

Query Match 79.5%; Score 30.2; DB 6; Length 46;
Best Local Similarity 91.4%; Pred. No. 0.032;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGGACTTCCAGGGGGACTT 35
| | | | | | | | | | | | | | | | | | | |
Db 6 GGGGACTTCCGCTGGGGACTTCCAGGGGGGGT 40
| | | | | | | | | | | | | | | | | | | |

RESULT 12
US-09-992-837-9
/ Sequence 9, Application US/09992837
/ Publication No. US20030039705A1
/ GENERAL INFORMATION:
/ APPLICANT: ARNTZEN, CHARLES J.
/ APPLICANT: BLAKE, MARY E.
/ APPLICANT: GUTTERMAN, JORDAN U.
/ APPLICANT: HOFFMANN, JOSEPH J.
/ APPLICANT: BAILEY, DAVID T.
/ APPLICANT: JAYATILAKE, GAMINI S.
/ TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF
/ FILE REFERENCE: CLFR:006
/ CURRENT APPLICATION NUMBER: US/09/992,837
/ CURRENT FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/314,691
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-19
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/085,997
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 9
/ LENGTH: 44
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Primer
/ US-09-992-837-9

Query Match 78.4%; Score 29.8; DB 3; Length 44;
Best Local Similarity 93.9%; Pred. No. 0.046;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGGACTTCCAGGGGGACT 34
| | | | | | | | | | | | | | | | | | | |
Db 10 GGGACTTCCGCTGGGGACTTCCAGGGGGGCT 42
| | | | | | | | | | | | | | | | | | | |

RESULT 13
US-09-999-495-9
/ Sequence 9, Application US/09999495
/ Publication No. US20030054052A1
/ GENERAL INFORMATION:
/ APPLICANT: ARNTZEN, CHARLES J.
/ APPLICANT: BLAKE, MARY E.
/ APPLICANT: GUTTERMAN, JORDAN U.
/ APPLICANT: HOFFMANN, JOSEPH J.
/ APPLICANT: BAILEY, DAVID T.
```

APPLICANT: JAYATILAKE, GAMINI S.  
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: CLFR:006  
; CURRENT APPLICATION NUMBER: US/09/999,495  
; CURRENT FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: 09/314,691  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: 60/099,066  
; PRIOR FILING DATE: 1998-09-03  
; PRIOR APPLICATION NUMBER: 60/085,997  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
US-09-999-495-9

Query Match 78.4%; Score 29.8; DB 3; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.046; 2; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCAGGGGACT 34  
|||||  
Db 10 GGGACTTTCGCTGGGACTTTCAGGGGACT 42  
|||||

RESULT 14  
US-10-000-720-9  
; Sequence 9, Application US/10000720  
; Publication No. US20030031738A1  
; GENERAL INFORMATION:  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: BLAKE, MARY E.  
; APPLICANT: GUTTERMAN, JORDAN U.  
; APPLICANT: HOFFMANN, JOSEPH J.  
; APPLICANT: BAILEY, DAVID T.  
; APPLICANT: JAYATILAKE, GAMINI S.  
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: CLFR:006  
; CURRENT APPLICATION NUMBER: US/10/000,720  
; CURRENT FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/314,691  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,066  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-03  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/085,997  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
US-10-000-720-9

Query Match 78.4%; Score 29.8; DB 5; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.046; 2; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCAGGGGACT 34  
|||||  
Db 10 GGGACTTTCGCTGGGACTTTCAGGGGACT 42  
|||||

RESULT 15

US-10-238-647-9  
; Sequence 9, Application US/10238647  
; Publication No. US20030203049A1  
; GENERAL INFORMATION:  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: BLAKE, MARY E.  
; APPLICANT: GUTTERMAN, JORDAN U.  
; APPLICANT: HOFFMANN, JOSEPH J.  
; APPLICANT: BAILEY, DAVID T.  
; APPLICANT: JAYATILAKE, GAMINI S.  
; TITLE OF INVENTION: TRITERPENE COMPOSITIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: CLFR:006  
; CURRENT APPLICATION NUMBER: US/10/238,647  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: US/09/314,691  
; PRIOR FILING DATE: 1999-05-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 44  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
US-10-238-647-9

Query Match 78.4%; Score 29.8; DB 6; Length 44;  
Best Local Similarity 93.9%; Pred. No. 0.046; 2; Indels 0; Gaps 0;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCAGGGGACT 34  
|||||  
Db 10 GGGACTTTCGCTGGGACTTTCAGGGGACT 42  
|||||

RESULT 16  
US-08-860-844-19  
; Sequence 19, Application US/08860844  
; Publication No. US20030104361A1  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,844  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/353,476  
; FILING DATE: 09-DEC-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 19;  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 45 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-860-844-19

Query Match 76.8%; Score 29.2; DB 2; Length 45;  
 Best Local Similarity 91.2%; Pred. No. 0.08;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 35  
 DB 7 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 40

RESULT 17  
 US-08-860-844-23  
 ; Sequence 23, Application US/08860844  
 ; Publication No. US20030104361A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weininger, Susan M  
 ; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 ; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
 ; NUMBER OF SEQUENCES: 118  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik & Saliwanchik  
 ; STREET: 2421 N.W. 41st St., Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/08/860,844  
 ; FILING DATE: 09-JUN-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/353,476  
 ; FILING DATE: 09-DEC-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 35,746  
 ; REFERENCE/DOCKET NUMBER: GP-100C1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (352) 375-8100  
 ; TELEFAX: (352) 372-5800  
 ; INFORMATION FOR SEQ ID NO: 23:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 45 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; US-08-860-844-23

Query Match 76.8%; Score 29.2; DB 2; Length 45;  
 Best Local Similarity 91.2%; Pred. No. 0.08;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 35  
 DB 7 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 40

RESULT 18  
 US-10-407-543-19  
 ; Sequence 19, Application US/10407543  
 ; Publication No. US20030175789A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weininger, Susan M  
 ; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 ; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
 ; NUMBER OF SEQUENCES: 118  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik & Saliwanchik  
 ; STREET: 2421 N.W. 41st St., Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/10/407,543  
 ; FILING DATE: 03-APR-2003  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/860,844  
 ; FILING DATE: 09-JUN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 35,746  
 ; REFERENCE/DOCKET NUMBER: GP-100C1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (352) 375-8100  
 ; TELEFAX: (352) 372-5800  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 45 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; US-10-407-543-19

Query Match 76.8%; Score 29.2; DB 2; Length 45;  
 Best Local Similarity 91.2%; Pred. No. 0.08;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 35  
 DB 7 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 40

Db 7 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 40

RESULT 18  
 US-10-407-543-19  
 ; Sequence 19, Application US/10407543  
 ; Publication No. US20030175789A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weininger, Susan M  
 ; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 ; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
 ; NUMBER OF SEQUENCES: 118  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik & Saliwanchik  
 ; STREET: 2421 N.W. 41st St., Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/10/407,543  
 ; FILING DATE: 03-APR-2003  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/860,844  
 ; FILING DATE: 09-JUN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 35,746  
 ; REFERENCE/DOCKET NUMBER: GP-100C1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (352) 375-8100  
 ; TELEFAX: (352) 372-5800  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 45 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; US-10-407-543-19

QY 2 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 35  
 DB 7 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 40

RESULT 19  
 US-10-407-543-23  
 ; Sequence 23, Application US/10407543  
 ; Publication No. US20030175789A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weininger, Susan M  
 ; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 ; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
 ; NUMBER OF SEQUENCES: 118  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik & Saliwanchik  
 ; STREET: 2421 N.W. 41st St., Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/10/407,543  
 ; FILING DATE: 03-APR-2003  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/860,844  
 ; FILING DATE: 09-JUN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 35,746  
 ; REFERENCE/DOCKET NUMBER: GP-100C1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (352) 375-8100  
 ; TELEFAX: (352) 372-5800  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 45 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; US-10-407-543-19

Query Match 76.8%; Score 29.2; DB 6; Length 45;  
 Best Local Similarity 91.2%; Pred. No. 0.08;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 35  
 DB 7 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 40

RESULT 19  
 US-10-407-543-23  
 ; Sequence 23, Application US/10407543  
 ; Publication No. US20030175789A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weininger, Susan M  
 ; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 ; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
 ; NUMBER OF SEQUENCES: 118  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik & Saliwanchik  
 ; STREET: 2421 N.W. 41st St., Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/10/407,543  
 ; FILING DATE: 03-APR-2003  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/860,844  
 ; FILING DATE: 09-JUN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 35,746  
 ; REFERENCE/DOCKET NUMBER: GP-100C1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (352) 375-8100  
 ; TELEFAX: (352) 372-5800  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 45 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; US-10-407-543-23

QY 2 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 35  
 DB 7 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 40



```
RESULT 23
US-08-860-844-20
; Sequence 20, Application US/08860844
; Publication No. US20030104361A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-860-844-20

Query Match 76.3%; Score 29; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACTTTCACAGGG 30
Db 7 GGGACTTTCGCTGGGGACTTTCACAGGG 35

RESULT 24
US-08-860-844-21
; Sequence 21, Application US/08860844
; Publication No. US20030104361A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-860-844-20

Query Match 76.3%; Score 29; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACTTTCACAGGG 30
Db 7 GGGACTTTCGCTGGGGACTTTCACAGGG 35

RESULT 25
US-08-860-844-22
; Sequence 22, Application US/08860844
; Publication No. US20030104361A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
```

```
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-860-844-21

Query Match 76.3%; Score 29; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACTTTCACAGGG 30
Db 7 GGGACTTTCGCTGGGGACTTTCACAGGG 35

RESULT 25
US-08-860-844-22
; Sequence 22, Application US/08860844
; Publication No. US20030104361A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
```

REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-860-844-22

Query Match 76.3%; Score 29; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.096;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGCTGGGACTTTCAGGG 30  
Db 7 GGGACTTTCGCTGGGACTTTCAGGG 35

## RESULT 26

US-08-860-844-27  
Sequence 27, Application US/08860844  
Publication No. US20030104361A1  
GENERAL INFORMATION:  
APPLICANT: Weininger, Susan  
ADDRESS: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st St., Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,844  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/353,476  
FILING DATE: 09-DEC-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-860-844-27

Query Match 76.3%; Score 29; DB 2; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.096;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 GGGACTTTCGCTGGGACTTTCAGGG 30  
Db 7 GGGACTTTCGCTGGGACTTTCAGGG 35

## RESULT 27

US-10-407-543-20  
Sequence 20, Application US/10407543  
Publication No. US20030175789A1  
GENERAL INFORMATION:  
APPLICANT: Weininger, Susan  
ADDRESS: Saliwanchik & Saliwanchik  
STREET: 2421 N.W. 41st St., Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: USA  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/407,543  
FILING DATE: 03-APR-2003  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,844  
FILING DATE: 09-JUN-1997  
APPLICATION NUMBER: 08/353,476  
FILING DATE: 09-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-10-407-543-20

Query Match 76.3%; Score 29; DB 6; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.096;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGCTGGGACTTTCAGGG 30  
Db 7 GGGACTTTCGCTGGGACTTTCAGGG 35

## RESULT 28

US-10-407-543-21  
Sequence 21, Application US/10407543  
Publication No. US20030175789A1  
GENERAL INFORMATION:





; MOLECULE I  
 ; HYPOTHETICA  
 ; ANTI-SENSE:  
 US-08-860-844-38

GENERAL INFORMATION:  
 APPLICANT: David Baltimore et al.  
 TITLE OF INVENTION: NUCLEAR FACTORS ASSOCIATED WITH TRANSCRIPTIONAL REGULATION  
 FILE REFERENCE: APBI-POS-035  
 CURRENT APPLICATION NUMBER: US/10/037,341  
 CURRENT FILING DATE: 2002-01-04  
 PRIOR APPLICATION NUMBER: 08/464364  
 PRIOR FILING DATE: 1995-06-05  
 NUMBER OF SEQ ID NOS: 59  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 53  
 TYPE: DNA  
 ORGANISM: HIV  
 US-10-037-341-53

Query Match 73.7%; Score 28; DB 8; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;  
 Matches 28; Conservative 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGG 29  
 Db 6 GGGACTTTCGGCTGGGACTTTCAGGG 33

RESULT 34  
 US-08-860-844-26  
 Sequence 26, Application US/08860844  
 Publication No. US20030104361A1  
 GENERAL INFORMATION:  
 APPLICANT: Weininger, Arthur M  
 TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
 NUMBER OF SEQUENCES: 118  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Saliwanchik & Saliwanchik  
 STREET: 2421 N.W. 41st St., Suite A-1  
 CITY: Gainesville  
 STATE: Florida  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION NUMBER: US/08/860,844  
 FILING DATE: 09-JUN-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/353,476  
 FILING DATE: 09-DEC-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: GP-100C1  
 REFERENCE/DOCKET NUMBER:  
 TELEPHONE: (352) 375-8100  
 TELEFAX: (352) 372-5800  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 45 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: cdNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-860-844-26

Query Match 72.6%; Score 27.6; DB 2; Length 45;  
 Best Local Similarity 88.2%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;  
 Matches 30; Conservative 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGACTT 35  
 Db 7 GGGACTTTCGGCTGGGACTTTCAGAGAGCGCT 40

RESULT 35  
 US-10-407-543-26  
 Sequence 26, Application US/10407543  
 Publication No. US20030175789A1  
 GENERAL INFORMATION:  
 APPLICANT: Weininger, Susan  
 TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
 TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
 NUMBER OF SEQUENCES: 118  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Saliwanchik & Saliwanchik  
 STREET: 2421 N.W. 41st St., Suite A-1  
 CITY: Gainesville  
 STATE: Florida  
 COUNTRY: USA  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION NUMBER: US/10/407,543  
 FILING DATE: 03-APR-2003  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/860,844  
 FILING DATE: 09-JUN-1997  
 APPLICATION NUMBER: 08/353,476  
 FILING DATE: 09-DEC-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 35,746  
 REFERENCE/DOCKET NUMBER: GP-100C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (352) 375-8100  
 TELEFAX: (352) 372-5800  
 INFORMATION FOR SEQ ID NO: 26:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 45 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: cdNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
 US-10-407-543-26

Query Match 72.6%; Score 27.6; DB 6; Length 45;  
 Best Local Similarity 88.2%; Pred. No. 0.34; Mismatches 0; Indels 0; Gaps 0;  
 Matches 30; Conservative 0;

QY 2 GGGACTTTCGGCTGGGACTTTCAGGGGACTT 35  
 Db 7 GGGACTTTCGGCTGGGACTTTCAGAGAGCGCT 40

RESULT 36  
 US-10-235-682-9/c  
 Sequence 9, Application US/10235682  
 Publication No. US20030108523A1  
 GENERAL INFORMATION:

APPLICANT: Lipton, James  
APPLICANT: Catania, Anna P.  
TITLE OF INVENTION: A CANCER TREATMENT SYSTEM  
FILE REFERENCE: 8022 US01  
CURRENT APPLICATION NUMBER: US/10/235,682  
CURRENT FILING DATE: 2002-09-05  
PRIOR FILING DATE: 2002-09-05  
PRIOR FILING DATE: 2002-09-05  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 35  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: NF-kappa B DNA binding site, negative strand  
US-10-235-682-9

Query Match 72.1%; Score 27.4; DB 5; Length 35;  
Best Local Similarity 96.6%; Pred. No. 0.41;  
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGACTTTCGGCTGGGACTTCCAGGG 29  
Db 32 GGGACTTTCGGCTGGGACTTTCATGG 4

RESULT 37  
US-08-860-844-24  
; Sequence 24, Application US/08860844  
; Publication No. US20030104361A1  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/860,844  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/353,476  
; FILING DATE: 09-DEC-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100C1  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO

US-08-860-844-24

Query Match 72.1%; Score 27.4; DB 2; Length 44;  
Best Local Similarity 83.8%; Pred. No. 0.41;  
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGACTTTCAGGGGACTTTC 38  
Db 7 GGGACTTTCGGCTGGGACTTTCAGGGGAGCGTGGCC 43

RESULT 38  
US-10-407-543-24  
; Sequence 24, Application US/10407543  
; Publication No. US20030175789A1  
; GENERAL INFORMATION:  
; APPLICANT: Weininger, Susan  
; APPLICANT: Weininger, Arthur M  
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A  
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st St., Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/10/407,543  
; FILING DATE: 03-Apr-2003  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/860,844  
; FILING DATE: 09-JUN-1997  
; APPLICATION NUMBER: 08/353,476  
; FILING DATE: 09-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100C1  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-10-407-543-24

Query Match 72.1%; Score 27.4; DB 6; Length 44;  
Best Local Similarity 83.8%; Pred. No. 0.41;  
Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGACTTTCAGGGGACTTTC 38  
Db 7 GGGACTTTCGGCTGGGACTTTCAGGGGAGCGTGGCC 43

RESULT 39  
US-08-860-844-25  
; Sequence 25, Application US/08860844

Publication No. US20030104361A1

GENERAL INFORMATION:

APPLICANT: Weininger, Susan

APPLICANT: Weininger, Arthur M

TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A

TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION

NUMBER OF SEQUENCES: 118

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st St., Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/860,844

FILING DATE: 09-JUN-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/353,476

FILING DATE: 09-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 35,746

REFERENCE/DOCKET NUMBER: GP-100C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (352) 375-8100

TELEFAX: (352) 372-5800

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 44 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-860-844-25

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/10/407,543
; FILING DATE: 03-Apr-2003
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
;
; INFORMATION FOR SEQ ID NO: 25:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 44 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA
;
; HYPOTHETICAL: NO
;
; ANTI-SENSE: NO
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
;
US-10-407-543-25

Query Match 71.6%; Score 27.2; DB 6; Length 44;
Best Local Similarity 90.6%; Pred.No. 0.49; 3; Indels 0;
Matches 29; Conservative 0; Mismatches 3; Indels 0;

QY 2 GGGACTTTCGCTGGGGACTTTCAGGGGAC 33
      |||||
Db 7 GGGACTTTCGCTGGGGACTTTCGGGGAGGC 38
      |||||

RESULT 41
US-10-235-682-8
; Sequence 8, Application US/10235682
; Publication No. US20030108523A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Lipton, James
;
; APPLICANT: Catania, Anna P.
;
; TITLE OF INVENTION: A CANCER TREATMENT SYSTEM
;
; FILE REFERENCE: 8022.US01
;
; CURRENT APPLICATION NUMBER: US/10/235,682
;
; CURRENT FILING DATE: 2002-09-05
;
; PRIOR APPLICATION NUMBER: US 60/317,514
;
; PRIOR FILING DATE: 2002-09-05
;
; NUMBER OF SEQ ID NOS: 9
;
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 8
;
; LENGTH: 35
;
; TYPE: DNA
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: NF-kappa B DNA binding site, positive strand
;
US-10-235-682-8

```

US-10-659-053-11  
; Sequence 11, Application US/10659053  
; Publication No. US20050037032A1  
; GENERAL INFORMATION:  
; APPLICANT: ZENGEN, INC.  
; APPLICANT: Catania, Anna P.  
; APPLICANT: Lipton, James M.  
; TITLE OF INVENTION: A COMPOSITION AND METHOD OF TREATMENT FOR UROGENITAL CONDITIONS  
; FILE REFERENCE: 54275.8005.US03  
; CURRENT APPLICATION NUMBER: US/10/659,053  
; CURRENT FILING DATE: 2003-09-08  
; PRIOR APPLICATION NUMBER: US 09/535,066  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: US 60/126,233  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: US 10/442,683  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/382,887  
; PRIOR FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide probes for NF-KB.  
US-10-659-053-11

Query Match 69.5%; Score 26.4; DB 8; Length 35;  
Best Local Similarity 96.4%; Pred. No. 1;  
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGGACTTTCGGCTGGGGACTTTCACG 28  
Db 8 GGGGACTTTCGGCTGGGGACTTTCACG 35

RESULT 43  
US-09-031-629A-5  
; Sequence 5, Application US/09031629A  
; Patent No. US20020106889A1  
; GENERAL INFORMATION:  
; APPLICANT: Faustman  
; APPLICANT: Havashi  
; TITLE OF INVENTION: Methods for Treating and Diagnosing Autoimmune Disease  
; FILE REFERENCE: MGH/Faustman 17633/1030  
; CURRENT APPLICATION NUMBER: US/09/031,629A  
; CURRENT FILING DATE: 1998-02-21  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Probe for  
; OTHER INFORMATION: wild-type kappa B1 sequence  
US-09-031-629A-5

Query Match 68.4%; Score 26; DB 3; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGGACTTTCACG 27  
Db 7 GGGACTTTCGGCTGGGGACTTTCACG 32

RESULT 44  
US-10-775-487A-1  
; Sequence 1, Application US/10775487A  
; Publication No. US20050158302A1

; GENERAL INFORMATION:  
; APPLICANT: Faustman, Denise L.  
; APPLICANT: Havashi, Takuma  
; TITLE OF INVENTION: Methods For Diagnosing Autoimmune  
; TITLE OF INVENTION: Disease  
; FILE REFERENCE: 00786/457003  
; CURRENT APPLICATION NUMBER: US/10/775,487A  
; CURRENT FILING DATE: 2004-02-10  
; PRIOR APPLICATION NUMBER: 09/358,682  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 09/031,629  
; PRIOR FILING DATE: 1998-02-27  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-775-487A-1

Query Match 68.4%; Score 26; DB 9; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGACTTTCGGCTGGGGACTTTCACG 27  
Db 7 GGGACTTTCGGCTGGGGACTTTCACG 32

RESULT 45  
US-10-659-053-12/c  
; Sequence 12, Application US/10659053  
; Publication No. US20050037032A1  
; GENERAL INFORMATION:  
; APPLICANT: ZENGEN, INC.  
; APPLICANT: Catania, Anna P.  
; APPLICANT: Lipton, James M.  
; TITLE OF INVENTION: A COMPOSITION AND METHOD OF TREATMENT FOR UROGENITAL CONDITIONS  
; FILE REFERENCE: 54275.8005.US03  
; CURRENT APPLICATION NUMBER: US/10/659,053  
; CURRENT FILING DATE: 2003-09-08  
; PRIOR APPLICATION NUMBER: US 09/535,066  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: US 60/126,233  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: US 10/442,683  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: US 60/382,887  
; PRIOR FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide probes for NF-KB.  
US-10-659-053-12

Query Match 67.9%; Score 25.8; DB 8; Length 35;  
Best Local Similarity 93.1%; Pred. No. 1.8;  
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGGACTTTCGGCTGGGGACTTTCACGG 29  
Db 32 GGGGAGTTTCCGCTGGGGACTTTCATGG 4

RESULT 46  
US-08-860-844-30  
; Sequence 30, Application US/08860844

```
; Publication No. US20030104361A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-860-844-30

Query Match 66.3%; Score 25.2; DB 2; Length 48;
Best Local Similarity 90.0%; Pred. No. 3;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CTTTCGCTGGGACTTCCAGGGGACTT 35
Db 1 CTTTCGCTGGGACTTCCAGGGGAGCGT 30

RESULT 47
US-10-407-543-30
; Sequence 30, Application US/10407543
; Publication No. US20030175789A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-860-844-30
```

```
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/407,543
; FILING DATE: 03-APR-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-407-543-30

Query Match 66.3%; Score 25.2; DB 6; Length 48;
Best Local Similarity 90.0%; Pred. No. 3;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CTTTCGCTGGGACTTTCAGGGGACTT 35
Db 1 CTTTCGCTGGGACTTTCAGGGAGCGT 30

RESULT 48
US-08-860-844-7
; Sequence 7, Application US/08860844
; Publication No. US20030104361A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
```

```
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-860-844-7

Query Match 65.8%; Score 25; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCCA 26
Db 3 GGGACTTTCGCTGGGACTTTCCA 27

RESULT 49
US-10-407-543-7
; Sequence 7, Application US/10407543
; Publication No. US20030175789A1
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; TITLE OF INVENTION: METHOD OF DETECTION OF NUCLEIC ACIDS WITH A
; SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/407,543
; FILING DATE: 03-Apr-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,844
; FILING DATE: 09-JUN-1997
; APPLICATION NUMBER: 08/353,476
; FILING DATE: 09-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-407-543-7

; REFERENCE/DOCKET NUMBER: GP-100C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-860-844-7

Query Match 65.8%; Score 25; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCCA 26
Db 3 GGGACTTTCGCTGGGACTTTCCA 27

RESULT 50
US-09-844-915-1
; Sequence 1, Application US/09844915
; Patent No. US20020048564A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, Paul D.
; APPLICANT: Lu, Lina
; APPLICANT: Giannoukakis, Nick
; TITLE OF INVENTION: THE USE OF TOLERGENIC DENDRITIC CELLS
; FOR ENHANCING TOLERGENICITY IN A HOST AND METHODS FOR
; MAKING THE SAME
; FILE REFERENCE: AP32737 / 072396.0225
; CURRENT APPLICATION NUMBER: US/09/844,915
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 60/200,479
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleotide sequence
US-09-844-915-1

Query Match 63.2%; Score 24; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGACTTTCC 25
Db 2 GGGACTTTCGCTGGGACTTTCC 25

Search completed: February 16, 2006, 02:34:12
Job time : 555.471 secs
```

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 02:03:53 ; Search time 354.248 Seconds  
(without alignments)  
98.157 Million cell updates/sec

Title: US-09-669-187A-148

Perfect score: 38

Sequence: 1 ggggactttccgtgggactttccgggggactttccc 38

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6247088 seqs, 457523669 residues

Total number of hits satisfying chosen parameters: 11812030

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications NA\_New.\*  
1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq3.\*  
11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq4.\*  
12: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	38	100.0	38	11	US-11-127-654-141
2	29.2	76.8	45	11	US-11-179-321-1
3	29.2	76.8	45	11	US-11-179-321-5
4	24	63.2	29	11	US-11-116-746-12
5	23	60.5	23	8	US-11-175-815-3
6	21.4	56.3	45	11	US-11-179-321-2
7	21.4	56.3	45	11	US-11-179-321-6
8	18	47.4	50	11	US-11-175-859-100529
9	17.2	45.3	25	11	US-11-136-527-200528
C 10	17.2	45.3	50	11	US-11-175-859-32817
C 11	16.4	43.2	50	11	US-11-175-859-66382
C 12	16	42.1	25	11	US-11-121-849-3916
C 13	16	42.1	25	11	US-11-121-849-43102
C 14	15.6	41.1	25	11	US-11-121-849-565799
C 15	15.6	41.1	25	11	US-11-136-527-273210
C 16	15.6	41.1	25	11	US-11-136-527-273212
C 17	15.6	41.1	50	11	US-11-175-859-21940
C 18	15.4	40.5	25	11	US-11-121-849-103498
C 19	15.4	40.5	25	11	US-11-121-849-260545
C 20	15.4	40.5	25	11	US-11-121-849-507340
C 21	15.4	40.5	25	11	US-11-121-849-528104

22	15.4	40.5	25	11	US-11-136-527-139991	Sequence 139991,
C 23	15.4	40.5	25	11	US-11-136-527-213042	Sequence 213042,
C 24	15.4	40.5	26	7	US-10-310-914A-767705	Sequence 767705,
C 25	15.4	40.5	41	11	US-11-032-236-2	Sequence 2, Appli
C 26	15.4	40.5	50	11	US-11-175-859-66869	Sequence 66869, A
C 27	15.4	40.5	50	11	US-11-175-859-103464	Sequence 103464,
28	15.2	40.0	23	7	US-10-310-914A-298241	Sequence 298241,
29	15.2	40.0	23	7	US-10-310-914A-663779	Sequence 663779,
C 30	15.2	40.0	25	11	US-11-121-849-454114	Sequence 454114,
C 31	15.2	40.0	26	7	US-10-310-914A-1226668	Sequence 1226668,
C 32	15.2	40.0	27	7	US-10-310-914A-1383495	Sequence 1383495,
C 33	15.2	40.0	50	11	US-11-175-859-43456	Sequence 43456, A
C 34	15.2	40.0	50	11	US-11-175-859-66764	Sequence 66764, A
C 35	15	39.5	24	7	US-10-310-914A-815249	Sequence 815249,
C 36	15	39.5	25	11	US-11-121-849-196232	Sequence 196232,
C 37	15	39.5	25	11	US-11-121-849-378884	Sequence 378884,
C 38	15	39.5	25	11	US-11-121-849-510666	Sequence 510666,
C 39	15	39.5	25	11	US-11-136-527-280766	Sequence 280766,
C 40	15	39.5	25	11	US-11-136-527-314081	Sequence 314081,
C 41	15	39.5	25	11	US-11-136-527-318283	Sequence 318283,
42	15	39.5	25	11	US-11-136-527-358480	Sequence 358480,
43	15	39.5	50	11	US-11-175-859-11173	Sequence 11173, A
44	15	39.5	50	11	US-11-175-859-74560	Sequence 74560, A
45	15	39.5	50	11	US-11-175-859-104360	Sequence 104360,
C 46	14.8	38.9	24	7	US-10-310-914A-252171	Sequence 252171,
47	14.8	38.9	25	11	US-11-121-849-508663	Sequence 508663,
48	14.8	38.9	25	11	US-11-121-849-569838	Sequence 569838,
49	14.8	38.9	25	11	US-11-121-849-571272	Sequence 571272,
C 50	14.8	38.9	50	11	US-11-175-859-1145	Sequence 1145, Ap
C 51	14.8	38.9	50	11	US-11-175-859-5345	Sequence 5345, Ap
C 52	14.8	38.9	50	11	US-11-175-859-5396	Sequence 5396, Ap
C 53	14.8	38.9	50	11	US-11-175-859-27611	Sequence 27611, A
C 54	14.8	38.9	50	11	US-11-175-859-68699	Sequence 68699, A
C 55	14.8	38.9	50	11	US-11-175-859-86367	Sequence 86367, A
C 56	14.6	38.4	21	7	US-10-310-914A-279653	Sequence 279653,
C 57	14.6	38.4	21	7	US-10-310-914A-905240	Sequence 905240,
C 58	14.6	38.4	21	7	US-10-310-914A-940420	Sequence 940420,
C 59	14.6	38.4	22	7	US-10-310-914A-1244998	Sequence 1244998,
C 60	14.6	38.4	22	7	US-10-310-914A-815248	Sequence 815248,
C 61	14.6	38.4	24	7	US-10-310-914A-400363	Sequence 400363,
C 62	14.6	38.4	24	7	US-10-310-914A-819776	Sequence 819776,
C 63	14.6	38.4	24	7	US-10-310-914A-915881	Sequence 915881,
C 64	14.6	38.4	25	11	US-11-121-849-369219	Sequence 369219,
C 65	14.6	38.4	25	11	US-11-121-849-411393	Sequence 411393,
C 66	14.6	38.4	25	11	US-11-121-849-577777	Sequence 577777,
C 67	14.6	38.4	50	11	US-11-175-859-34784	Sequence 34784, A
C 68	14.6	38.4	50	11	US-11-175-859-47813	Sequence 47813, A
C 69	14.6	38.4	50	11	US-11-175-859-96013	Sequence 96013, A
C 70	14.4	37.9	21	7	US-10-310-914A-845785	Sequence 845785,
C 71	14.4	37.9	22	7	US-10-310-914A-93496	Sequence 93496, A
C 72	14.4	37.9	23	7	US-10-310-914A-300956	Sequence 300956,
C 73	14.4	37.9	23	7	US-10-310-914A-856110	Sequence 856110,
C 74	14.4	37.9	24	7	US-10-310-914A-767653	Sequence 767653,
C 75	14.4	37.9	25	7	US-10-310-914A-860553	Sequence 860553,
C 76	14.4	37.9	25	11	US-11-121-849-48612	Sequence 48612, A
C 77	14.4	37.9	25	11	US-11-121-849-152849	Sequence 152849,
C 78	14.4	37.9	25	11	US-11-121-849-194663	Sequence 194663,
C 79	14.4	37.9	25	11	US-11-121-849-201921	Sequence 201921,
C 80	14.4	37.9	25	11	US-11-121-849-454205	Sequence 454205,
C 81	14.4	37.9	25	11	US-11-136-527-139973	Sequence 139973,
C 82	14.4	37.9	25	11	US-11-136-527-139984	Sequence 139984,
C 83	14.4	37.9	25	11	US-11-136-527-148772	Sequence 148772,
C 84	14.4	37.9	25	11	US-11-136-527-213033	Sequence 213033,
C 85	14.4	37.9	25	11	US-11-136-527-213054	Sequence 213054,
C 86	14.4	37.9	25	11	US-11-136-527-255943	Sequence 255943,
C 87	14.4	37.9	25	11	US-11-136-527-284919	Sequence 284919,
C 88	14.4	37.9	25	11	US-11-136-527-264938	Sequence 264938,
C 89	14.4	37.9	25	11	US-11-136-527-295909	Sequence 295909,
C 90	14.4	37.9	25	11	US-11-136-527-318422	Sequence 318422,
C 91	14.4	37.9	25	11	US-11-136-527-323032	Sequence 323032,
C 92	14.4	37.9	25	11	US-11-136-527-337618	Sequence 337618,
C 93	14.4	37.9	27	7	US-10-310-914A-1042809	Sequence 1042809,
C 94	14.4	37.9	28	7	US-10-310-914A-860573	Sequence 860573,

C	95	14.4	37.9	50	11	US-11-175-859-16894	Sequence 16894, A	168	14	36.8	50	11	US-11-175-859-115454	Sequence 115454,
	96	14.4	37.9	50	11	US-11-175-859-29564	Sequence 29564, A	C 169	13.8	36.3	18	7	US-10-310-914A-515523	Sequence 515523,
	97	14.4	37.9	50	11	US-11-175-859-78404	Sequence 78404, A	C 170	13.8	36.3	18	7	US-10-310-914A-603980	Sequence 603980,
	98	14.4	37.9	50	11	US-11-175-859-108242	Sequence 108242, A	C 171	13.8	36.3	19	7	US-10-310-914A-1286243	Sequence 1286243,
	99	14.4	37.9	50	11	US-11-175-859-111846	Sequence 111846,	C 172	13.8	36.3	19	9	US-11-101-244-662609	Sequence 662609,
	100	14.2	37.4	50	11	US-10-310-914A-481857	Sequence 481857, A	C 173	13.8	36.3	19	9	US-11-101-244-664250	Sequence 664250,
	101	14.2	37.4	50	11	US-10-310-914A-663781	Sequence 663781, A	C 174	13.8	36.3	19	10	US-11-083-784-662609	Sequence 662609,
	102	14.2	37.4	50	11	US-10-310-914A-940417	Sequence 940417, A	C 175	13.8	36.3	19	10	US-11-083-784-664250	Sequence 664250,
	103	14.2	37.4	19	9	US-11-101-244-1342196	Sequence 1342196,	C 176	13.8	36.3	20	7	US-10-310-914A-197603	Sequence 197603,
	104	14.2	37.4	19	10	US-11-083-784-1342196	Sequence 1342196,	C 177	13.8	36.3	20	7	US-10-310-914A-515599	Sequence 515599,
	105	14.2	37.4	20	7	US-10-310-914A-400362	Sequence 400362, A	C 178	13.8	36.3	20	7	US-10-310-914A-1084298	Sequence 1084298,
	106	14.2	37.4	20	7	US-10-310-914A-880143	Sequence 880143, A	C 179	13.8	36.3	20	7	US-10-310-914A-1084528	Sequence 1084528,
	107	14.2	37.4	20	7	US-10-310-914A-983911	Sequence 983911, A	C 180	13.8	36.3	20	7	US-10-310-914A-1216378	Sequence 1216378,
	108	14.2	37.4	21	7	US-10-770-726-1531	Sequence 1531, Ap	C 181	13.8	36.3	21	7	US-10-310-914A-1216655	Sequence 1216655,
	109	14.2	37.4	21	7	US-10-310-914A-470528	Sequence 470528, A	C 182	13.8	36.3	21	7	US-10-310-914A-487014	Sequence 487014,
	110	14.2	37.4	21	7	US-10-310-914A-1229615	Sequence 1229615, A	C 183	13.8	36.3	22	7	US-10-310-914A-226394	Sequence 226394,
	111	14.2	37.4	21	11	US-11-001-347-2195	Sequence 2195, Ap	C 184	13.8	36.3	23	7	US-10-310-914A-1139580	Sequence 1139580,
	112	14.2	37.4	22	7	US-10-310-914A-1229664	Sequence 1229664, A	C 185	13.8	36.3	24	7	US-10-310-914A-38730	Sequence 38730, A
	113	14.2	37.4	22	7	US-10-310-914A-515600	Sequence 515600, A	C 186	13.8	36.3	24	7	US-10-310-914A-603981	Sequence 603981,
	114	14.2	37.4	23	7	US-10-310-914A-920517	Sequence 920517, A	C 187	13.8	36.3	25	7	US-10-310-914A-257305	Sequence 257305,
	115	14.2	37.4	23	7	US-10-310-914A-1227854	Sequence 1227854, A	C 188	13.8	36.3	25	7	US-10-310-914A-765370	Sequence 765370,
	116	14.2	37.4	25	11	US-11-121-849-92973	Sequence 92973, A	C 189	13.8	36.3	25	7	US-10-310-914A-1334567	Sequence 1334567,
	117	14.2	37.4	25	11	US-11-121-849-123890	Sequence 123890, A	C 190	13.8	36.3	25	11	US-11-121-849-2166	Sequence 2166, Ap
	118	14.2	37.4	25	11	US-11-121-849-245310	Sequence 245310, A	C 191	13.8	36.3	25	11	US-11-121-849-56581	Sequence 56581, A
	119	14.2	37.4	25	11	US-11-121-849-351482	Sequence 351482, A	C 192	13.8	36.3	25	11	US-11-121-849-63156	Sequence 63156, A
	120	14.2	37.4	25	11	US-11-121-849-392406	Sequence 392406, A	C 193	13.8	36.3	25	11	US-11-121-849-76904	Sequence 76904, A
	121	14.2	37.4	25	11	US-11-121-849-480753	Sequence 480753, A	C 194	13.8	36.3	25	11	US-11-121-849-87010	Sequence 87010, A
	122	14.2	37.4	25	11	US-11-121-849-514563	Sequence 514563, A	C 195	13.8	36.3	25	11	US-11-121-849-150850	Sequence 150850,
	123	14.2	37.4	25	11	US-11-121-849-514564	Sequence 514564, A	C 196	13.8	36.3	25	11	US-11-121-849-210823	Sequence 210823,
	124	14.2	37.4	25	11	US-11-121-849-574900	Sequence 574900, A	C 197	13.8	36.3	25	11	US-11-121-849-232914	Sequence 232914,
	125	14.2	37.4	25	11	US-11-121-849-574901	Sequence 574901, A	C 198	13.8	36.3	25	11	US-11-121-849-234662	Sequence 234662,
	126	14.2	37.4	25	11	US-11-136-527-53210	Sequence 53210, A	C 199	13.8	36.3	25	11	US-11-121-849-236300	Sequence 236300,
	127	14.2	37.4	25	11	US-11-136-527-53215	Sequence 53215, A	C 200	13.8	36.3	25	11	US-11-121-849-277374	Sequence 277374,
	128	14.2	37.4	25	11	US-11-136-527-53220	Sequence 53220, A	C 201	13.8	36.3	25	11	US-11-121-849-509586	Sequence 509586,
	129	14.2	37.4	25	11	US-11-136-527-247224	Sequence 247224, A	C 202	13.8	36.3	25	11	US-11-121-849-585616	Sequence 585616,
	130	14.2	37.4	50	11	US-11-175-859-241	Sequence 241, App	C 203	13.8	36.3	25	11	US-11-121-849-585617	Sequence 585617,
	131	14.2	37.4	50	11	US-11-175-859-24603	Sequence 24603, A	C 204	13.8	36.3	25	11	US-11-136-527-139988	Sequence 139988,
	132	14.2	37.4	50	11	US-11-175-859-62229	Sequence 62229, A	C 205	13.8	36.3	25	11	US-11-136-527-139994	Sequence 139994,
	133	14.2	37.4	50	11	US-11-175-859-73037	Sequence 73037, A	C 206	13.8	36.3	25	11	US-11-136-527-200554	Sequence 200554,
	134	14.2	37.4	50	11	US-11-175-859-94754	Sequence 94754, A	C 207	13.8	36.3	25	11	US-11-136-527-216717	Sequence 216717,
	135	14.2	37.4	50	11	US-11-175-859-114859	Sequence 114859, A	C 208	13.8	36.3	25	11	US-11-136-527-218537	Sequence 218537,
	136	14	36.8	22	7	US-10-310-914A-458309	Sequence 458309, A	C 209	13.8	36.3	25	11	US-11-136-527-228021	Sequence 228021,
	137	14	36.8	23	7	US-10-310-914A-643683	Sequence 643683, A	C 210	13.8	36.3	25	11	US-11-136-527-243777	Sequence 243777,
	138	14	36.8	23	7	US-10-310-914A-1017158	Sequence 1017158, A	C 211	13.8	36.3	25	11	US-11-136-527-264917	Sequence 264917,
	139	14	36.8	23	7	US-10-310-914A-1020590	Sequence 1020590, A	C 212	13.8	36.3	25	11	US-11-136-527-344781	Sequence 344781,
	140	14	36.8	24	7	US-10-310-914A-24012	Sequence 24012, A	C 213	13.8	36.3	25	11	US-11-136-527-344817	Sequence 344817,
	141	14	36.8	24	7	US-10-310-914A-1090819	Sequence 1090819, A	C 214	13.8	36.3	25	11	US-11-136-527-348675	Sequence 348675,
	142	14	36.8	24	7	US-10-310-914A-1242049	Sequence 1242049, A	C 215	13.8	36.3	26	7	US-10-310-914A-758648	Sequence 758648,
	143	14	36.8	24	7	US-10-310-914A-1298143	Sequence 1298143, A	C 216	13.8	36.3	36	11	US-11-195-109-5	Sequence 5, Appli
	144	14	36.8	25	7	US-10-750-185-8519	Sequence 8519, Ap	C 217	13.8	36.3	36	11	US-11-175-859-4612	Sequence 4612, Ap
	145	14	36.8	25	7	US-10-750-623-8519	Sequence 623-8519, Ap	C 218	13.8	36.3	50	11	US-11-175-859-14338	Sequence 14338, A
	146	14	36.8	25	7	US-10-310-914A-166305	Sequence 166305, A	C 219	13.8	36.3	50	11	US-11-175-859-23877	Sequence 23877, A
	147	14	36.8	25	11	US-11-121-849-23916	Sequence 23916, A	C 220	13.8	36.3	50	11	US-11-175-859-26652	Sequence 26652, A
	148	14	36.8	25	11	US-11-121-849-50786	Sequence 50786, A	C 221	13.8	36.3	50	11	US-11-175-859-30372	Sequence 30372, A
	149	14	36.8	25	11	US-11-121-849-60898	Sequence 60898, A	C 222	13.8	36.3	50	11	US-11-175-859-30641	Sequence 30641, A
	150	14	36.8	25	11	US-11-121-849-61350	Sequence 61350, A	C 223	13.8	36.3	50	11	US-11-175-859-34982	Sequence 34982, A
	151	14	36.8	25	11	US-11-121-849-363099	Sequence 363099, A	C 224	13.8	36.3	50	11	US-11-175-859-49871	Sequence 49871, A
	152	14	36.8	25	11	US-11-121-849-374844	Sequence 374844, A	C 225	13.8	36.3	50	11	US-11-175-859-63177	Sequence 63177, A
	153	14	36.8	25	11	US-11-121-849-399270	Sequence 399270, A	C 226	13.8	36.3	50	11	US-11-175-859-78145	Sequence 78145, A
	154	14	36.8	25	11	US-11-121-849-423422	Sequence 423422, A	C 227	13.8	36.3	50	11	US-11-175-859-88574	Sequence 88574, A
	155	14	36.8	25	11	US-11-136-527-148785	Sequence 148785, A	C 228	13.8	36.3	50	11	US-11-175-859-92135	Sequence 92135, A
	156	14	36.8	25	11	US-11-136-527-225946	Sequence 225946, A	C 229	13.8	36.3	50	11	US-11-175-859-105891	Sequence 105891,
	157	14	36.8	25	11	US-11-136-527-273444	Sequence 273444, A	C 230	13.6	35.8	20	7	US-10-517-544-66	Sequence 66, Appl
	158	14	36.8	25	11	US-11-136-527-323329	Sequence 323329, A	C 231	13.6	35.8	20	7	US-10-310-914A-394854	Sequence 394854,
	159	14	36.8	28	7	US-10-310-914A-637718	Sequence 637718, A	C 232	13.6	35.8	20	7	US-10-310-914A-416467	Sequence 416467,
	160	14	36.8	50	11	US-11-175-859-19585	Sequence 19585, A	C 233	13.6	35.8	20	7	US-10-310-914A-877642	Sequence 877642,
	161	14	36.8	50	11	US-11-175-859-27865	Sequence 27865, A	C 234	13.6	35.8	20	7	US-10-310-914A-982390	Sequence 982390, A
	162	14	36.8	50	11	US-11-175-859-34114	Sequence 34114, A	C 235	13.6	35.8	21	7	US-10-310-914A-67829	Sequence 67829, A
	163	14	36.8	50	11	US-11-175-859-44652	Sequence 44652, A	C 236	13.6	35.8	21	7	US-10-310-914A-277280	Sequence 277280,
	164	14	36.8	50	11	US-11-175-859-63852	Sequence 63852, A	C 237	13.6	35.8	21	7	US-10-310-914A-442560	Sequence 442560,
	165	14	36.8	50	11	US-11-175-859-66866	Sequence 66866, A	C 238	13.6	35.8	21	7	US-10-310-914A-1011495	Sequence 1011495,
	166	14	36.8	50	11	US-11-175-859-73803	Sequence 73803, A	C 239	13.6	35.8	21	7	US-10-310-914A-1020589	Sequence 1020589,
	167	14	36.8	50	11	US-11-175-859-86934	Sequence 86934, A	C 240	13.6	35.8	22	7	US-10-310-914A-277229	Sequence 277229,



```

; CURRENT APPLICATION NUMBER: US/11/179,321
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: 60/587,187
; PRIOR FILING DATE: 2004-07-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-179-321-5

Query Match
Best Local Similarity 76.8%; Score 29.2; DB 11; Length 45;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGGACTTCCAGGGGACTT 35
Db 10 GGGACTTCCGCTGGGGACTTCCAGGGGCGT 43

RESULT 4
US-11-116-746-12
; Sequence 12, Application US/11/116746
; Publication No. US20060020114A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2Dcr
; FILE REFERENCE: P1110
; CURRENT APPLICATION NUMBER: US/11/116,746
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/08/878,168
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 12
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-116-746-12

Query Match
Best Local Similarity 63.2%; Score 24; DB 11; Length 29;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGGACTTCC 25
Db 5 GGGACTTCCGCTGGGGACTTCC 28

RESULT 5
US-11-175-815-3
; Sequence 3, Application US/11/175815
; Publication No. US20060029932A1
; GENERAL INFORMATION:
; APPLICANT: Graham P. Allaway et al.
; TITLE OF INVENTION: A METHOD FOR PREVENTING HIV-1 INFECTION OF CD4 CELLS
; FILE REFERENCE: 2048/50875-DA/JPW/AJD
; CURRENT APPLICATION NUMBER: US/11/175,815
; CURRENT FILING DATE: 2005-07-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-175-815-3

Query Match
Best Local Similarity 60.5%; Score 23; DB 8; Length 23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGGACTTTC 24
Db 1 GGGACTTCCGCTGGGGACTTTC 23

RESULT 6
US-11-179-321-2
; Sequence 2, Application US/11/179321
; Publication No. US20060019907A1
; GENERAL INFORMATION:
; APPLICANT: AGGARWAL, BHARAT
; APPLICANT: SHISHODIA, SHISHIR
; TITLE OF INVENTION: GUGGULSTERONE: AN INHIBITOR OF NUCLEAR FACTOR- B AND
; TITLE OF INVENTION: I B KINASE
; TITLE OF INVENTION: ACTIVATION AND USES THEREOF
; FILE REFERENCE: CLFR:255US
; CURRENT APPLICATION NUMBER: US/11/179,321
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: 60/587,187
; PRIOR FILING DATE: 2004-07-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-179-321-2

Query Match
Best Local Similarity 56.3%; Score 21.4; DB 11; Length 45;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 ACTTCCGCTGGGGACTTCCAGGGGACTT 35
Db 13 ACTTCCGCTGCTCACTTCCAGGGAGCGT 43

RESULT 7
US-11-179-321-6
; Sequence 6, Application US/11/179321
; Publication No. US20060019907A1
; GENERAL INFORMATION:
; APPLICANT: AGGARWAL, BHARAT
; APPLICANT: SHISHODIA, SHISHIR
; TITLE OF INVENTION: GUGGULSTERONE: AN INHIBITOR OF NUCLEAR FACTOR- B AND
; TITLE OF INVENTION: I B KINASE
; TITLE OF INVENTION: ACTIVATION AND USES THEREOF
; FILE REFERENCE: CLFR:255US
; CURRENT APPLICATION NUMBER: US/11/179,321
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: 60/587,187
; PRIOR FILING DATE: 2004-07-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-179-321-6

Query Match
Best Local Similarity 56.3%; Score 21.4; DB 11; Length 45;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 ACTTCCGCTGGGGACTTCCAGGGGACTT 35
Db 13 ACTTCCGCTGCTCACTTCCAGGGAGCGT 43
```

Best Local Similarity 80.6%; Pred. No. 17;  
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 ACTTCCGCTGGGACTTTCCAGGGGACTTT 35  
|||||  
Db 13 ACTTCCGCTGCTCATTTCAGGGAGGCGT 43

RESULT 8

US-11-175-859-100529  
; Sequence 100529, Application US/11175859  
; Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; CURRENT FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 100529  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-100529

Query Match 47.4%; Score 18; DB 11; Length 50;  
Best Local Similarity 66.7%; Pred. No. 3.5e+02;  
Matches 24; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGACTTTCCAGGGGACTTT 36  
|||||  
Db 1 GGACAGTTTGGGTTGGGACTTACCRGGGTGATGT 36

RESULT 9

US-11-136-527-200528  
; Sequence 200528, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 200528  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-200528

Query Match 45.3%; Score 17.2; DB 11; Length 25;  
Best Local Similarity 86.4%; Pred. No. 6.4e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 TTCCGCTGGGACTTTCCAGG 29  
|||||  
Db 1 TTCTCTGGGACTTTCTGGG 22

RESULT 10

US-11-175-859-32817/c  
; Sequence 32817, Application US/11175859

Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; APPLICANT: Liu, Guoying et al.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; CURRENT FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 32817  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-32817

Query Match 45.3%; Score 17.2; DB 11; Length 50;  
Best Local Similarity 68.8%; Pred. No. 7e+02;  
Matches 22; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 5 ACTTCCGCTGGGACTTTCCAGGGGACTTT 36  
|||||  
Db 42 ACTTCTGATAGCTACWTTCAGGCACATT 11

RESULT 11

US-11-175-859-66382/c  
; Sequence 66382, Application US/11175859  
; Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; APPLICANT: Liu, Guoying et al.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; CURRENT FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 66382  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-66382

Query Match 43.2%; Score 16.4; DB 11; Length 50;  
Best Local Similarity 71.4%; Pred. No. 1.4e+03;  
Matches 20; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGACTTTCCAGG 28  
|||||  
Db 48 GGGACATTCACTTGGGACTTCTATG 21

RESULT 12

US-11-121-849-3916/c  
; Sequence 3916, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 3916

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-3916

Query Match      42.1%; Score 16; DB 11; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 10 CCCTGGGAGCTTTCACGGGGGAC 33
    ||||| ||| ||| ||| ||| |||
Db 24 CCCTGAAGACCTTTCAGTGGGAC 1

RESULT 13
US-11-121-849-43102
; Sequence 43102, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 43102
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-43102

Query Match      42.1%; Score 16; DB 11; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 12 GCTGGGAGCTTTCACGGGGGACTT 35
    ||||| ||| ||| ||| ||| |||
Db 1 GCTGAGGCAATCCAGGGGGAGCT 24

RESULT 14
US-11-121-849-565799/c
; Sequence 565799, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 565799
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-565799

Query Match      41.1%; Score 15.6; DB 11; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 TTTCGGCTGGGAGCTTTCAGG 28
    ||||| ||| ||| ||| ||| |||
Db 25 TTTCAGCTTTGAAGCTTTCAGG 4
```

```
RESULT 15
US-11-136-527-273210/c
; Sequence 273210, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 273210
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-273210

Query Match      41.1%; Score 15.6; DB 11; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 16 GGGACTTTCAGGGGGAGCTTTC 37
    || ||||| ||| ||| ||| |||
Db 23 GGTACTTTCAGGCGCGCTTC 2

RESULT 16
US-11-136-527-273212/c
; Sequence 273212, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 273212
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-273212

Query Match      41.1%; Score 15.6; DB 11; Length 25;
Best Local Similarity 81.8%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 16 GGGACTTTCAGGGGGAGCTTTC 37
    || ||||| ||| ||| ||| |||
Db 22 GGTACTTTCAGGCGCGCTTC 1

RESULT 17
US-11-175-859-21940/c
; Sequence 21940, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
```

```

; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21940
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-21940

```

Query Match 41.1%; Score 15.6; DB 11; Length 50;  
Best Local Similarity 75.0%; Pred. No. 2.9e+03;  
Matches 18; Conservative 1; Mismatches 5; Indels

Qy 4 GACTTTCGCTGGGGACTTTCCAG 27  
||||||| : ||| ||  
Db 37 GACTTTCCTCTGTGGATTTGTAG 14

RESULT 18  
US-11-121-849-103498/c  
; Sequence 103498, Application US/11121849  
; Publication No. US20050272080A1

Query Match 40.5%; Score 15.4; DB 11; Length 25;  
Best Local Similarity 76.0%; Pred. No. 3.2e+03;  
Matches 19: Conservative 0; Mismatches 6; Indels

Qy 13 CTGGGGACTTTCAGGGGACTTTC 37  
||| | ||| | ||| | ||| |  
Db 25 CTAGGGCCGCTCCAGTGGGACTTCC 1

RESULT 19  
US-11-121-849-260545/c  
; Sequence 260545, Application US/11121849  
; Publication No. US20050272080A1

; LENGTH: 23  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 US-11-121-849-260545

RESULT 22  
US-11-136-527-139991  
; Sequence 139991, Application US/11136527  
; Publication No. US20050287570A1

Query Match 40.5%; Score 15.4; DB 11; Length 25;  
Best Local Similarity 76.0%; Pred. No. 3.2e+03;  
Matches 19; Conservative 0; Mismatches 6; Indels

Qy 11 CGCTGGGACTTTCAGGGGACTT 35  
Db 25 CGCTGGGGTCTTACCAGTGGTGTTT 1

RESULT 20  
US-11-121-849-507340  
; Sequence 507340, Application US/11121849  
; Publication No. US20050272080A1

Query Match 40.5%; Score 15.4; DB 11; Length 25;  
Best Local Similarity 76.0%; Pred. No. 3.2e+03;  
Matches 19: Conservative 0; Mismatches 6; Indels

Qy 14 TGGGGACTTTCAGGGGGACTTTCC 38  
||| ||| ||| ||| ||| ||| ||| |||  
db 1 TGCGGGCTTACCAGGAGGCCTGTCC 25

RESULT 21  
US-11-121-849-528104/c  
; Sequence 528104, Application US/11121849  
; Publication No. US20050272080A1

Query Match 40.5%; Score 15.4; DB 11; Length 25;  
Best Local Similarity 76.0%; Pred. No. 3.2e+03;  
Matches 19: Conservative 0; Mismatches 6; Indels

Qy 7 TTTCGCTGGGGACTTTCAGGGG 31  
|||  
Db 25 TCTCAGCTGGGACTTCTCAGAGG 1

```
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139991
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-139991

Query Match          40.5%; Score 15.4; DB 11; Length 25;
Best Local Similarity 76.0%; Pred. No. 3.2e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGGACTTCCGCTGGGGACTTTCC 25
    ||||| ||||| ||||| |||||
Db 1 GGGGACTTTCAGATGTTTATTTC 25

RESULT 23
US-11-136-527-213042/c
; Sequence 213042, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 213042
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
US-11-136-527-213042

Query Match          40.5%; Score 15.4; DB 11; Length 25;
Best Local Similarity 76.0%; Pred. No. 3.2e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 ACTTTCGCTGGGGACTTTCCAGGG 29
    ||||| ||||| ||||| |||||
Db 25 ACTTCAGCTGAGACTTCCGGGG 1

RESULT 24
US-10-310-914A-767705/c
; Sequence 767705, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 767705
; LENGTH: 26
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-767705

Query Match          40.5%; Score 15.4; DB 7; Length 26;
Best Local Similarity 76.0%; Pred. No. 3.2e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CTTTCGCTGGGGACTTTCCAGGG 30
    ||||| ||||| ||||| |||||
Db 26 CTCTGGGTGGGGCTTTCAGGG 2

RESULT 25
US-11-032-236-2/c
; Sequence 2, Application US/11032236
; Publication No. US20050273867A1
; GENERAL INFORMATION:
; APPLICANT: BROULET, PHILIPPE
; APPLICANT: ROGERS, KELLY
; APPLICANT: PICAUD, SANDRINE
; TITLE OF INVENTION: NON-INVASIVE REAL-TIME IN VIVO BIOLUMINESCENCE IMAGING
; TITLE OF INVENTION: OF LOCAL CA2+ DYNAMICS IN LIVING ORGANISMS
; FILE REFERENCE: 03495.0328
; CURRENT APPLICATION NUMBER: US/11/032,236
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 60/543,659
; PRIOR FILING DATE: 2004-02-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: flexible linker sequence
US-11-032-236-2

Query Match          40.5%; Score 15.4; DB 11; Length 41;
Best Local Similarity 66.7%; Pred. No. 3.4e+03;
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCCAGGGGGAC 33
    ||||| ||||| ||||| |||||
Db 39 GGGGACTGGCCGCGATCCGCTCCGCGCGAC 7

RESULT 26
US-11-175-859-66869/c
; Sequence 66869, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66869
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-66869

Query Match          40.5%; Score 15.4; DB 11; Length 50;
```



Best Local Similarity 70.4%; Pred. No. 3.4e+03; Indels 0; Gaps 0; Mismatches 7;  
Matches 19; Conservative 1;  
QY 10 CCCTGGGACTTTCAGGGGACTTT 36  
Db 35 CCCTGTCCCTTCCATTTGGGACTT 9  
RESULT 27  
US-11-175-859-103464  
; Sequence 103464, Application US/11175859  
; Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affimetrix, Inc.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; CURRENT FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 103464  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-103464  
Query Match 40.5%; Score 15.4; DB 11; Length 50;  
Best Local Similarity 70.4%; Pred. No. 3.4e+03; Indels 0; Gaps 0; Mismatches 7;  
Matches 19; Conservative 1;  
QY 3 GGACTTTCGCTGGGACTTTCAGGG 29  
Db 9 GGACTTTCCTGTGATTCCTGGG 35  
RESULT 28  
US-10-310-914A-298241  
; Sequence 298241, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 298241  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-298241  
Query Match 40.0%; Score 15.2; DB 7; Length 23;  
Best Local Similarity 70.0%; Pred. No. 3.7e+03; Indels 0; Gaps 0; Mismatches 3;  
Matches 14; Conservative 3;  
QY 10 CCCTGGGACTTTCAGGG 29  
Db 3 CUGCUGGUGACUCUCCAGGG 22  
RESULT 29  
US-10-310-914A-663779  
; Sequence 663779, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 663779  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-663779  
Query Match 40.0%; Score 15.2; DB 7; Length 23;  
Best Local Similarity 55.0%; Pred. No. 3.7e+03; Indels 0; Gaps 0; Mismatches 11; Conservative 6;  
Matches 11; Conservative 6;  
QY 3 GGACTTTCGCTGGGACTT 22  
Db 1 GGACUUUCCUGGGAACUU 20  
RESULT 30  
US-11-121-849-454114/C  
; Sequence 454114, Application US/1121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; TITLE OF INVENTION: Microarrays  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 454114  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-454114  
Query Match 40.0%; Score 15.2; DB 11; Length 25;  
Best Local Similarity 85.0%; Pred. No. 3.8e+03; Indels 0; Gaps 0; Mismatches 17; Conservative 0;  
Matches 17; Conservative 0;  
QY 16 GGACTTTCAGGGGACTT 35  
Db 23 GGGACTCTCCATGGGAGTT 4  
RESULT 31  
US-10-310-914A-1226668  
; Sequence 1226668, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvazat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1226668  
; LENGTH: 26  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1226668

```
Query Match          40.0%; Score 15.2; DB 7; Length 26;
Best Local Similarity 65.0%; Pred. No. 3.8e+03;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGAC 20
    |||||:|:|:|||||
Db 7 GAGGACUUGCCUGGGGAC 26

RESULT 32
US-10-310-914A-1383495
; Sequence 1383495, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1383495
; LENGTH: 27
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1383495

Query Match          40.0%; Score 15.2; DB 7; Length 27;
Best Local Similarity 60.0%; Pred. No. 3.8e+03;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGACTTTCGCTGGGGACT 21
    |||||:|:|:|:|:|
Db 8 GGGACUUCGCCUGAGGCCU 27

RESULT 33
US-11-175-859-43456/c
; Sequence 43456, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43456
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-43456

Query Match          40.0%; Score 15.2; DB 11; Length 50;
Best Local Similarity 66.7%; Pred. No. 4.1e+03;
Matches 20; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 7 TTTCCTCGGGGACTTTCAGGGGGACTTTT 36
    |||||:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 30 TTGSGATGACTACTTTCAGGAGCTACTTT 1

RESULT 34
US-11-175-859-66764
; Sequence 66764, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66764
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-66764

Query Match          40.0%; Score 15.2; DB 11; Length 50;
Best Local Similarity 63.9%; Pred. No. 4.1e+03;
Matches 23; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GGGGACTTTCGCTGGGGACTTTCAGGGGGACTTT 36
    |||||:|:|:|:|:|:|:|:|:|:|:|:|
Db 7 GGTCACTTACCTTAGAGARGTTCAAGAGGGACTGT 42

RESULT 35
US-10-310-914A-815249
; Sequence 815249, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 815249
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-815249

Query Match          39.5%; Score 15; DB 7; Length 24;
Best Local Similarity 65.2%; Pred. No. 4.5e+03;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 15 GGGGACTTTCAGGGGGACTTTC 37
    |||||:|:|:|:|:|:|:|
Db 1 GGGGAGUGUCCAGGGGCACCUGC 23

RESULT 36
US-11-121-849-196232/c
; Sequence 196232, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 196232
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
```

## US-11-121-849-196232

Query Match 39.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACTTTCGCTGGGGA 19  
|||||  
DB 22 ACTTTCGCTGGGGA 8

## RESULT 37

US-11-121-849-378884/c  
; Sequence 378884, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 378884  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-378884

Query Match 39.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 78.3%; Pred. No. 4.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 15 GGGGACTTCCAGGGGACTTC 37  
|||||  
DB 23 GGGGCTTTCAGACTGAGTTC 1

## RESULT 38

US-11-121-849-510666  
; Sequence 510666, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 510666  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-510666

Query Match 39.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 78.3%; Pred. No. 4.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 12 GCTGGGCACTTCCAGGGGACT 34  
|||||  
DB 3 GCTGGGCACTTCCGGGAGTCCT 25

## RESULT 39

US-11-136-527-280766/c

; Sequence 280766, Application US/11136527  
; Publication No. US20050287570A1

; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 280766  
; LENGTH: 25

; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-280766

Query Match 39.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 78.3%; Pred. No. 4.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 13 CTGGGCACTTCCAGGGGACTT 35  
|||||  
DB 23 CAGGGCACTCATCTGGGGACTT 1

## RESULT 40

US-11-136-527-314081/c  
; Sequence 314081, Application US/11136527  
; Publication No. US20050287570A1

; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 314081  
; LENGTH: 25

; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-11-136-527-314081

Query Match 39.5%; Score 15; DB 11; Length 25;  
Best Local Similarity 78.3%; Pred. No. 4.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 11 CGCTGGGCACTTCCAGGGGAC 33  
|||||  
DB 23 CGCTGAGAGCTTTCAGGGCGGC 1

## RESULT 41

US-11-136-527-318283  
; Sequence 318283, Application US/11136527  
; Publication No. US20050287570A1

; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25

```

; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 318283
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
;
US-11-136--527-318283

Query Match          39.5%; Score 15; DB 11; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GGACTTCCGCTGGGACTTTCC 25
    ||||| ||||| ||||| |||||
Db 2 GGACTAGCAGCTGGGGTCTTTAC 24

RESULT 42
US-11-136-527-358480
; Sequence 358480, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 358480
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Probe
;
US-11-136-527-358480

Query Match          39.5%; Score 15; DB 11; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 TTTCCTGGGACTTTCCAGG 29
    ||||| ||||| ||||| |||||
Db 3 TTTCCTGAAGACTTCCCAAG 25

RESULT 43
US-11-175-859-11173
; Sequence 11173, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11173
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
;
US-11-175-859-11173

Query Match          39.5%; Score 15; DB 11; Length 25;
Best Local Similarity 78.3%; Pred. No. 4.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 TTTCCTGGGACTTTCCAGG 29
    ||||| ||||| ||||| |||||
Db 3 TTTCCTGAAGACTTCCCAAG 25

RESULT 43
US-11-175-859-104360
; Sequence 104360, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104360
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
;
US-11-175-859-104360

Query Match          39.5%; Score 15; DB 11; Length 50;
Best Local Similarity 78.3%; Pred. No. 4.9e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 GGGACTTCCGCTGGGACTTTCCAGGGGA 32
    ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GGGAAATATCTGCTGAGTTCTACCAAYGGCA 31

RESULT 45
US-11-175-859-104360
; Sequence 104360, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104360
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
;
US-11-175-859-104360

Query Match          39.5%; Score 15; DB 11; Length 50;
Best Local Similarity 78.3%; Pred. No. 4.9e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGGACTTTCCTGGGACTTTT 23
    ||||| ||||| ||||| |||||
Db 21 GGGGARTTTCCGCACTGTACTGT 43

RESULT 46
US-10-310-914A-252171/C
; Sequence 252171, Application US/10310914A
```

```

; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 252171
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-252171

Query Match      38.9%; Score 14.8; DB 7; Length 24;
Best Local Similarity 88.9%; Pred. No. 5.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 16 GGACACTTCCAGGGGAC 33
Db 21 GGACTAGCCAGGGGAC 4

RESULT 47
US-11-121-849-508663
; Sequence 508663, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 508663
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-508663

Query Match      38.9%; Score 14.8; DB 11; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ACTTCCGCTGGGACTT 22
Db 1 ACTCCGCTGGGACTT 18

RESULT 48
US-11-121-849-569838
; Sequence 569838, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 569838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-569838
```

```

; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-569838

Query Match      38.9%; Score 14.8; DB 11; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 TGGGGACTTTCAGGGG 31
Db 4 TGGGGACTTTCAGGTGG 21

RESULT 49
US-11-121-849-571272
; Sequence 571272, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; PRIOR FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 571272
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-571272

Query Match      38.9%; Score 14.8; DB 11; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 TGGGGACTTTCAGGGG 31
Db 4 TGGGGACTTTCAGGTGG 21

RESULT 50
US-11-175-859-1145/c
; Sequence 1145, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1145
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-1145

Query Match      38.9%; Score 14.8; DB 11; Length 50;
Best Local Similarity 61.1%; Pred. No. 5.9e+03;
Matches 22; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Qy 3 GGACTTTCGGTGGGACTTCCAGGGGACTTTC 38
Db 36 GGTCCTCTCATYCTAGGACTTTTCACCCACACTTTC 1
```

Search completed: February 16, 2006, 02:53:06  
Job time : 357.248 secs

---

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:51:58 ; Search time 479.835 Seconds  
(without alignments)  
2369.293 Million cell updates/sec

Title: US-09-669-187A-906

Perfect score: 20

Sequence: 1 aggggaggggagggagggg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 2097806

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vl.\*

14: gb\_htg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	20	100.0	20	6	AX104714 Sequence
2	20	100.0	20	6	AX547767 Sequence
3	20	100.0	50	6	AX058549 Sequence
C 4	20	100.0	50	6	AX058550 Sequence
C 5	17.4	87.0	27	6	AR091424 Sequence
6	17.4	87.0	27	6	AR091425 Sequence
C 7	17.4	87.0	27	6	AR125629 Sequence
8	17.4	87.0	27	6	AR125630 Sequence
9	17.4	87.0	30	6	AX477591 Sequence
10	17.4	87.0	30	6	AX050511 Sequence
11	17.4	87.0	39	6	AR091423 Sequence
12	17.4	87.0	39	6	AR125628 Sequence
C 13	16.4	82.0	50	6	AR356035 Sequence
C 14	16.4	82.0	50	6	AR537591 Sequence
C 15	16	80.0	17	6	BD202728 Method an
16	15.8	79.0	20	6	ES9332
17	15.8	79.0	26	6	BD078154 Modulator
18	15.8	79.0	42	6	AR362756 Sequence

A28677	Oligonucleo
A28678	Oligonucleo
A28674	dsRNA with
A28685	Oligonucleo
CQ003486	Sequence
CQ003487	Sequence
CQ006699	Sequence
CQ006700	Sequence
BD202727	Method an
AR110134	Sequence
I41099	Sequence 2
A23688	L. monocyto
A23689	L. monocyto
AX058552	Sequence
AX514983	Sequence
AX519178	Sequence
BD078171	Modulator
BD078223	Modulator
AR121366	Sequence
AR213275	Sequence
AR202976	Sequence
AR643452	Sequence
AX158892	Sequence
AR121583	Sequence
AR630012	Sequence
CS130448	Sequence
CS130449	Sequence
E12675	Ant i-HTLV-1
AR182883	Sequence
AR607446	Sequence
AX045778	Sequence
AX045788	Sequence
AX045791	Sequence
AX104065	Sequence
AX104338	Sequence
AX104339	Sequence
AX104619	Sequence
AX104795	Sequence
AX105235	Sequence
AX355140	Sequence
AX355141	Sequence
AX355401	Sequence
AX355402	Sequence
AX477342	Sequence
AX547118	Sequence
AX547391	Sequence
AX547392	Sequence
AX547672	Sequence
AX547848	Sequence
AX664309	Sequence
AX664310	Sequence
AX786642	Sequence
A28676	dsRNA with
AR074234	Sequence
AR084522	Sequence
AR084523	Sequence
I21020	Sequence 3
AX575156	Sequence
AX023407	Sequence
AX032596	Sequence
AX133266	Sequence
AX0420	Sequence 47
AR010036	Sequence
AR034771	Sequence
AR152031	Sequence
BD138633	Soluble M
I05045	Sequence 8
I24744	Sequence 7
AX104236	Sequence
AX104771	Sequence

C 92	14.2	71.0	24	6	AX355142 Sequence	AX355142 Sequence	C 165	13.8	69.0	37	6	AR080892	AR080892 Sequence
C 93	14.2	71.0	24	6	AX547289 Sequence	AX547289 Sequence	C 166	13.8	69.0	37	6	AR173722	AR173722 Sequence
C 94	14.2	71.0	24	6	AX547824 Sequence	AX547824 Sequence	C 167	13.8	69.0	38	6	AX033315	AX033315 Sequence
C 95	14.2	71.0	25	6	BD087484	BD087484 De novo o	C 168	13.8	69.0	40	6	AX520121	AX520121 Sequence
C 96	14.2	71.0	25	6	BD105777	BD105777 Conjgate	C 169	13.8	69.0	41	6	AX513947	AX513947 Sequence
C 97	14.2	71.0	25	6	AR182077	AR182077 Sequence	C 170	13.8	69.0	41	6	AX515756	AX515756 Sequence
C 98	14.2	71.0	25	6	AR261501	AR261501 Sequence	C 171	13.8	69.0	41	6	AX518351	AX518351 Sequence
C 99	14.2	71.0	26	6	BD078156	BD078156 Modulator	C 172	13.8	69.0	41	6	AX519286	AX519286 Sequence
C 100	14.2	71.0	27	6	E04986	E04986 DNA sequenc	C 173	13.8	69.0	41	6	AX520120	AX520120 Sequence
C 101	14.2	71.0	27	6	E04987	E04987 DNA sequenc	C 174	13.8	69.0	45	6	AR080900	AR080900 Sequence
C 102	14.2	71.0	28	6	I06458	I06458 Sequence 1	C 175	13.8	69.0	45	6	AR173730	AR173730 Sequence
C 103	14.2	71.0	28	6	AX104578	AX104578 Sequence	C 176	13.8	69.0	47	6	AR288550	AR288550 Sequence
C 104	14.2	71.0	28	6	AX355143	AX355143 Sequence	C 177	13.8	69.0	47	6	AR291483	AR291483 Sequence
C 105	14.2	71.0	28	6	AX547631	AX547631 Sequence	C 178	13.8	69.0	47	6	AR582752	AR582752 Sequence
C 106	14.2	71.0	30	6	A62990	A62990 Sequence 2	C 179	13.8	69.0	50	6	AX158894	AX158894 Sequence
C 107	14.2	71.0	30	6	A62996	A62996 Sequence 8	C 180	13.8	69.0	50	8	HSTPE31A4	HSTPE31A4 Sequence
C 108	14.2	71.0	30	6	AR179065	AR179065 Sequence	C 181	13.6	68.0	21	6	AR006855	AR006855 Sequence
C 109	14.2	71.0	30	6	AR179071	AR179071 Sequence	C 182	13.6	68.0	21	6	AR080893	AR080893 Sequence
C 110	14.2	71.0	30	6	CS130457	CS130457 Sequence	C 183	13.6	68.0	21	6	AR173723	AR173723 Sequence
C 111	14.2	71.0	30	6	AX104904	AX104904 Sequence	C 184	13.6	68.0	23	6	AX033314	AX033314 Sequence
C 112	14.2	71.0	30	6	AX477343	AX477343 Sequence	C 185	13.6	68.0	24	6	AR094559	AR094559 Sequence
C 113	14.2	71.0	31	6	A40435	A40435 Sequence 62	C 186	13.6	68.0	24	6	BD138044	BD138044 Expressio
C 114	14.2	71.0	31	6	A62992	A62992 Sequence 4	C 187	13.6	68.0	24	6	BD237692	BD237692 Therapeut
C 115	14.2	71.0	31	6	AR179067	AR179067 Sequence	C 188	13.6	68.0	24	6	AR473408	AR473408 Sequence
C 116	14.2	71.0	32	6	A62993	A62993 Sequence 5	C 189	13.6	68.0	24	6	AX278210	AX278210 Sequence
C 117	14.2	71.0	32	6	AR179068	AR179068 Sequence	C 190	13.6	68.0	25	6	AR609154	AR609154 Sequence
C 118	14.2	71.0	35	6	AX104579	AX104579 Sequence	C 191	13.6	68.0	26	6	BD078200	BD078200 Modulator
C 119	14.2	71.0	35	6	AX355144	AX355144 Sequence	C 192	13.6	68.0	30	6	AR018187	AR018187 Sequence
C 120	14.2	71.0	35	6	AX547632	AX547632 Sequence	C 193	13.6	68.0	30	6	AR430823	AR430823 Sequence
C 121	14.2	71.0	37	6	AR078293	AR078293 Sequence	C 194	13.6	68.0	40	6	AX150214	AX150214 Sequence
C 122	14.2	71.0	37	6	BD135456	BD135456 Fatty aci	C 195	13.6	68.0	50	9	MMU41989	MMU41989 Sequence
C 123	14.2	71.0	37	6	BD135459	BD135459 Fatty aci	C 196	13.6	68.0	50	9	AX737059	AX737059 Sequence
C 124	14.2	71.0	37	6	AR285611	AR285611 Sequence	C 197	13.6	68.0	22	6	AR594206	AR594206 Sequence
C 125	14.2	71.0	37	6	AR285614	AR285614 Sequence	C 198	13.6	68.0	36	6	AX356948	AX356948 Sequence
C 126	14.2	71.0	38	6	AR054965	AR054965 Sequence	C 199	13.6	68.0	41	6	AX513870	AX513870 Sequence
C 127	14.2	71.0	39	6	A23696	A23696 L. monocyto	C 200	13.6	68.0	41	6	AX515849	AX515849 Sequence
C 128	14.2	71.0	40	6	AR149456	AR149456 Sequence	C 201	13.6	68.0	41	6	AX516477	AX516477 Sequence
C 129	14.2	71.0	40	6	AR149458	AR149458 Sequence	C 202	13.6	68.0	41	6	AX519146	AX519146 Sequence
C 130	14.2	71.0	40	6	CS130458	CS130458 Sequence	C 203	13.6	68.0	41	6	AX520098	AX520098 Sequence
C 131	14.2	71.0	40	6	E05618	E05618 Primer for	C 204	13.4	67.0	41	6	AX521106	AX521106 Sequence
C 132	14.2	71.0	40	6	E49428	E49428 Method for	C 205	13.4	67.0	41	6	AR288788	AR288788 Sequence
C 133	14.2	71.0	40	6	E49430	E49430 Method for	C 206	13.4	67.0	47	6	CS052981	CS052981 Sequence
C 134	14.2	71.0	41	6	AR080642	AR080642 Sequence	C 207	13.4	67.0	48	6	AX600119	AX600119 Sequence
C 135	14.2	71.0	42	6	AX033316	AX033316 Sequence	C 208	13.4	67.0	50	8	AF057511	AF057511 Homo sapi
C 136	14.2	71.0	45	6	AR071841	AR071841 Sequence	C 209	13.4	67.0	18	6	A87890	A87890 Sequence 38
C 137	14.2	71.0	45	6	AR112581	AR112581 Sequence	C 210	13.4	67.0	18	6	A89857	A89857 Sequence 38
C 138	14.2	71.0	45	6	BD087459	BD087459 De novo o	C 211	13.4	67.0	18	6	AR034902	AR034902 Sequence
C 139	14.2	71.0	45	6	AR182052	AR182052 Sequence	C 212	13.4	67.0	18	6	AR168816	AR168816 Sequence
C 140	14.2	71.0	45	6	AR261476	AR261476 Sequence	C 213	13.4	67.0	18	6	AR168817	AR168817 Sequence
C 141	14.2	71.0	45	6	AX055492	AX055492 Sequence	C 214	13.4	67.0	18	6	BD065403	BD065403 An antise
C 142	14.2	71.0	47	6	AR071857	AR071857 Sequence	C 215	13.4	67.0	18	6	I27810	I27810 Sequence 42
C 143	14.2	71.0	47	6	AR112597	AR112597 Sequence	C 216	13.2	66.0	18	6	I27811	I27811 Sequence 43
C 144	14.2	71.0	49	6	A21777	A21777 oligonucleo	C 217	13.2	66.0	18	6	AR200285	AR200285 Sequence
C 145	14.2	71.0	49	6	C0758887	C0758887 Sequence	C 218	13.2	66.0	18	6	AR200286	AR200286 Sequence
C 146	14.2	71.0	50	6	AR032910	AR032910 Sequence	C 219	13.2	66.0	18	6	AR262417	AR262417 Sequence
C 147	14.2	71.0	50	6	AR137494	AR137494 Sequence	C 220	13.2	66.0	18	6	AR262418	AR262418 Sequence
C 148	14.2	71.0	50	6	AR137495	AR137495 Sequence	C 221	13.2	66.0	18	6	AR612302	AR612302 Sequence
C 149	14.2	71.0	50	6	BD087487	BD087487 De novo o	C 222	13.2	66.0	18	6	AR613539	AR613539 Sequence
C 150	14.2	71.0	50	6	I29650	I29650 Sequence 52	C 223	13.2	66.0	18	6	AR648018	AR648018 Sequence
C 151	14.2	71.0	50	6	I91324	I91324 Sequence 52	C 224	13.2	66.0	18	6	AX047272	AX047272 Sequence
C 152	14.2	71.0	50	6	AR182080	AR182080 Sequence	C 225	13.2	66.0	18	6	AR20286	AR20286 Sequence
C 153	14.2	71.0	50	6	AR209574	AR209574 Sequence	C 226	13.2	66.0	18	6	AR262417	AR262417 Sequence
C 154	14.2	71.0	50	6	AR261504	AR261504 Sequence	C 227	13.2	66.0	18	6	AR612302	AR612302 Sequence
C 155	14.2	71.0	50	6	AR646888	AR646888 Sequence	C 228	13.2	66.0	18	6	AR613539	AR613539 Sequence
C 156	14.2	71.0	50	6	AX147411	AX147411 Sequence	C 229	13.2	66.0	18	6	AR648018	AR648018 Sequence
C 157	13.8	69.0	27	6	AR091427	AR091427 Sequence	C 230	13.2	66.0	18	6	AX047272	AX047272 Sequence
C 158	13.8	69.0	27	6	AR125632	AR125632 Sequence	C 231	13.2	66.0	18	6	AX047274	AX047274 Sequence
C 159	13.8	69.0	27	6	AR125635	AR125635 Sequence	C 232	13.2	66.0	18	6	AX599745	AX599745 Sequence
C 160	13.8	69.0	27	6	AX298100	AX298100 Sequence	C 233	13.2	66.0	18	6	AX599746	AX599746 Sequence
C 161	13.8	69.0	29	6	AX655758	AX655758 Sequence	C 234	13.2	66.0	19	6	AR300315	AR300315 Sequence
C 162	13.8	69.0	36	6	AX496099	AX496099 Sequence	C 235	13.2	66.0	19	6	AX104367	AX104367 Sequence
C 163	13.8	69.0	37	6	AR006854	AR006854 Sequence	C 236	13.2	66.0	19	6	AX547420	AX547420 Sequence
C 164	13.8	69.0	37	6	AR006854	AR006854 Sequence	C 237	13.2	66.0	19	6	AX547420	AX547420 Sequence







```

VERSION      AR125630.1  GI:14111692
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 27)
AUTHORS      Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.
TITLE        Nucleic acid transporter systems
JOURNAL      Patent: US 6177554-A 15 23-JAN-2001;
FEATURES     Location/Qualifiers
             1..27
             /organism="unknown"
             /mol_type="unassigned DNA"

ORIGIN
Query Match      87.0%; Score 17.4; DB 6; Length 27;
Best Local Similarity 94.7%; Pred. No. 8.8e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGG 19
    |||||
Db 4 AAGGGAGGGGAGGGAGGG 22
    |||||

RESULT 9
LOCUS      AX477591          30 bp      DNA      linear      PAT 12-AUG-2002
DEFINITION Sequence 43 from Patent WO0246433.
ACCESSION  AX477591
VERSION     AX477591.1  GI:22216771
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.

REFERENCE   1
AUTHORS     Saus,J.
TITLE       Tnf-Inducible promoters and methods for using
JOURNAL     Patent: WO 0246433-A 43 13-JUN-2002;
            Saus, Juan (ES)
FEATURES     Location/Qualifiers
             1..30
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="Primer ON-TATADel"

ORIGIN
Query Match      87.0%; Score 17.4; DB 6; Length 30;
Best Local Similarity 94.7%; Pred. No. 8.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGG 19
    |||||
Db 2 AGGGAGGGGAGGGAGGG 20
    |||||

RESULT 10
LOCUS      AX505011          30 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 43 from Patent WO0246378.
ACCESSION  AX505011
VERSION     AX505011.1  GI:23386333
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.

REFERENCE   1
AUTHORS     Saus,J.
TITLE       Alternative pol k nucleotide and amino acid sequence and methods
            for using
JOURNAL     Patent: WO 0246378-A 43 13-JUN-2002;
            Saus, Juan (ES)
FEATURES     Location/Qualifiers
             1..30
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="Primer ON-TATADel"

ORIGIN
Query Match      87.0%; Score 17.4; DB 6; Length 30;
Best Local Similarity 94.7%; Pred. No. 8.7e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGG 19
    |||||
Db 2 AGGGAGGGGAGGGAGGG 20
    |||||

RESULT 11
LOCUS      AR091423          39 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 13 from patent US 5994109.
ACCESSION  AR091423
VERSION     AR091423.1  GI:10018178
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 39)
AUTHORS     Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.
TITLE       Nucleic acid transporter system and methods of use
JOURNAL     Patent: US 5994109-A 13 30-NOV-1999;
FEATURES     Location/Qualifiers
             1..39
             /organism="unknown"
             /mol_type="unassigned DNA"

ORIGIN
Query Match      87.0%; Score 17.4; DB 6; Length 39;
Best Local Similarity 94.7%; Pred. No. 8.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGG 19
    |||||
Db 10 AAGGGAGGGGAGGGAGGG 28
    |||||

RESULT 12
LOCUS      AR125628          39 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 13 from patent US 6177554.
ACCESSION  AR125628
VERSION     AR125628.1  GI:14111690
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 39)
AUTHORS     Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.
TITLE       Nucleic acid transporter systems
JOURNAL     Patent: US 6177554-A 13 23-JAN-2001;
FEATURES     Location/Qualifiers
             1..39
             /organism="unknown"
             /mol_type="unassigned DNA"

ORIGIN
Query Match      87.0%; Score 17.4; DB 6; Length 39;
Best Local Similarity 94.7%; Pred. No. 8.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGG 19
    |||||
Db 10 AAGGGAGGGGAGGGAGGG 28
    |||||
```

```
RESULT 13
LOCUS AR356035/c 50 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 2153 from patent US 6593114.
ACCESSION AR356035
VERSION AR356035.1 GI:33762119
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 50)
AUTHORS Kunsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and
  Rosen,C.A.
TITLE Scaphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6593114-A 2153 15-JUL-2003;
  Human Genome Sciences, Inc.; Rockville, MD
FEATURES
  source 1..50
    /organism="unknown"
    /mol_type="genomic DNA"
ORIGIN
Query Match 82.0%; Score 16.4; DB 6; Length 50;
Best Local Similarity 89.5%; Pred. No. 1.9e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGAGGGGGAGGGAGGGG 20
    |||||
Db 28 GGGGGGGGGGGAGGGGGG 10

RESULT 14
LOCUS AR537591/c 50 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 2153 from patent US 6737248.
ACCESSION AR537591
VERSION AR537591.1 GI:53928808
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 50)
AUTHORS Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and
  Rosen,C.A.
TITLE Scaphylococcus aureus polynucleotides and sequences
JOURNAL Patent: US 6737248-A 2153 18-MAY-2004;
  Human Genome Sciences, Inc.; Rockville, MD
FEATURES
  source 1..50
    /organism="unknown"
    /mol_type="genomic DNA"
ORIGIN
Query Match 82.0%; Score 16.4; DB 6; Length 50;
Best Local Similarity 89.5%; Pred. No. 1.9e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGAGGGGGAGGGAGGGG 20
    |||||
Db 28 GGGGGGGGGGGAGGGGGG 10

RESULT 15
LOCUS BD202728/c 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning
  molecule participating in vasculogenic response.
ACCESSION BD202728
VERSION BD202728.1 GI:33012498
KEYWORDS JP 2002509721-A/5754.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
```

```
REFERENCE
  1 (bases 1 to 17)
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning
  molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 5754 02-APR-2002;
  RIBOZYME PHARMACEUTICALS INC
COMMENT
  OS Homo sapiens (human)
  PN JP 2002509721-A/5754
  PD 02-APR-2002
  PF 24-MAR-1999 JP 2000541291
  PR 27-MAR-1998 US 60/079678
  PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
  PJ JAMES A MCSWIGGEN
  PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
  A61P29/00,
  PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
  C12N5/00
  CC Method and reagent for treating diseases or conditions CC
  concerning molecule
  CC participating in vasculogenic response
  FH Key Location/Qualifiers
  FT source 1..17
  FT /organism='Homo sapiens (human)'.
FEATURES
  source 1..17
    /organism="Homo sapiens"
    /mol_type="genomic RNA"
    /db_xref="taxon:9606"
ORIGIN
Query Match 80.0%; Score 16; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGGAGGGGGAGGGAGG 18
    |||||
Db 16 GGGAGGGGGAGGGAGG 1

RESULT 16
LOCUS ES9332 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for purifying oligonucleotide.
ACCESSION ES9332
VERSION ES9332.1 GI:18622509
KEYWORDS JP 2000342265-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
  other sequences; artificial sequences.
REFERENCE
  1 (bases 1 to 20)
AUTHORS Hirose,K. and Yoshida,T.
TITLE Method for purifying oligonucleotide
JOURNAL Patent: JP 2000342265-A 13 12-DEC-2000;
  TOAGOSEI CHEM IND CO LTD
COMMENT
  OS Artificial Sequence
  PN JP 2000342265-A/13
  PD 12-DEC-2000
  PF 02-JUN-1999 JP 1999154974
  PR KUNIHICO HIROSE,TADAO YOSHIDA
  PI C12N15/09,B01D15/08,C12N15/00
  PC C12N15/09,B01D15/08,C12N15/00
  CC Key Location/Qualifiers
  FH Key 1..20
  FH /organism='Artificial Sequence'.
  FT source Location/Qualifiers
  FT 1..20
    /organism="synthetic construct"
    /mol_type="genomic DNA"
```

/db\_xref="taxon:32630"

## ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 20;  
Best Local Similarity 89.5%; Pred. No. 3.7e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 2 GGGGCGGGGGGAGGGG 20

RESULT 17  
BD078154  
LOCUS BD078154.1 GI:22623757 26 bp DNA linear PAT 27-AUG-2002  
DEFINITION Modulator of DNA cytosine-5 methyltransferase and method of using  
the same.

ACCESSION BD078154  
VERSION JP 2001514862-A/38.  
KEYWORDS unclassified  
SOURCE unclassified  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 26)  
AUTHORS Reich,N.O. and Flynn,J.  
TITLE Modulator of DNA cytosine-5 methyltransferase and method of using  
the same

JOURNAL Patent: JP 2001514862-A 38 18-SEP-2001;  
COMMENT THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
OS 'Unidentified  
PN JP 2001514862-A/38  
PD 18-SEP-2001

PF 12-JUN-1998 JP 2000508978  
PR 29-AUG-1997 US 60/057411  
PI NORBERT O REICH,JAMES FLYNN  
PC C12N9/10,C12Q1/48//C12N15/09,C12N15/00  
CC Strandedness: Double;  
CC Topology: Linear;

CC Modulator of DNA cytosine-5 methyltransferase and method of  
using the same

FT Key Location/Qualifiers  
FT source 1..26  
/organism='Unidentified'.  
Location/Qualifiers  
1..26  
/organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref="taxon:32644"

FEATURES  
source

## ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 26;  
Best Local Similarity 89.5%; Pred. No. 3.5e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 2 GGGGCGGGGAGGGAGGGG 20

RESULT 18  
AR362756  
LOCUS AR362756 42 bp DNA linear PAT 03-SEP-2003  
DEFINITION Sequence 21 from patent US 5182196.

ACCESSION AR362756  
VERSION AR362756.1 GI:34423141  
KEYWORDS Unknown.  
SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 42)  
AUTHORS Allet,B. and Kawashima,B.H.  
TITLE Expression systems for overproduction of desired proteins  
JOURNAL Patent: US 5182196-A 21 26-JAN-1993;

Biogen, Inc.; Cambridge, MA;  
EPX;

FEATURES  
source Location/Qualifiers  
1..42  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 42;  
Best Local Similarity 89.5%; Pred. No. 3.3e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 17 GGGGCGGGGGGAGGGG 35

## RESULT 19

A28677  
LOCUS A28677 43 bp DNA linear PAT 04-JUN-1995  
DEFINITION Oligonucleotide 1.  
ACCESSION A28677  
VERSION A28677.1 GI:1248716  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 43)  
AUTHORS SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE  
TITLE Patent: WO 9014090-A 5 29-NOV-1990;  
JOURNAL Location/Qualifiers  
FEATURES source 1..43  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

## ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 43;  
Best Local Similarity 89.5%; Pred. No. 3.3e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 11 GGGGCGGGGAGGGAGGGG 29

## RESULT 20

A28678/c  
LOCUS A28678 43 bp DNA linear PAT 04-JUN-1995  
DEFINITION Oligonucleotide 2 (comp.).  
ACCESSION A28678  
VERSION A28678.1 GI:1248717  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 43)  
AUTHORS SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE  
TITLE Patent: WO 9014090-A 6 29-NOV-1990;  
JOURNAL Location/Qualifiers  
FEATURES source 1..43  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

## ORIGIN

Query Match 79.0%; Score 15.8; DB 6; Length 43;  
Best Local Similarity 89.5%; Pred. No. 3.3e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20

```
Db          37 GGGGGGGGAGGGGGGGG 19
||||| ||||| ||||| ||||| |||||
RESULT 21
A28674/c
LOCUS      A28674          44 bp      RNA      linear      PAT 04-JUN-1995
DEFINITION dsRNA with terminal locks (comp.).
ACCESSION  A28674
VERSION    A28674.1 GI:1248713
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1 (bases 1 to 44)
AUTHORS    .
TITLE      SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE
JOURNAL    Patent: WO 9014090-A 2 29-NOV-1990;
FEATURES   Location/Qualifiers
            source
            1..44
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      79.0%; Score 15.8; DB 6; Length 44;
Best Local Similarity 89.5%; Pred. No. 3.2e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      2 GGGGAGGGGAGGGGAGGGG 20
        ||||| ||||| ||||| |||||
Db      43 GGGGGGGGAGGGGGGGG 25
        ||||| ||||| ||||| |||||
RESULT 22
A28685/c
LOCUS      A28685          47 bp      RNA      linear      PAT 04-JUN-1995
DEFINITION Oligonucleotide 9.
ACCESSION  A28685
VERSION    A28685.1 GI:1248724
KEYWORDS   .
SOURCE     .
ORGANISM   .
REFERENCE  1 (bases 1 to 47)
AUTHORS    .
TITLE      SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE
JOURNAL    Patent: WO 9014090-A 13 29-NOV-1990;
FEATURES   Location/Qualifiers
            source
            1..47
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      79.0%; Score 15.8; DB 6; Length 47;
Best Local Similarity 89.5%; Pred. No. 3.2e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      2 GGGGAGGGGAGGGGAGGGG 20
        ||||| ||||| ||||| |||||
Db      40 GGGGGGGGAGGGGGGGG 22
        ||||| ||||| ||||| |||||
RESULT 23
CQ003486/c
LOCUS      CQ003486          50 bp      DNA      linear      PAT 16-JAN-2004
DEFINITION Sequence 2126 from Patent WO0147944.
ACCESSION  CQ003486
VERSION    CQ003486.1 GI:41010118
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
```

```
REFERENCE 1
AUTHORS    Shimkets,R.A. and Leach,M.
TITLE      Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL    Patent: WO 0147944-A 2126 05-JUL-2001;
            Curagen Corporation (US)
FEATURES   Location/Qualifiers
            source
            1..50
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            misc_feature
            25..26
            /note="Nucleotide deleted between bases 25 and 26
            Accession number cg44131752"
ORIGIN
Query Match      79.0%; Score 15.8; DB 6; Length 50;
Best Local Similarity 89.5%; Pred. No. 3.2e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      2 GGGGAGGGGAGGGGAGGGG 20
        ||||| ||||| ||||| |||||
Db      44 GGGGAGGGGAAGGGGGG 26
        ||||| ||||| ||||| |||||
RESULT 24
CQ003487/c
LOCUS      CQ003487          50 bp      DNA      linear      PAT 16-JAN-2004
DEFINITION Sequence 2127 from Patent WO0147944.
ACCESSION  CQ003487
VERSION    CQ003487.1 GI:41010119
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE 1
AUTHORS    Shimkets,R.A. and Leach,M.
TITLE      Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
JOURNAL    Patent: WO 0147944-A 2127 05-JUL-2001;
            Curagen Corporation (US)
FEATURES   Location/Qualifiers
            source
            1..50
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            misc_feature
            25..26
            /note="Nucleotide deleted between bases 25 and 26
            Accession number cg44131752"
ORIGIN
Query Match      79.0%; Score 15.8; DB 6; Length 50;
Best Local Similarity 89.5%; Pred. No. 3.2e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      2 GGGGAGGGGAGGGGAGGGG 20
        ||||| ||||| ||||| |||||
Db      36 GGGGAGGGGAAGGGGGG 18
        ||||| ||||| ||||| |||||
RESULT 25
CQ006699
LOCUS      CQ006699          50 bp      DNA      linear      PAT 16-JAN-2004
DEFINITION Sequence 5339 from Patent WO0147944.
ACCESSION  CQ006699
VERSION    CQ006699.1 GI:41013331
KEYWORDS   .
SOURCE     Homo sapiens (human)
```



```
RESULT 29
I41099/c
LOCUS           I41099          38 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION      Sequence 2 from patent US 5624803.
ACCESSION       I41099
VERSION         I41099.1 GI:2081689
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 38)
AUTHORS        Noonberg S.B. and Hunt C.Anthony.
TITLE          In vivo oligonucleotide generator, and methods of testing the
               binding affinity of triplex forming oligonucleotides derived
               therefrom
JOURNAL
FEATURES       Patent: US 5624803-A 2 29-APR-1997;
               Location/Qualifiers
               1..38
               /organism="unknown"
               /mol_type="unassigned DNA"
ORIGIN
Query Match    76.0%; Score 15.2; DB 6; Length 38;
Best Local Similarity 85.0%; Pred. No. 5.6e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 27 AGGGGAAGGAAGGAAGGG 8

RESULT 30
A23688/c
LOCUS           A23688          41 bp      DNA      linear      PAT 25-NOV-1994
DEFINITION      L. monocytogenes HlyA gene probe-primer.
ACCESSION       A23688
VERSION         A23688.1 GI:641736
KEYWORDS        .
SOURCE          synthetic construct
ORGANISM        other sequences; artificial sequences.
REFERENCE       1 (bases 1 to 41)
AUTHORS
TITLE          METHODS OF DETECTING OR QUANTITATING NUCLEIC ACIDS AND OF PRODUCING
               LABELLED IMMOBILISED NUCLEIC ACIDS
JOURNAL
FEATURES       Patent: WO 9304199-A 4 04-MAR-1993;
               Location/Qualifiers
               1..41
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
ORIGIN
Query Match    76.0%; Score 15.2; DB 6; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 21 AGGGGGGGGGGGGGGGGGG 2

RESULT 31
A23689/c
LOCUS           A23689          41 bp      DNA      linear      PAT 25-NOV-1994
DEFINITION      L. monocytogenes HlyA gene probe-primer.
ACCESSION       A23689
VERSION         A23689.1 GI:641737
KEYWORDS        .
SOURCE          synthetic construct
ORGANISM        synthetic construct
```

```
other sequences; artificial sequences.
REFERENCE       1 (bases 1 to 41)
AUTHORS
TITLE          METHODS OF DETECTING OR QUANTITATING NUCLEIC ACIDS AND OF PRODUCING
               LABELLED IMMOBILISED NUCLEIC ACIDS
JOURNAL
FEATURES       Patent: WO 9304199-A 5 04-MAR-1993;
               Location/Qualifiers
               1..41
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
ORIGIN
Query Match    76.0%; Score 15.2; DB 6; Length 41;
Best Local Similarity 85.0%; Pred. No. 5.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 21 AGGGGGGGGGGGGGGGGGG 2

RESULT 32
AX058552
LOCUS           AX058552          15 bp      DNA      linear      PAT 17-JAN-2001
DEFINITION      Sequence 4 from Patent WO0077250.
ACCESSION       AX058552
VERSION         AX058552.1 GI:12310894
KEYWORDS        .
SOURCE          synthetic construct
ORGANISM        synthetic construct
               other sequences; artificial sequences.
REFERENCE       1
AUTHORS        Escude, C., Garestier, T., Helene, C. and Roulon, T.
TITLE          Method for circularizing oligonucleotides around a double stranded
               nucleic acid, resulting structures and uses thereof
JOURNAL
FEATURES       Patent: WO 0077250-A 4 21-DEC-2000;
               INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
               (FR) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
               Location/Qualifiers
               1..15
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Oligonucleotide"
ORIGIN
Query Match    75.0%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GAGGGGAGGGGAGGGG 19
    ||||| ||||| ||||| |||||
Db 1 GAGGGGAGGGGAGGGG 15

RESULT 33
AX514983
LOCUS           AX514983          41 bp      DNA      linear      PAT 05-OCT-2002
DEFINITION      Sequence 1181 from Patent WO02052044.
ACCESSION       AX514983
VERSION         AX514983.1 GI:23561811
KEYWORDS        .
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE       1
AUTHORS        Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE          Detection of genetic polymorphisms
JOURNAL
FEATURES       Patent: WO 02052044-A 1181 04-JUL-2002;
               Riken (JP)
```



```

FEATURES
  source
    Location/Qualifiers
      1..41
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
ORIGIN
  Query Match      75.0%; Score 15; DB 6; Length 41;
  Best Local Similarity 88.2%; Pred. No. 6.6e+04;
  Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
  Qy 4 GGAGGGGAGGGAGGGG 20
  Db 10 GGAAGGGAGGGAGGGG 26
  RESULT 14
  AX519178
  LOCUS AX519178 41 bp DNA linear PAT 05-OCT-2002
  DEFINITION Sequence 5376 from Patent WO02052044.
  ACCESSION AX519178
  VERSION AX519178.1 GI:23569300
  KEYWORDS
  SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominidae; Homo.
  REFERENCE
  AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
  TITLE Detection of genetic polymorphisms
  JOURNAL Patent: WO 02052044-A 5376 04-JUL-2002;
  Riken (JP)
  FEATURES
    source
      Location/Qualifiers
        1..41
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"
ORIGIN
  Query Match      75.0%; Score 15; DB 6; Length 41;
  Best Local Similarity 88.2%; Pred. No. 6.6e+04;
  Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
  Qy 4 GGAGGGGAGGGAGGGG 20
  Db 10 GGAAGGGAGGGAGGGG 26
  RESULT 35
  BD078171
  LOCUS BD078171 26 bp DNA linear PAT 27-AUG-2002
  DEFINITION Modulator of DNA cytosine-5 methyltransferase and method of using
    the same.
  ACCESSION BD078171
  VERSION BD078171.1 GI:22623774
  KEYWORDS JP 2001514862-A/55.
  SOURCE unidentified
  ORGANISM unidentified
    unclassified.
  REFERENCE
  AUTHORS Reich,N.O. and Flynn,J.
  TITLE Modulator of DNA cytosine-5 methyltransferase and method of using
    the same
  JOURNAL Patent: JP 2001514862-A 55 18-SEP-2001;
    THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
  COMMENT OS Unidentified
    PN JP 2001514862-A/55
    PF 12-JUN-1998 JP 2000508978
    PR 29-AUG-1997 US 60/057411
    PI NORBERT O REICH,JAMES FLYNN
    PC C12N9/10,C12Q1/48//C12N15/09,C12N15/00
    CC Strandedness: Double;
    CC Topology: Linear;
    CC Modulator of DNA cytosine-5 methyltransferase and method of
      using the same
    FH Key Location/Qualifiers
    FT source 1..26
      /organism="Unidentified".
  FEATURES
    source
      Location/Qualifiers
        1..26
          /organism="unidentified"
          /mol_type="genomic DNA"
          /db_xref="taxon:32644"
ORIGIN
  Query Match      74.0%; Score 14.8; DB 6; Length 26;
  Best Local Similarity 88.9%; Pred. No. 8.4e+04;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  Qy 3 GGGAGGGGAGGGAGGGG 20
  Db 3 GGGGGGGAGCGAGGGG 20
  RESULT 36
  BD078223
  LOCUS BD078223 26 bp DNA linear PAT 27-AUG-2002
  DEFINITION Modulator of DNA cytosine-5 methyltransferase and method of using
    the same.
  ACCESSION BD078223
  VERSION BD078223.1 GI:22623826
  KEYWORDS JP 2001514862-A/107.
  SOURCE unidentified
  ORGANISM unidentified
    unclassified.
  REFERENCE
  AUTHORS Reich,N.O. and Flynn,J.
  TITLE Modulator of DNA cytosine-5 methyltransferase and method of using
    the same
  JOURNAL Patent: JP 2001514862-A 107 18-SEP-2001;
    THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
  COMMENT OS Unidentified
    PN JP 2001514862-A/107
    PF 12-JUN-1998 JP 2000508978
    PR 29-AUG-1997 US 60/057411
    PI NORBERT O REICH,JAMES FLYNN
    PC C12N9/10,C12Q1/48//C12N15/09,C12N15/00
    CC Strandedness: Double;
    CC Topology: Linear;
    CC Modulator of DNA cytosine-5 methyltransferase and method of
      using the same
    FH Key Location/Qualifiers
    FT source 1..26
      /organism="Unidentified".
  FEATURES
    source
      Location/Qualifiers
        1..26
          /organism="unidentified"
          /mol_type="genomic DNA"
          /db_xref="taxon:32644"
ORIGIN
  Query Match      74.0%; Score 14.8; DB 6; Length 26;
  Best Local Similarity 88.9%; Pred. No. 8.4e+04;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  Qy 3 GGGAGGGGAGGGAGGGG 20
  Db 3 GGGGGGGAGCGAGGGG 20
  RESULT 37
  AR121366/c
  LOCUS AR121366 30 bp DNA linear PAT 16-MAY-2001

```

DEFINITION Sequence 18 from patent US 6159720.  
ACCESSION AR121366  
VERSION AR121366.1 GI:14104942  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Murashima,K., Moriya,T., Hamaya,T., Koga,J., Sumida,N., Aoyagi,K., Murakami,T. and Kono,T.  
TITLE Enzyme endoglucanase and cellulase preparations containing the same  
JOURNAL Patent: US 6159720-A 18 12-DEC-2000;  
FEATURES Location/Qualifiers  
source 1..30  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 30;  
Best Local Similarity 88.9%; Pred. No. 8.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCGAGGGGAGGGAGG 18  
||| ||||| ||||| |||||  
Db 25 AGCGAGGGAGGGAGG 8

RESULT 38  
AR213275/c  
LOCUS AR213275 30 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 25 from patent US 6403362.  
ACCESSION AR213275  
VERSION AR213275.1 GI:23310445  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Moriya,T., Murashima,K., Aoyagi,K., Sumida,N., Watanabe,M., Hamaya,T., Koga,J., Kono,T. and Murakami,T.  
TITLE Systems for the mass production of proteins or peptides by microorganisms of the genus humicola  
JOURNAL Patent: US 6403362-A 25 11-JUN-2002;  
Meiji Seika Kaisha, Ltd.; Tokyo;  
JPX;

FEATURES Location/Qualifiers  
source 1..30  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 30;  
Best Local Similarity 88.9%; Pred. No. 8.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCGAGGGGAGGGAGG 18  
||| ||||| ||||| |||||  
Db 25 AGCGAGGAGAGGGAGG 8

RESULT 39  
AR202976  
LOCUS AR202976 31 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 31 from patent US 6365350.  
ACCESSION AR202976  
VERSION AR202976.1 GI:21499243  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Hayashizaki,Y.  
TITLE Method of DNA sequencing

JOURNAL Patent: US 6365350-A 31 02-APR-2002;  
FEATURES Location/Qualifiers  
source 1..31  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 88.9%; Pred. No. 8.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGGAGGGGAGGGAGGG 20  
||| ||||| ||||| |||||  
Db 1 GGGAGGGGGGGGGGGG 18

RESULT 40  
AR643452  
LOCUS AR643452 31 bp DNA linear PAT 20-APR-2005  
DEFINITION Sequence 17 from patent US 6867027.  
ACCESSION AR643452  
VERSION AR643452.1 GI:62781753  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Hayashizaki,Y. and Watahiki,M.  
TITLE RNA polymerase  
JOURNAL Patent: US 6867027-A 17 15-MAR-2005;  
The Institute of Physical and Chemical Research, Nippon Gene Co., Ltd. and Nippon Genetech Co., Ltd.; Wako;  
JPX;

FEATURES Location/Qualifiers  
source 1..31  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 74.0%; Score 14.8; DB 6; Length 31;  
Best Local Similarity 88.9%; Pred. No. 8.2e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGGAGGGGAGGGAGGG 20  
||| ||||| ||||| |||||  
Db 1 GGGAGGGGGGGGGGGG 18

RESULT 41  
AX158892/c  
LOCUS AX158892 50 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 2220 from Patent WO0140521.  
ACCESSION AX158892  
VERSION AX158892.1 GI:14540223  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Shimkets,R.A. and Leach,M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof  
JOURNAL Patent: WO 0140521-A 2220 07-JUN-2001;  
Curagen Corporation (US)

FEATURES Location/Qualifiers  
source 1..50  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
25..26  
/note="Nucleotide deleted between bases 25 and 26  
misc\_feature

```
misc_feature      Accession number cg39331132"
26
/note="2 of 2 allelic variants (2219 is other entry)"
ORIGIN
Query Match      74.0%; Score 14.8; DB 6; Length 50;
Best Local Similarity 88.9%; Pred. No. 7.6e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 GGGAGGGAGGGAGGGG 20
|||||
Db 39 GGGAGGAGGGAGGGG 22
|||||
RESULT 42
AR121583/c
LOCUS      AR121583      20 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 16 from patent US 6159934.
ACCESSION  AR121583
VERSION     AR121583.1 GI:14105159
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Pescovitz,O.H.
TITLE      Use of GHRH-RP to stimulate stem cell factor production
JOURNAL    Patent: US 6159934-A 16 12-DEC-2000;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match      72.0%; Score 14.4; DB 6; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GAGGGAGGGAGGGG 20
|||||
Db 20 GAGGGAGGTGAGGGG 5
|||||
RESULT 43
AR630012
LOCUS      AR630012      25 bp      DNA      linear      PAT 14-FEB-2005
DEFINITION Sequence 66 from patent US 6838556.
ACCESSION  AR630012
VERSION     AR630012.1 GI:59762204
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS    Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
            Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
            Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE      Promoters for regulated gene expression
JOURNAL    Patent: US 6838556-A 66 04-JAN-2005;
FEATURES   Location/Qualifiers
            source
            1..25
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN
Query Match      72.0%; Score 14.4; DB 6; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGGAGGGAGGGAGGGG 17
|||||
Db 1 GGTGAGGGAGGGGAG 16
|||||
RESULT 44
AX351114
LOCUS      AX351114      25 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 66 from Patent WO0194600.
ACCESSION  AX351114
VERSION     AX351114.1 GI:18616468
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS    Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
            Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
            Sheppard,L.T., Lim,M.Y. and Bruice,T.W.
TITLE      Promoters for regulated gene expression
JOURNAL    Patent: WO 0194600-A 66 13-DEC-2001;
FEATURES   Location/Qualifiers
            source
            1..25
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
ORIGIN
Query Match      72.0%; Score 14.4; DB 6; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.2e+05;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GGGAGGGAGGGAGGGG 17
|||||
Db 1 GGTGAGGGAGGGGAG 16
|||||
RESULT 45
AR137709/c
LOCUS      AR137709      20 bp      DNA      linear      PAT 16-JUN-2001
DEFINITION Sequence 2 from patent US 6197554.
ACCESSION  AR137709
VERSION     AR137709.1 GI:14479218
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Lin,S.-L., Chuong,C.-M. and Ying,S.-Y.
TITLE      Method for generating full-length cDNA library from single cells
JOURNAL    Patent: US 6197554-A 2 06-MAR-2001;
FEATURES   Location/Qualifiers
            source
            1..20
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match      71.0%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GGGAGGGAGGGAGGGG 20
|||||
Db 20 GGGGGGGGGGGGGGGG 2
|||||
RESULT 46
CQ892090
LOCUS      CQ892090      20 bp      DNA      linear      PAT 01-NOV-2004
DEFINITION Sequence 133 from Patent WO2004087203.
ACCESSION  CQ892090
VERSION     CQ892090.1 GI:55164648
KEYWORDS
```

```

SOURCE      synthetic construct
ORGANISM     synthetic construct
REFERENCE    1
AUTHORS      Davis,H.L. and Mccluskie,M.J.
TITLE        Immunostimulatory nucleic acid oil-in-water formulations and
              related methods of use
JOURNAL      Patent: WO 2004087203-A 133 14-OCT-2004;
              Coley Pharmaceutical Group, Ltd. (CA)
FEATURES     Location/Qualifiers
              1..20
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Oligonucleotide"
ORIGIN
Query Match      71.0%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 1 GGGGGGGGGGGGGGGGGG 19

RESULT 47
CS130448/c
LOCUS          CS130448      20 bp      DNA      linear      PAT 02-AUG-2005
DEFINITION     Sequence 3 from Patent WO2005063300.
ACCESSION      CS130448
VERSION        CS130448.1 GI:71792416
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      1
AUTHORS        Kippenberger,S.
TITLE          Cosmetics or pharmaceutical preparations containing nucleic acid
              sequences forming a superstructure
JOURNAL        Patent: WO 2005063300-A 3 14-JUL-2005;
              Phenion GmbH & Co KG (DE)
FEATURES       Location/Qualifiers
              1..20
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="phosphorothioate or phosphodiester"
ORIGIN
Query Match      71.0%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 20 GGGGGGGGGGGGGGGGGG 2

RESULT 48
CS130449
LOCUS          CS130449      20 bp      DNA      linear      PAT 02-AUG-2005
DEFINITION     Sequence 4 from Patent WO2005063300.
ACCESSION      CS130449
VERSION        CS130449.1 GI:71792417
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      1
AUTHORS        Kippenberger,S.
TITLE          Cosmetic or pharmaceutical preparations containing nucleic acid
              sequences forming a superstructure
SOURCE      synthetic construct
ORGANISM     synthetic construct
REFERENCE    1
AUTHORS      Davis,H.L. and Mccluskie,M.J.
TITLE        Immunostimulatory nucleic acid oil-in-water formulations and
              related methods of use
JOURNAL      Patent: WO 2004087203-A 133 14-OCT-2004;
              Coley Pharmaceutical Group, Ltd. (CA)
FEATURES     Location/Qualifiers
              1..20
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="phosphorothioate or phosphodiester"
ORIGIN
Query Match      71.0%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 20 GGGGGGGGGGGGGGGGGG 2

RESULT 49
E12675/c
LOCUS          E12675      20 bp      DNA      linear      PAT 27-APR-1998
DEFINITION     Anti-HTLV-1 antisense oligonucleotide.
ACCESSION      E12675
VERSION        E12675.1 GI:3251507
KEYWORDS       JP 1997052898-A/9.
SOURCE         unidentified
ORGANISM       unidentified
REFERENCE      1 (bases 1 to 20)
AUTHORS        Mizuguchi,M., Kurosaki,N., Makino,K., Koyanagi,Y. and Yamamoto,N.
TITLE          ANTI-HTLV-1 ANTI-SENSE OLIGONUCLEOTIDE
JOURNAL        Patent: JP 1997052898-A 9 25-FEB-1997;
              SOYAKU GIJUTSU KENKYUSHO:KK
COMMENT        OS None
              OC Artificial sequences.
              PN JP 1997052898-A/9
              PD 25-FEB-1997
              PF 09-AUG-1995 JP 1995224606
              PI MIZUGUCHI MASATSUGU, KUROSAKI NAOKO, MAKINO KEISUKE, PI
              KOYANAGI YOSHIO,
              YAMAMOTO NAOKI
              PC C07H21/04//A61K31/70;
              CC strandedness: Single;
              CC topology: Linear;
              CC hypothetical: No;
              CC anti-sense: Yes;
              FH Key
              FT source
              1..20
              /organism='Artificial sequences'.
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
FEATURES       Location/Qualifiers
              1..20
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
ORIGIN
Query Match      71.0%; Score 14.2; DB 6; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.5e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 20 GGGGGGGGGGGGGGGGGG 2

RESULT 50
AR182883/c
LOCUS          AR182883      20 bp      DNA      linear      PAT 20-APR-2002
DEFINITION     Sequence 55 from patent US 6339068.
ACCESSION      AR182883
VERSION        AR182883.1 GI:20226090
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
REFERENCE      1
AUTHORS        Kippenberger,S.
TITLE          Cosmetic or pharmaceutical preparations containing nucleic acid
              sequences forming a superstructure
```

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Krieg.A.M., Davis,H.L., Wu,T. and Schorr,J.  
TITLE Vectors and methods for immunization or therapeutic protocols  
JOURNAL Patent: US 6339068-A 55 15-JAN-2002;  
FEATURES Location/Qualifiers  
source  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
  
ORIGIN  
Query Match 71.0%; Score 14.2; DB 6; Length 20;  
Best Local Similarity 84.2%; Pred. No. 1.5e+05;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 GGGGAGGGGGGGGGGGGG 20  
||| ||| ||| ||| |||  
Db 20 GGGGGGGGGGGGGGGGG 2

Search completed: February 15, 2006, 18:56:04  
Job time : 486.835 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 17:25:23 ; Search time 150.744 Seconds  
(without alignments)  
884.241 Million cell updates/sec

Title: US-09-669-187A-906

Perfect score: 20

Sequence: 1 aggggaggggagggagggg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 4879314

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

N\_Geneseq\_21.\*

1: geneseqn1980s.\*

2: geneseqn1990s.\*

3: geneseqn2000s.\*

4: geneseqn2001as.\*

5: geneseqn2001bs.\*

6: geneseqn2002as.\*

7: geneseqn2002bs.\*

8: geneseqn2003as.\*

9: geneseqn2003bs.\*

10: geneseqn2003cs.\*

11: geneseqn2003ds.\*

12: geneseqn2004as.\*

13: geneseqn2004bs.\*

14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	4	Aaf99701 Immunosti
2	20	100.0	20	6	Abf78422 Angiogene
3	20	100.0	20	9	Ach03340 Immunosti
4	20	100.0	20	9	Ach37203 Immunosti
5	20	100.0	20	13	Adu90222 Allergic
6	20	100.0	50	4	Abf56735 Sequence
7	20	100.0	50	4	Abf56736 Sequence
8	17.4	87.0	27	3	Aaa36647 Nucleic a
9	17.4	87.0	27	3	Aaa36646 Nucleic a
10	17.4	87.0	27	3	Aaz39496 Template
11	17.4	87.0	27	3	Aaz39497 Template
12	17.4	87.0	27	4	Aac82867 Nucleic a
13	17.4	87.0	27	4	Aac82866 Nucleic a
14	17.4	87.0	27	4	Aas08476 Pyrimidin
15	17.4	87.0	27	4	Aas08477 Purine-ri
16	17.4	87.0	30	6	Aad41066 Primer ON
17	17.4	87.0	30	6	Abc03901 Human pol
18	17.4	87.0	30	9	Adc13504 Human bl-
19	17.4	87.0	30	9	Ada97805 Human tum

20	17.4	87.0	39	3	AAA36645	Aaa36645 Nucleic a
21	17.4	87.0	39	3	AAZ39495	Aaz39495 Target se
22	17.4	87.0	39	4	AAC82865	Aac82865 Nucleic a
23	17.4	87.0	39	4	AAO8475	Aas08475 Vector ta
24	17.4	87.0	39	6	ABK98155	Abk98155 Triple he
25	17.4	87.0	39	6	ABK98154	Abk98154 Triple he
c	25	87.0	39	6	ABK98106	Abk98106 Triple he
26	17.4	87.0	43	6	ABK98104	Abk98104 Triple he
27	17	85.0	19	6	ABK98105	Abk98105 Human Vbe
c	28	16.8	23	12	ADH70505	Adh70505 39mer dup
29	16.8	84.0	23	12	AAQ46253	Aaq46253 Duplex fo
30	16.4	82.0	43	2	AAQ46257	Aaq46257 Duplex fo
31	16.4	82.0	43	2	AAQ46256	Aaq46256 Duplex fo
c	31	16.4	43	2	ABK98158	Abk98158 Triple he
c	33	16.4	43	6	ABK98112	Abk98112 Triple he
34	16.4	82.0	43	6	ABK98111	Abk98111 Triple he
35	16.4	82.0	43	6	ABK98107	Abk98107 Triple he
36	16.4	82.0	45	6	ABK98157	Abk98157 Triple he
c	37	16.4	50	2	AAV76464	Aav76464 Staphyloc
c	38	16	80.0	17	AAZ25258	Aaz25258 Integrin
39	15.8	79.0	19	12	ADH70729	Adh70729 Human Vbe
40	15.8	79.0	20	4	AAF99947	Aaf99947 Synthetici
41	15.8	79.0	26	2	AAK40753	Aax40753 Oligonuc1
c	42	15.8	27	4	AAF28800	Aaf28800 Human GAB
43	15.8	79.0	27	4	AAF28801	Aaf28801 Human GAB
c	44	15.8	50	4	AAI28918	Aai28918 Human SNP
45	15.8	79.0	50	4	AAI32132	Aai32132 Human SNP
46	15.8	79.0	50	4	AAI32131	Aai32131 Human SNP
c	47	15.8	50	4	AAI28919	Aai28919 Human SNP
c	48	15.4	17	2	AAZ25257	Aaz25257 Integrin
49	15.4	77.0	41	6	ABZ44397	Abz44397 Human cat
50	15.4	77.0	41	6	ABZ48593	Abz48593 Human cat
c	51	15.2	21	6	ABK87618	Abk87618 MALDI-TOF
52	15.2	76.0	22	10	ADE86192	Ade86192 Ret gene
53	15.2	76.0	22	13	ADT92592	Adt92592 Quadruple
54	15.2	76.0	22	13	ADT92592	Adt92592 Quadruple
55	15.2	76.0	24	10	ADE86193	Ade86193 Ret gene
c	56	15.2	25	13	ADV99319	Adv99319 PCR prime
c	57	15.2	31	6	ABK87619	Abk87619 MALDI-TOF
c	58	15.2	35	12	ADJ87120	Adj87120 Nucleotid
c	59	15.2	35	12	ADL92249	Adl92249 MBL gene
60	15.2	76.0	37	3	AA94626	Aa94626 Poly(dG) -
c	61	15.2	38	2	AAQ8038	Aaq8038 U6-type R
c	62	15.2	38	2	AAK36436	Aax36436 U6 specif
c	63	15.2	39	12	ADJ87110	Adj87110 Probe C-2
c	64	15.2	40	2	AAQ25021	Aaq25021 Anti-sens
c	65	15.2	40	2	AAQ25025	Aaq25025 Anti-sens
c	66	15.2	40	5	AAF28723	Aaf28723 Template
c	67	15.2	41	2	AAQ37807	Aaq37807 Sequence
c	68	15.2	41	2	AAQ37806	Aaq37806 Sequence
c	69	15.2	41	6	ABL60242	Abi60242 Citrate s
c	70	15.2	41	12	ADF82773	Adf82773 Antiviral
c	71	15.2	44	13	ADV99324	Adv99324 PCR prime
c	72	15.2	47	13	ADV99325	Adv99325 PCR prime
c	73	15.2	49	12	ADJ87111	Adj87111 Probe C-3
74	15	75.0	15	4	ABL56738	Abi56738 Sequence
c	75	15	15	12	ADH70249	Adh70249 Human Vbe
76	14.8	74.0	26	2	AAK40770	Aax40770 Oligonuc1
77	14.8	74.0	26	2	AAK40822	Aax40822 Genomic s
c	78	14.8	30	2	AAV19382	Aav19382 Humicola
c	79	14.8	30	2	AAV13428	Aav13428 Primer NC
c	80	14.8	36	2	AAAT35032	Aat35032 HSV-1 exo
81	14.8	74.0	36	2	AAAT35026	Aat35026 Triplex-f
82	14.8	74.0	40	9	ACC42064	Acc42064 Human SCN
c	83	14.8	41	6	ABZ49535	Abz49535 Human glu
84	14.8	74.0	43	12	ADL72598	Adl72598 Hairpin s
c	85	14.8	50	4	AAI75279	Aai75279 Human sil
86	14.6	73.0	19	6	ABK98156	Abk98156 Triple he
87	14.6	73.0	19	6	ABK98105	Abk98105 Triple he
c	88	14.4	25	6	AAV02552	Aav02552 Transcrip
89	14.4	72.0	28	6	ABK29917	Abk29917 Androgen
90	14.4	72.0	39	12	ADO60970	Ado60970 Human deb
91	14.4	72.0	39	12	ADO60971	Ado60971 Human deb
92	14.2	71.0	20	2	AAK99571	Aak99571 Fusion re

C 93	14.2	71.0	20	2	AAAT63648	Aat63648	Anti-HTLV	166	14.2	71.0	23	2	AAQ44149	Aa44149	Sequence
C 94	14.2	71.0	20	2	AAV74241	Aav74241	CpG-N mot	167	14.2	71.0	23	2	AAQ43985	Aa43985	HIV-1 LTR
C 95	14.2	71.0	20	3	AAZ57147	Aaz57147	Exemplary	168	14.2	71.0	24	2	AAQ49955	Aa49955	Sequence
C 96	14.2	71.0	20	3	AAZ57136	Aaz57136	Quadruple	169	14.2	71.0	24	2	AAQ36277	Aa36277	APPpar,
C 97	14.2	71.0	20	4	AAC87242	Aac87242	Poly C ol	170	14.2	71.0	24	2	AAQ36278	Aa36278	APPtanti,
C 98	14.2	71.0	20	4	AAC87229	Aac87229	Digoxigen	171	14.2	71.0	24	2	AAT99285	Aat99285	POLYG, a
C 99	14.2	71.0	20	4	AAC87239	Aac87239	Phosphoro	172	14.2	71.0	24	2	AAV31742	Aav31742	Nucleotid
C 100	14.2	71.0	20	4	AAF77533	Aaf77533	CDNA libr	173	14.2	71.0	24	2	AAX04085	Aax04085	Oligonucl
C 101	14.2	71.0	20	4	AAF98853	Aaf98853	Poly-G im	C 174	14.2	71.0	24	4	AAF99299	Aaf99299	Immunosti
C 102	14.2	71.0	20	4	AAF99402	Aaf99402	Immunosti	C 175	14.2	71.0	24	4	AAF99758	Aaf99758	Immunosti
C 103	14.2	71.0	20	4	AAF99782	Aaf99782	Immunosti	C 176	14.2	71.0	24	6	ABS78479	Ab578479	Angiogene
C 104	14.2	71.0	20	4	AAF99608	Aaf99608	Immunosti	C 177	14.2	71.0	24	6	ABS77944	Ab577944	Angiogene
C 105	14.2	71.0	20	4	AAF99130	Aaf99130	Immunosti	C 178	14.2	71.0	24	6	ABL38793	Ab138793	Immunosti
C 106	14.2	71.0	20	4	AAF99401	Aaf99401	Immunosti	C 179	14.2	71.0	24	9	ACH03286	Ach03286	Immunosti
C 107	14.2	71.0	20	5	AAD18515	Adi18515	Biotinyla	C 180	14.2	71.0	24	9	ACD99724	Acd99724	Immunosti
C 108	14.2	71.0	20	6	ABS78046	Ab578046	Angiogene	C 181	14.2	71.0	24	9	ADB36801	Adb36801	Immunosti
C 109	14.2	71.0	20	6	ABS78327	Ab578327	Angiogene	C 182	14.2	71.0	24	9	ADB37260	Adb37260	Immunosti
C 110	14.2	71.0	20	6	ABS77773	Ab577773	Angiogene	C 183	14.2	71.0	24	12	ADF82754	Adf82754	Antiviral
C 111	14.2	71.0	20	6	ABS78047	Ab578047	Angiogene	C 184	14.2	71.0	24	13	ADRA48247	Adr48247	Microarra
C 112	14.2	71.0	20	6	ABS78503	Ab578503	Angiogene	C 185	14.2	71.0	24	13	ADRA48248	Adr48248	Microarra
C 113	14.2	71.0	20	6	ABL38792	Ab138792	Immunosti	C 186	14.2	71.0	24	13	ADU89744	Adu89744	Allergic
C 114	14.2	71.0	20	6	ABL39026	Ab139026	Immunosti	C 187	14.2	71.0	24	13	ADU90279	Adu90279	Allergic
C 115	14.2	71.0	20	6	ABL38791	Ab138791	Immunosti	C 188	14.2	71.0	25	2	AAX76435	Aax76435	Sequencin
C 116	14.2	71.0	20	6	ABL39025	Ab139025	Immunosti	C 189	14.2	71.0	25	6	ABK99282	Abk99282	Hepatitis
C 117	14.2	71.0	20	8	ABX89934	Abx89934	Cancer me	C 190	14.2	71.0	25	11	ADL99557	Adl99557	Single ch
C 118	14.2	71.0	20	9	ACA92790	Aca92790	Immunosti	C 191	14.2	71.0	26	2	AAX40755	Aax40755	Oligonucl
C 119	14.2	71.0	20	9	ACD99822	Acd99822	Immunosti	C 192	14.2	71.0	26	8	AAD48367	Aad48367	Oligonucl
C 120	14.2	71.0	20	9	ACD99562	Acd99562	Immunosti	C 193	14.2	71.0	26	12	ADF82755	Adf82755	Antiviral
C 121	14.2	71.0	20	9	ACD99821	Acd99821	Immunosti	C 194	14.2	71.0	26	13	ADV51233	Adv51233	Hepatitis
C 122	14.2	71.0	20	9	ADB37284	Adb37284	Immunosti	C 195	14.2	71.0	27	2	AAQ40855	Aa40855	DNA seque
C 123	14.2	71.0	20	9	ADB37110	Adb37110	Immunosti	C 196	14.2	71.0	27	2	AAQ40856	Aa40856	DNA seque
C 124	14.2	71.0	20	9	ADB36903	Adb36903	Immunosti	C 197	14.2	71.0	28	4	AAF99570	Aaf99570	Immunosti
C 125	14.2	71.0	20	9	ADB36632	Adb36632	Immunosti	C 198	14.2	71.0	28	6	ABS78286	Ab578286	Angiogene
C 126	14.2	71.0	20	9	ADB36904	Adb36904	Immunosti	C 199	14.2	71.0	28	6	ABL38794	Ab138794	Immunosti
C 127	14.2	71.0	20	10	ADD71314	Add71314	Nucleic a	C 200	14.2	71.0	28	9	ACH03108	Ach03108	Immunosti
C 128	14.2	71.0	20	10	ADE86164	Ade86164	HRAS gene	C 201	14.2	71.0	28	9	ADB37072	Adb37072	Immunosti
C 129	14.2	71.0	20	10	ADE86160	Ade86160	RET gene	C 202	14.2	71.0	28	12	ADF82756	Adf82756	Antiviral
C 130	14.2	71.0	20	10	ABZ98602	Abz98602	Human oli	C 203	14.2	71.0	28	13	ADU90086	Adu90086	Allergic
C 131	14.2	71.0	20	10	ABX98602	Abx98602	Human oli	C 204	14.2	71.0	30	2	AAT09304	Aat09304	Murine an
C 132	14.2	71.0	20	10	ACA58787	Aca58787	Gastric u	C 205	14.2	71.0	30	4	AAF99890	Aaf99890	Immunosti
C 133	14.2	71.0	20	10	ADJ94141	Adj94141	Oligonucl	C 206	14.2	71.0	30	6	ABK10417	Abk10417	Synthetic
C 134	14.2	71.0	20	10	ADK17359	Adk17359	Human CCR	C 207	14.2	71.0	30	6	ABK10411	Abk10411	Synthetic
C 135	14.2	71.0	20	11	ADL99556	Adl99556	Single ch	C 208	14.2	71.0	30	9	ACC58754	Acc58754	Anti-rest
C 136	14.2	71.0	20	11	ABD24832	Abd24832	AT092623-	C 209	14.2	71.0	30	10	ADG70063	Adg70063	Terminal
C 137	14.2	71.0	20	12	ADL57919	Adl57919	Human ESM	C 210	14.2	71.0	30	12	ADP82757	Adp82757	Antiviral
C 138	14.2	71.0	20	12	ADL57899	Adl57899	Human ESM	C 211	14.2	71.0	30	13	ADU87448	Adu87448	Target ge
C 139	14.2	71.0	20	12	ADQ07551	Adq07551	Immunosti	C 212	14.2	71.0	30	14	ADV26181	Adv26181	Human dl9
C 140	14.2	71.0	20	13	ADT08004	Adt08004	Spacer se	C 213	14.2	71.0	30	14	ADZ36927	Adz36927	Rice zmCe
C 141	14.2	71.0	20	13	ADS75744	Ads75744	DNA molec	C 214	14.2	71.0	30	14	ABE28261	Aeb28261	Oligonucl
C 142	14.2	71.0	20	13	ADS08444	Ads08444	Poly-C pr	C 215	14.2	71.0	31	6	ABK10413	Abk10413	Synthetic
C 143	14.2	71.0	20	13	ADT04251	Adt04251	Novel imm	C 216	14.2	71.0	31	14	ADZ67901	Adz67901	HiPLA-31
C 144	14.2	71.0	20	13	ADU90127	Adu90127	Allergic	C 217	14.2	71.0	32	6	ABK10414	Abk10414	Synthetic
C 145	14.2	71.0	20	13	ADU90303	Adu90303	Allergic	C 218	14.2	71.0	32	9	ACC58756	Acc58756	Anti-rest
C 146	14.2	71.0	20	13	ADU89847	Adu89847	Allergic	C 219	14.2	71.0	32	12	ADF82758	Adf82758	Antiviral
C 147	14.2	71.0	20	13	ADU89846	Adu89846	Allergic	C 220	14.2	71.0	32	14	ADY51623	Ady51623	Transcrip
C 148	14.2	71.0	20	13	ADU89573	Adu89573	Allergic	C 221	14.2	71.0	33	2	AAQ44777	Aaq44777	Steroid h
C 149	14.2	71.0	20	14	ADZ67881	Adz67881	Quadruple	C 222	14.2	71.0	34	2	AAQ36326	Aaq36326	NGPR5anti
C 150	14.2	71.0	20	14	ADZ67885	Adz67885	Quadruple	C 223	14.2	71.0	34	2	AAT42899	Aat42899	ss circul
C 151	14.2	71.0	20	14	AEA39362	Aea39362	RET gene	C 224	14.2	71.0	34	12	ADF82759	Adf82759	Antiviral
C 152	14.2	71.0	20	14	AEA39366	Aea39366	H-RAS gen	C 225	14.2	71.0	35	4	AAF99571	Aaf99571	Immunosti
C 153	14.2	71.0	20	14	ABE38253	Aeb38253	Oligonucl	C 226	14.2	71.0	35	6	ABS78287	Ab578287	Angiogene
C 154	14.2	71.0	20	14	ABE38252	Aeb38252	Oligonucl	C 227	14.2	71.0	35	6	ABL38795	Ab138795	Immunosti
C 155	14.2	71.0	21	2	AAQ50950	Aaq50950	Synthetic	C 228	14.2	71.0	35	9	ACH03109	Ach03109	Immunosti
C 156	14.2	71.0	21	2	AAQ61901	Aaq61901	HSV repli	C 229	14.2	71.0	35	9	ADB37073	Adb37073	Immunosti
C 157	14.2	71.0	21	2	AAQ97967	Aaq97967	Peptide n	C 230	14.2	71.0	35	12	ADU87115	Adj87115	Nucleotid
C 158	14.2	71.0	21	2	AAT35038	Aat35038	Triplex-f	C 231	14.2	71.0	35	12	ADL92244	Adl92244	MXA gene
C 159	14.2	71.0	21	3	AAZ99630	Aaz99630	Protypic	C 232	14.2	71.0	35	13	ADU90087	Adu90087	Allergic
C 160	14.2	71.0	21	5	AAH88948	Aah88948	Human pol	C 233	14.2	71.0	36	12	ADF82760	Adf82760	Antiviral
C 161	14.2	71.0	21	5	AAH62060	Aah62060	PDGF A ha	C 234	14.2	71.0	37	2	AAQ98446	Aaq98446	Antisense
C 162	14.2	71.0	21	5	ACC58752	Acc58752	Anti-rest	C 235	14.2	71.0	37	2	AAX06500	Aax06500	G-free bi
C 163	14.2	71.0	21	13	ADW24473	Adw24473	Nucleotid	C 236	14.2	71.0	37	2	AZ06497	Aaz06497	Competito
C 164	14.2	71.0	22	8	ACF03717	Acf03717	PCR prime	C 237	14.2	71.0	37	2	AZ24985	Aaz24985	Oligonucl
C 165	14.2	71.0	23	2	AAQ33897	Aaq33897	Microsate	C 238	14.2	71.0	37	12	ADF82770	Adf82770	Antiviral



```
239 14.2 71.0 38 2 AAV03769 Hepatitis
c 240 14.2 71.0 38 12 Adf82761 Antiviral
c 241 14.2 71.0 38 13 ADS75741 DNA molec
c 242 14.2 71.0 38 13 ADS08441 Poly-C pr
c 243 14.2 71.0 38 13 ADV93321 PCR prime
c 244 14.2 71.0 40 2 AaQ25029 Oligonuc1
c 245 14.2 71.0 40 2 AaQ22624 Sense oli
c 246 14.2 71.0 40 2 AaQ25022 Anti-sens
c 247 14.2 71.0 40 2 AaQ25026 Anti-sens
c 248 14.2 71.0 40 2 AaQ25030 Oligonuc1
c 249 14.2 71.0 40 2 AaQ25017 Sense oli
c 250 14.2 71.0 40 2 AaQ22626 Sense oli
c 251 14.2 71.0 40 2 AaQ25018 Sense oli
c 252 14.2 71.0 40 2 AaQ50877 HSV2 prim
c 253 14.2 71.0 40 4 AaC83643 Human c-f
c 254 14.2 71.0 40 4 AaC83641 Human c-f
c 255 14.2 71.0 40 12 Adf82762 Antiviral
c 256 14.2 71.0 40 13 Adv51231 Linker ol
c 257 14.2 71.0 40 14 Aeb28262 Oligonuc1
c 258 14.2 71.0 41 2 AaQ72283 Rat serot
c 259 14.2 71.0 41 6 AbQ79324 Human pro
c 260 14.2 71.0 41 12 AdK17714 Cytochrom
c 261 14.2 71.0 41 13 Adv25730 Primer BA
c 262 14.2 71.0 42 3 AaA71923 E. coli 2
c 263 14.2 71.0 42 6 AbZ50869 Human ATP
c 264 14.2 71.0 42 6 AbZ48406 Human ATP
c 265 14.2 71.0 42 6 AbZ44642 Human ATP
c 266 14.2 71.0 45 2 AaX76410 Sequencin
c 267 14.2 71.0 45 5 AaC91549 Human PRO
c 268 14.2 71.0 45 13 Adv25731 Primer BA
c 269 14.2 71.0 46 7 AdI94435 Human IL-
c 270 14.2 71.0 46 7 AdI94432 Human IL-
c 271 14.2 71.0 47 3 AaZ65938 Human map
c 272 14.2 71.0 47 3 AaZ68865 Human map
c 273 14.2 71.0 47 7 AdI93449 Human bet
c 274 14.2 71.0 48 2 AaQ12358 Europium-
c 275 14.2 71.0 49 2 AaC80463 Hepatoma
c 276 14.2 71.0 49 7 AdI94426 Human IL-
c 277 14.2 71.0 49 7 AdI94427 Human IL-
c 278 14.2 71.0 49 7 AdI93448 Human bet
c 279 14.2 71.0 49 12 AdH76831 MCHR1 loc
c 280 14.2 71.0 49 12 AdH76662 MCHR1 loc
c 281 14.2 71.0 49 13 Adv25732 Primer BA
c 282 14.2 71.0 50 2 AaQ69772 Herpes si
c 283 14.2 71.0 50 2 AaT64234 HSV-1 b'g
c 284 14.2 71.0 50 2 AaX76438 Sequencin
c 285 14.2 71.0 50 2 AaX17522 Test sequ
c 286 14.2 71.0 50 3 AaA38175 Primer us
c 287 14.2 71.0 50 4 AaH4830 Probe use
c 288 14.2 71.0 50 6 AbK83013 DNA bindi
c 289 14.2 71.0 50 6 AbZ02124 Human leu
c 290 14.2 71.0 50 6 AbZ04174 Human leu
c 291 14.2 71.0 50 10 AdC56858 Micro gol
c 292 14.2 71.0 50 10 AdC56859 Micro gol
c 293 14.2 71.0 50 10 AdG33323 Human DNA
c 294 14.2 71.0 50 12 Ade80552 Duplex ol
c 295 14.2 71.0 50 14 AdV97064 Chimeric
c 296 14.2 71.0 50 14 AdZ71296 Human ACh
c 297 14 70.0 14 12 AdH70438 Human Vbe
c 298 14 70.0 50 6 AbZ04828 Human leu
c 299 14 70.0 50 6 AbZ04829 Human leu
c 300 13.8 69.0 17 12 AdI83485 HCV DNaza
```

## ALIGNMENTS

```
RESULT 1
AAF99701
ID AAF99701 standard; DNA; 20 BP.
XX
AC AAF99701;
XX
```

```
DT 12-JUN-2001 (first entry)
XX Immunostimulatory nucleic acid #817.
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX Synthetic.
OS WO200122972-A2.
PN 05-APR-2001.
PD 25-SEP-2000; 2000WO-US026383.
PF 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
XX Krieg AM, Schetter C, Vollmer J;
XX WPI; 2001-273485/28.
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
XX using immunostimulatory Py-rich and TG nucleic acids.
XX
XX Claim 101; Page 56; 338pp; English.
XX
XX The present invention relates to a method for stimulating an immune
XX response. The method comprises administering an immunostimulatory nucleic
XX acid to a non-rodent subject in sufficient quantity to stimulate an
XX immune response. The present sequence is one such immunostimulatory
XX nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX also useful for preventing cancer, asthma, infectious disease, allergy or
XX immune deficiency. The present sequence can also be used to redirect a
XX Th2 to a Th1 immune response and to activate immune cells. Note: the
XX present sequence may have a phosphorothioate backbone
XX
XX Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 4; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AGGGGAGGGGAGGGGAGGGG 20
Db 1 AGGGGAGGGGAGGGGAGGGG 20
RESULT 2
ABS78422
ID ABS78422 standard; DNA; 20 BP.
XX
XX ABS78422;
XX
XX 13-DEC-2002 (first entry)
XX
XX Angiogenesis inhibitory oligonucleotide #906.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;
XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
```

KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KW plaque neovascularisation; telangiectasia; haemophilic joint;  
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KW scleroderma; hypertrophic scar.  
 XX Synthetic.  
 XX OS  
 XX WO200253141-A2.  
 PN  
 XX  
 XX 11-JUL-2002.  
 PD  
 XX  
 XX 14-DEC-2001; 2001WO-US048458.  
 PF  
 XX  
 XX 14-DEC-2000; 2000US-0255534P.  
 PR  
 XX  
 XX (COLE-) COLEY PHARM GROUP INC.  
 FA  
 XX  
 XX Bratzler RL;  
 PI  
 XX  
 XX WPI; 2002-566690/60.  
 DR  
 XX  
 XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 XX  
 XX Claim 2; Page 35; 276pp; English.  
 PS  
 XX  
 XX The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth.  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 XX  
 XX SQ Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AGGGAGGGGAGGGAGGGG 20  
 Db 1 AGGGAGGGGAGGGAGGGG 20  
 RESULT 3  
 ACH03240  
 ID ACH03240 standard; DNA; 20 BP.  
 XX  
 XX ACH03240;  
 AC  
 XX  
 XX 25-SEP-2003 (first entry)  
 DT  
 XX  
 XX Immunostimulatory nucleic acid #875.  
 DE  
 XX  
 XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX US2003050268-A1.  
 PN  
 XX  
 XX 13-MAR-2003.  
 PD  
 XX

PF 29-MAR-2002; 2002US-00112653.  
 XX  
 PR 29-MAR-2001; 2001US-0279642P.  
 XX  
 PA (KRIE/) KRIEG A M.  
 PA (BERG/) BERG D J.  
 XX  
 XX Krieg AM, Berg DJ;  
 PI  
 XX WPI; 2003-521815/49.  
 DR  
 XX  
 XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.  
 XX  
 XX Disclosure; Page 32; 229pp; English.  
 PS  
 XX  
 XX The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid  
 XX  
 XX SQ Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 9; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 6e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AGGGAGGGGAGGGAGGGG 20  
 Db 1 AGGGAGGGGAGGGAGGGG 20  
 RESULT 4  
 ADB37203  
 ID ADB37203 standard; DNA; 20 BP.  
 XX  
 XX ADB37203;  
 AC  
 XX  
 XX 04-DEC-2003 (first entry)  
 DT  
 XX  
 XX Immunostimulatory nucleic acid #817.  
 DE  
 XX  
 XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
 KW hypo-responsive subject; immunostimulatory.  
 KW  
 XX Synthetic.  
 OS  
 XX  
 XX US2003087848-A1.  
 PN  
 XX  
 XX 08-MAY-2003.  
 PD  
 XX  
 XX 02-FEB-2001; 2001US-00776479.  
 PF  
 XX  
 XX 03-FEB-2000; 2000US-0179991P.  
 PR  
 XX  
 XX (BRAT/) BRATZLER R L.  
 PA (PETE/) PETERSEN D M.  
 PA (FOUR/) FOURON Y.  
 XX  
 XX Bratzler RL, Petersen DM, Fouron Y;  
 PI  
 XX WPI; 2003-657977/62.  
 DR  
 XX  
 XX Treating and/or preventing allergy or asthma using an immunostimulatory  
 PT nucleic acid alone or in combination with an asthma/allergy medicament.  
 PT  
 XX Disclosure; Page 17; 221pp; English.  
 PS  
 XX

CC The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.

XX SQ Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGGGAGGGGAGGGAGGGG 20  
|||||  
Db 1 AGGGAGGGGAGGGAGGGG 20

## RESULT 5

ADU90222

ID ADU90222 standard; DNA; 20 BP.  
AC ADU90222;  
DT 10-FEB-2005 (first entry)  
XX Allergic response suppressor oligonucleotide #906.

XX ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;  
XX antibacterial; virucide; immunoglobulin E antagonist; allergy;  
XX immunostimulator; asthma; rhinitis; urticaria; dermatitis;  
XX bacterial infection; viral infection.

XX OS Synthetic.

XX PN US2004235774-A1.

XX PD 25-NOV-2004.

XX PF 23-APR-2004; 2004US-00831778.

XX PR 03-FEB-2000; 2000US-0179991P.

XX FR 02-FEB-2001; 2001US-00776479.

XX (BRAT/) BRATZLER R L.

XX PA (PETE/) PETERSEN D M.

XX PA (FOUR/) FOURON Y.

XX XX Bratzler RL, Petersen DM, Fouron Y;

XX WPI; 2004-833006/82.

XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
XX dermatitis, in a subject, comprises administering a first and second dose  
XX of an immunostimulatory nucleic acid.

XX Disclosure; SEQ ID NO 906; 235pp; English.

XX The invention relates to a method of suppressing a symptom of an allergic  
XX response in a subject by administering a first and second dose of an  
XX immunostimulatory nucleic acid that comprises a nucleotide sequence  
XX comprising 5'-cg-3', and where the second dose is administered from 1 day  
XX to 8 weeks after the first dose. The methods and compositions of the  
XX present invention are useful for the treatment or prevention of asthma  
XX and allergy, including rhinitis, urticaria and atopic dermatitis, using  
XX an immunostimulatory nucleic acid alone or in combination with other  
XX medicaments. This can also be used in preventing bacterial and viral  
XX infections. This sequence represents an oligonucleotide used in the  
XX method of the invention.

XX SQ Sequence 20 BP; 4 A; 0 C; 16 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 13; Length 20;

Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGGGAGGGGAGGGAGGGG 20  
|||||  
Db 1 AGGGAGGGGAGGGAGGGG 20

## RESULT 6

ABL56735

ID ABL56735 standard; DNA; 50 BP.

XX AC ABL56735;

XX DT 20-AUG-2002 (first entry)

XX DE Sequence of a fragment of the murine androgen receptor promoter.

XX KW Nucleic acid detection; nucleic acid labelling; gene therapy;  
XX KW nucleic acid purification; androgen receptor promoter; triple helix; ss.

XX OS Synthetic.

XX OS Mus sp.

XX PN WO200077250-A2.

XX PD 21-DEC-2000.

XX PF 14-JUN-2000; 2000WO-FR001655.

XX PR 14-JUN-1999; 99FR-00007503.

XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

XX PA (CNRS ) CNRS CENT NAT RECH SCI.

XX PI Escude C, Garestier T, Helene C, Roulon T;

XX WPI; 2001-080698/09.

XX Circularizing oligonucleotide around double-stranded nucleic acid, useful  
XX e.g. for detecting mutations, using target-binding oligonucleotide with  
XX complementary end sequences.

XX Disclosure; Page 20; 91pp; French.

XX The specification describes a process for circularizing an  
XX oligonucleotide around a double-stranded nucleic acid that contains a  
XX target sequence. The method is used to detect or label nucleic acids,  
XX particularly plasmids, to detect target sequences in the nucleic acid,  
XX and to distinguish between two sequences that differ in only 1 or 2  
XX mutations. It can be used to select, e.g. from degenerate single-stranded  
XX nucleic acids, sequences that can bind to the nucleic acid, particularly  
XX sequences that promote entry of the nucleic acid into cells or can target  
XX the nucleic acid to specific cellular compartments. The method can also  
XX be used to purify nucleic acids, particularly plasmids, and in gene  
XX therapy for specific inhibition of a gene contained in the nucleic acid.  
XX ABL56735-36 represent a fragment of the murine androgen receptor  
XX promoter. They were used in the course of the invention, during  
XX construction of triple helices

XX SQ Sequence 50 BP; 19 A; 0 C; 30 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 50;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGGGAGGGGAGGGAGGGG 20  
|||||  
Db 16 AGGGAGGGGAGGGAGGGG 35

## RESULT 7

ABL56736/c



```
XX 20-MAR-1992; 92US-00855389.
PR 19-MAR-1993; 93WO-US002725.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX Gottchalk S, Sparrow J, Cristiano RJ, Woo SLC, Smith LC;
XX WPI; 2000-281993/24.
XX System for transporting nucleic acid into cells, useful e.g. in gene
PT therapy and for generating transgenic animals, comprises binding agent
PT linked to nucleic acid, surface ligand and lytic agent.
XX Disclosure; Fig 15a; 108pp; English.
XX The present invention relates to a transporter system for delivering
CC nucleic acid to a cell. The system comprises a nucleic acid binding
CC complex, consisting of a binding molecule bonded non-covalently to the
CC nucleic acid, and covalently to a surface ligand, and a lytic agent. The
CC binding molecule is spermine or a spermidine derivative. Nucleotide
CC sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used
CC in the construction of the transporter system of the invention. The
CC transporter system is used in gene therapy, particularly to deliver
CC nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g. for
CC treating cardiovascular disease, cancer, and infection. The transporter
CC systems are also used to create transgenic animals (as models for human
CC carcinogenesis or disease or for drug testing). Other uses include
CC transforming cells to produce proteins, or transfecting cells in vitro
CC to study the function of the nucleic acid. The use of a surface ligand
CC allows specific targeting of selected cells and tissues. The lytic agent
CC provides for release of the nucleic acid into the cellular interior, from
CC endosomes, without requiring endosomal or lysosomal degradation
XX
XX Sequence 27 BP; 0 A; 14 C; 0 G; 13 T; 0 U; 0 Other;
SQ Query Match 87.0%; Score 17.4; DB 3; Length 27;
Best Local Similarity 94.7%; Pred. No. 4.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGGGGAGGGGAGGGGAGGG 19
DB 24 AAGGGAGGGGAGGGGAGGG 6
RESULT 10
AAZ39496/C
ID AAZ39496 standard; DNA; 27 BP.
XX AAZ39496;
XX 07-MAR-2000 (first entry)
XX Template pyrimidine series sequence in a ligand.
DE Nucleic acid transport system; NTS; cell surface receptor; cytosol;
XX nuclear membrane; lysis moiety; transgenic animal; human disease;
XX nucleic acid delivery; cancer; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..27
FT /*tag= a
FT /note= "all C's are methylcytosines"
XX US5994109-A.
XX 30-NOV-1999.
XX 03-JUN-1995; 95US-00460890.
XX 20-MAR-1992; 92US-00855389.
XX
```

```
PR 19-MAR-1993; 93WO-US002725.
PR 14-DEC-1993; 93US-00167641.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX Woo SLC, Cristiano RJ, Gottchalk S, Sparrow J, Smith LC;
XX WPI; 2000-038262/03.
XX Nucleic acid transport system, useful for creating transgenic animals for
PT assessing human disease such as cancer in an animal model.
XX Disclosure; Fig 15A; 107pp; English.
XX The invention relates to a nucleic acid transport system (NTS) for
CC delivering nucleic acid into a cell. The NTS contains but is not limited
CC to 5 components: (a) the nucleic acid or a macromolecule to be delivered;
CC (b) a moiety that recognizes and binds to a cell surface receptor or
CC antigen or is capable of entering a cell through cytosol; (c) a nucleic
CC acid or macromolecular molecule binding moiety; (d) a moiety that is
CC capable of moving or initiating movement through a nuclear membrane; and/
CC or (e) a lysis moiety that enables the transport of the entire complex
CC from the cell surface directly into the cytoplasm of the cell. The NTS
CC delivers nucleic acid into the cellular interior as well as the nucleus
CC of specific cells. The NTS can be used to treat disorders by targeting
CC specific nucleic acid accordingly. The NTS can also be used to create
CC transgenic animals for assessing human disease, such as cancer, in an
CC animal model. The NTS can be used in vitro with tissue culture cells
CC which allows the role of various nucleic acids to be studied by targeting
CC specific expression into specifically targeted tissue culture cells. The
CC lysis agent within the NTS avoids the problem of endosomal/lysosomal
CC degradation
XX
XX Sequence 27 BP; 0 A; 14 C; 0 G; 13 T; 0 U; 0 Other;
SQ Query Match 87.0%; Score 17.4; DB 3; Length 27;
Best Local Similarity 94.7%; Pred. No. 4.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AGGGGAGGGGAGGGGAGGG 19
DB 24 AAGGGAGGGGAGGGGAGGG 6
RESULT 11
AAZ39497
ID AAZ39497 standard; DNA; 27 BP.
XX AAZ39497;
XX 07-MAR-2000 (first entry)
XX Template purine series sequence in a ligand.
XX Nucleic acid transport system; NTS; cell surface receptor; cytosol;
XX nuclear membrane; lysis moiety; transgenic animal; human disease;
XX nucleic acid delivery; cancer; ss.
XX Synthetic.
XX US5994109-A.
XX 30-NOV-1999.
XX 03-JUN-1995; 95US-00460890.
XX 20-MAR-1992; 92US-00855389.
XX 19-MAR-1993; 93WO-US002725.
XX 14-DEC-1993; 93US-00167641.
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX Woo SLC, Cristiano RJ, Gottchalk S, Sparrow J, Smith LC;
XX
```



```
FT modified_base 13 /*tag= g
FT /mod_base= Other
FT /note= "5-methylcytosine"
FT modified_base 15 /*tag= h
FT /mod_base= Other
FT /note= "5-methylcytosine"
FT modified_base 16 /*tag= i
FT /mod_base= Other
FT /note= "5-methylcytosine"
FT modified_base 17 /*tag= j
FT /mod_base= Other
FT /note= "5-methylcytosine"
FT modified_base 18 /*tag= k
FT /mod_base= Other
FT /note= "5-methylcytosine"
FT modified_base 20 /*tag= l
FT /mod_base= Other
FT /note= "5-methylcytosine"
FT modified_base 21 /*tag= m
FT /mod_base= Other
FT /note= "5-methylcytosine"
FT modified_base 22 /*tag= n
FT /mod_base= Other
FT /note= "5-methylcytosine"
XX US6150168-A.
XX
XX 21-NOV-2000.
XX
XX 05-JUN-1995; 95US-00460971.
XX
XX 20-MAR-1992; 92US-00855389.
XX 19-MAR-1993; 93WO-US002725.
XX 14-DEC-1993; 93US-00167641.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Gottchalk S, Sparrow J, Cristiano RJ, Smith LC, Woo SLC;
XX WPI; 2001-049093/06.
XX
XX Nucleic acid transporter system for delivering nucleic acid into a cell,
XX useful for delivering proteins and polypeptides to cells, including
XX growth factors, enzymes, hormones, and tumor suppressors.
XX
XX Disclosure; Col 97-98; 105pp; English.
XX
XX This invention describes a novel system (I) for delivering a nucleic acid
XX to a cell, comprising a binding complex comprising a ligand binding
XX molecule noncovalently bound to a nucleic acid and covalently linked to a
XX surface ligand, and a second binding complex comprising a second binding
XX molecule noncovalently bound to a nucleic acid and covalently linked to a
XX nuclear ligand. The complexes are simultaneously bound to the nucleic
XX acid. The nucleic acid transporter system can also be used in a method
XX for the in vivo targeting of the insertion of DNA into a cell. It can
XX also be used in processes for producing transformed cell lines. The
XX system can be used to deliver a variety of proteins and polypeptides,
XX such as hormones, growth factors, enzymes, clotting factors,
XX apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor
XX suppressors, viral antigens, parasitic antigens, and bacterial antigens.
XX The transporter system uses lysis agents to overcome the problems of
XX endosomal/lysosomal degradation seen with prior art systems
XX
XX Sequence 27 BP; 0 A; 14 C; 0 G; 13 T; 0 U; 0 Other;
```

---

```
Query Match 87.0%; Score 17.4; DB 4; Length 27;
Best Local Similarity 94.7%; Pred. No. 4.2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AGGGGAGGGAGGGAGGG 19
    |||||
Db 24 AAGGGAGGGAGGGAGGG 6
    |||||

RESULT 14
AAS08476/C
ID AAS08476 standard; DNA; 27 BP.
XX
XX AC AAS08476;
XX
XX DT 23-OCT-2001 (first entry)
XX
XX DE Pyrimidine-rich oligonucleotide #5 used in nucleic acid transport system.
XX
XX KW Nucleic acid transport; cytosine; ligand; lysis agent; spacer molecule;
XX gene therapy; hepatocyte; muscle; bone forming cell; oligonucleotide; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
FT modified_base 6 /*tag= a
FT /mod_base= m5c
FT modified_base 9 /*tag= b
FT /mod_base= m5c
FT modified_base 11 /*tag= c
FT /mod_base= m5c
FT modified_base 14 /*tag= d
FT /mod_base= m5c
FT modified_base 16 /*tag= e
FT /mod_base= m5c
FT modified_base 19 /*tag= f
FT /mod_base= m5c
FT modified_base 21..22 /*tag= g
FT /mod_base= m5c
XX
XX US6177554-B1.
XX
XX PD 23-JAN-2001.
XX
XX PF 05-JUN-1995; 95US-00462040.
XX
XX PR 20-MAR-1992; 92US-00855389.
XX PR 19-MAR-1993; 93WO-US002725.
XX PR 14-DEC-1993; 93US-00167641.
XX
XX PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX PI Woo SLC, Smith LC, Cristiano RJ, Gottchalk S, Sparrow J;
XX WPI; 2001-365933/38.
XX
XX Nucleic acid transport system, useful for creating transgenic animals for
XX assessing human disease such as cancer in an animal model.
XX
XX Disclosure; Fig 15; 111pp; English.
XX
XX The sequence represents the pyrimidine-rich oligonucleotide #5 used in a
XX nucleic acid transporter system. The nucleic acid transporter system uses
XX nucleic acid binding complexes containing surface ligands which are
XX capable of binding to a cell surface receptor and entering the cell
XX through cytosine. The compounds of the invention are either ligands,
```

CC binding molecules (surface ligands), lysis agents, spacer molecules or  
CC their intermediates. The ligands, binding molecules, lysis agents and  
CC spacer molecules are used in nucleic acid transporter systems to deliver  
CC nucleic acid into specific cells e.g. in gene therapy to deliver nucleic  
CC acid into hepatocytes, muscle cells or bone forming cells  
XX  
SQ Sequence 27 BP; 0 A; 14 C; 0 G; 13 T; 0 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 4; Length 27;  
Best Local Similarity 94.7%; Pred. No. 4.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 24 AAGGAGGGAGGGAGGG 6

RESULT 15  
AAS08477  
ID AAS08477 standard; DNA; 27 BP.

XX  
AC AAS08477;

DT 23-OCT-2001 (first entry)

DE Purine-rich oligonucleotide #5 used in nucleic acid transporter system.

XX Nucleic acid transport; cytosine; ligand; lysis agent; spacer molecule;  
KW gene therapy; hepatocyte; muscle; bone forming cell; oligonucleotide; ss.  
XX Synthetic.

PN US6177554-B1.

PD 23-JAN-2001.

XX 05-JUN-1995; 95US-00462040.

PR 20-MAR-1992; 92US-00855389.

PR 19-MAR-1993; 93WO-US002725.

XX 14-DEC-1993; 93US-00167641.

PA (BAYU) BAYLOR COLLEGE MEDICINE.

PI Woo SLC, Smith LC, Cristiano RJ, Gottchalk S, Sparrow J;

DR WPI; 2001-365933/38.

XX Nucleic acid transport system, useful for creating transgenic animals for  
PT assessing human disease such as cancer in an animal model.

PS Disclosure; Fig 15; 11pp; English.

XX The sequence represents the purine-rich oligonucleotide #5 used in used  
CC in a nucleic acid transporter system. The nucleic acid transporter system  
CC uses nucleic acid binding complexes containing surface ligands which are  
CC capable of binding to a cell surface receptor and entering the cell  
CC through cytosine. The compounds of the invention are either ligands,  
CC binding molecules (surface ligands), lysis agents, spacer molecules or  
CC their intermediates. The ligands, binding molecules, lysis agents and  
CC spacer molecules are used in nucleic acid transporter systems to deliver  
CC nucleic acid into specific cells e.g. in gene therapy to deliver nucleic  
CC acid into hepatocytes, muscle cells or bone forming cells  
XX

SQ Sequence 27 BP; 13 A; 0 C; 14 G; 0 T; 0 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 4; Length 27;  
Best Local Similarity 94.7%; Pred. No. 4.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 4 AAGGAGGGAGGGAGGG 22

RESULT 16  
AAD41066  
ID AAD41066 standard; DNA; 30 BP.  
XX  
AC AAD41066;  
XX  
DT 30-OCT-2002 (first entry)  
XX  
DE Primer ON-TAPAdel used for DNA sequencing.

XX Tumour necrosis-factor; TNF; promoter; autoimmune disorder; cancer;  
KW therapy; primer; ss.

XX Unidentified.

PN WO200246433-A2.

XX 13-JUN-2002.

XX 07-DEC-2001; 2001WO-EP014412.

XX 08-DEC-2000; 2000US-0254649P.

XX (SAUS/) SAUS J.

XX Saus J;

DR WPI; 2002-519670/55.

XX Novel tumor necrosis-factor inducible promoter useful for identifying  
PT candidate compounds for treating/preventing autoimmune disorders/cancer,  
PT or for identifying promoters that are regulated by tumor necrosis factor.  
XX  
XX Example; Page 17; 95pp; English.

XX The invention relates to a tumour necrosis-factor TNF inducible promoter.  
CC The invention is useful for identifying candidate TNF inducible promoters  
CC by aligning a test sequence consisting of a nucleic acid sequence with a  
CC comparison sequence selected from the invention, using a gap opening  
CC penalty of 50 and a gap extension penalty of 3 to define a test  
CC alignment, shuffling the nucleic sequence of the test sequence at least  
CC one hundred times, while maintaining its length and composition, to  
CC produce a series of randomised sequences, aligning the randomised  
CC sequences with the comparison sequence using a gap opening penalty of 50  
CC and a gap extension penalty of 3, to produce a series of randomised  
CC alignments, determining an average alignment quality of the randomised  
CC alignments, where the average alignment quality of the randomised  
CC alignments represent an alignment expected by chance, comparing the test  
CC alignment with the average alignment quality of the randomised alignments  
CC and identifying a test alignment with a probability value of less than  
CC 0.05 that the alignment is obtained by chance as a candidate TNF  
CC inducible promoter. The invention is useful for identifying candidate  
CC compounds for treating or preventing autoimmune disorders or cancer. The  
CC present sequence is a primer used in the exemplification of the invention  
XX  
SQ Sequence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;

Query Match 87.0%; Score 17.4; DB 6; Length 30;  
Best Local Similarity 94.7%; Pred. No. 4.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 2 AGGGAGGGAGGGAGGG 20

RESULT 17  
ABT03901  
ID ABT03901 standard; DNA; 30 BP.

XX  
AC ABT03901;



```
XX 18-SEP-2002 (first entry)
XX Human pol kappa 76 DNA polymerase sequencing primer #7.
XX
XX Human; pol kappa 76; Goodpasture antigen binding protein; GPBP;
XX chromosome 5q12-13; apoptosis; autoimmune disorder; cancer; cytostatic;
XX immunosuppressive; PCR; primer; sequencing; ss.
XX
XX Homo sapiens.
XX WO200246378-A2.
XX
XX 13-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-EP014409.
XX
XX 08-DEC-2000; 2000US-0254649P.
XX (SAUS/) SAUS J.
XX Saus J;
XX WPI; 2002-537563/57.
XX
XX Novel isolated pol kappa76 polypeptide, a 76 kDa alternatively spliced
XX variant of DNA polymerase kappa, useful as target for treating a patient
XX with autoimmune disorder or cancer.
XX
XX Example; Page 15; 90pp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX DNA polymerase pol kappa 76. The gene is found on human chromosome 5q12-
XX 13, in a head-to-head arrangement with the Goodpasture antigen binding
XX protein (GPBP). The detection of the coding sequence can be used for
XX diagnosing an autoimmune condition and identifying cells undergoing
XX apoptosis, and the sequences can be used in the treatment of autoimmune
XX diseases and cancer. The present sequence is a sequencing primer
XX described in the invention
XX
XX Sequence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 87.0%; Score 17.4; DB 6; Length 30;
XX Best Local Similarity 94.7%; Pred. No. 4.2e+03;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 AGGGAGGGGAGGGAGGG 19
XX 2 AGGGAGGGGAGGGGTGGG 20
XX
XX
XX RESULT 18
XX ACD13504
XX ID ACD13504 standard; DNA; 30 BP.
XX
XX AC ACD13504;
XX
XX 14-AUG-2003 (first entry)
XX
XX Human bi-directional promoter PCR/sequencing primer ON-TATAdel.
XX
XX Human; ss; Goodpasture antigen binding protein; GPBP; COL4A3BP;
XX collagen 4 alpha 3 binding protein; DNA polymerase kappa; Pol kappa;
XX Goodpasture disease; cutaneous lupus; polk76; bi-directional promoter;
XX autoimmune disease; cancer; antisense therapy; PCR; primer.
XX
XX Homo sapiens.
XX
XX US2003027165-A1.
XX
XX 06-FEB-2003.
XX
XX 07-DEC-2001; 2001US-00010920.
XX
```

```
XX 08-DEC-2000; 2000US-0254649P.
XX (SAUS/) SAUS J.
XX Saus J;
XX WPI; 2003-479531/45.
XX
XX New isolated DNA polymerase, pol kappa 76, useful in identifying
XX autoimmune disorders and in treating cancer and autoimmune disorders by
XX modifying its expression.
XX
XX Example; Page 6; 54pp; English.
XX
XX The invention relates to an isolated pol kappa (k) 76 polypeptide (an
XX alternatively spliced form of DNA polymerase kappa), appearing as
XX AB007327 (encoded by the cDNA appearing as ACD13492). The gene for
XX Polkappa is located on chromosome 5q12-13 in a head-head arrangement with
XX the gene encoding Goodpasture antigen binding protein (GPBP or collagen 4
XX alpha 3 binding protein (COL4A3bp), associated with autoimmune diseases
XX such as Goodpasture's disease and cutaneous lupus) i.e. has a bi-
XX directional promoter. Also included are a recombinant expression vector
XX comprising the polk76 cDNA, a host cell transfected with the vector,
XX detecting (M1) polk76 (comprising providing a protein sample to be
XX screened, contacting the protein sample to be screened with an anti-
XX polk76 antibody and detecting the formation of an antibody- polypeptide
XX complexes, where the presence of the antibody-polypeptide complexes
XX indicates the presence of polk76), detecting (M2) the polk76 nucleic acid
XX in a sample (comprising contacting the sample with one or more polk76 PCR
XX primer, carrying out PCR to generate PCR products, and identifying the
XX polk76-specific PCR), detecting an autoimmune condition in a patient
XX (comprising providing a tissue or body fluid sample from the patient,
XX providing a control tissue or body fluid sample in which no autoimmune
XX condition is present, and detecting an increase in pol k76 RNA expression
XX in the tissue of body fluid samples compared to the control sample, where
XX the increase indicates the presence of an autoimmune condition) and
XX treating (M3) a patient with an autoimmune disorder or cancer by
XX modifying the expression or activity of pol k76 in the patient. Modifying
XX the expression or activity of polk76 or polk76 nucleic acid, such as by
XX increasing or decreasing their expression or activity using antibodies or
XX antisense therapy, is useful for treating an autoimmune disorder or
XX cancer. The present sequence is a PCR and/or sequencing primer used in
XX the analysis of bi-directional promoters of other genes (and/or of
XX polkappa/GPBP), whose structure and sequence were compared to the
XX polkappa/GPBP bi-directional promoter
XX
XX Sequence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 87.0%; Score 17.4; DB 9; Length 30;
XX Best Local Similarity 94.7%; Pred. No. 4.2e+03;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 AGGGAGGGGAGGGAGGG 19
XX 2 AGGGAGGGGAGGGGTGGG 20
XX
XX
XX RESULT 19
XX ADA97805
XX ID ADA97805 standard; DNA; 30 BP.
XX
XX AC ADA97805;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human tumour necrosis factor (TNF) inducible promoter PCR primer #7.
XX
XX Human; tumour necrosis factor inducible promoter; TNF;
XX autoimmune disorder; cancer; PCR; immunosuppressive; cytostatic; ss;
XX primer.
XX
XX Homo sapiens.
XX
```

XX US2003082745-A1.  
XX 01-MAY-2003.  
XX 07-DEC-2001; 2001US-00008721.  
XX 08-DEC-2000; 2000US-0254649P.  
XX (SAUS/) SAUS J.  
XX Saus J;  
XX WPI; 2003-606062/57.  
XX New tumor necrosis factor inducible promoters, useful for identifying  
PT promoters that are regulated by tumor necrosis factor, or for identifying  
PT candidate compounds for treating or preventing autoimmune disorders or  
PT cancer.  
XX Example; Page 7; 57pp; English.  
XX The invention relates to a tumour necrosis factor (TNF) inducible  
CC promoter. Also disclosed are an expression vector comprising one or more  
CC tumour necrosis factor inducible promoters and a recombinant host cell  
CC transfected with one or more expression vectors. The TNF inducible  
CC promoters, expression vectors and host cells are useful for identifying  
CC promoters that are regulated by tumour necrosis factor or for identifying  
CC candidate compounds for treating or preventing autoimmune disorders or  
CC cancer. This sequence represents a PCR primer used for isolating a tumour  
CC necrosis factor inducible promoter of the invention.  
XX Sequence 30 BP; 6 A; 4 C; 17 G; 3 T; 0 U; 0 Other;  
SQ

Query Match 87.0%; Score 17.4; DB 9; Length 30;  
Best Local Similarity 94.7%; Pred. No. 4.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 AGGGGAGGGGAGGGAGGG 19  
Db 2 AGGGGAGGGGAGGGGTGGG 20

RESULT 20  
AAA36645  
ID AAA36645 standard; cDNA; 39 BP.  
XX AAA36645;  
AC  
XX  
DT 31-JUL-2000 (first entry)  
XX Nucleic acid transporter system target sequence #5.  
XX  
KW Transporter system; nucleic acid delivery; gene therapy; cancer;  
KW carcinogenesis; cardiovascular disease; infection; ss.  
XX Synthetic.  
XX  
XX US6033884-A.  
XX  
XX 07-MAR-2000.  
XX  
XX 14-DEC-1993; 93US-00167641.  
XX  
XX 20-MAR-1992; 92US-00855389.  
XX 19-MAR-1993; 93WO-US0002725.  
XX  
XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX  
XX Gottchalk S, Sparrow J, Cristiano RJ, Woo SLC, Smith LC;  
XX WPI; 2000-281993/24.  
XX

PT System for transporting nucleic acid into cells, useful e.g. in gene  
PT therapy and for generating transgenic animals, comprises binding agent  
PT linked to nucleic acid, surface ligand and lytic agent.  
XX Disclosure; Fig 15a; 108pp; English.  
XX  
XX The present invention relates to a transporter system for delivering  
CC nucleic acid to a cell. The system comprises a nucleic acid binding  
CC complex, consisting of a binding molecule bonded non-covalently to the  
CC nucleic acid, and covalently to a surface ligand, and a lytic agent. The  
CC binding molecule is spermine or a spermidine derivative. Nucleotide  
CC sequences AAA36633-A36652 and peptide sequences AAY98456-Y98500 are used  
CC in the construction of the transporter system of the invention. The  
CC transporter system is used in gene therapy, particularly to deliver  
CC nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for  
CC treating cardiovascular disease, cancer, and infection. The transporter  
CC systems are also used to create transgenic animals (as models for human  
CC carcinogenesis or disease or for drug testing). Other uses include  
CC transforming cells to produce proteins, or transfecting cells in vitro  
CC to study the function of the nucleic acid. The use of a surface ligand  
CC allows specific targeting of selected cells and tissues. The lytic agent  
CC provides for release of the nucleic acid into the cellular interior, from  
CC endosomes, without requiring endosomal or lysosomal degradation  
XX Sequence 39 BP; 13 A; 6 C; 14 G; 6 T; 0 U; 0 Other;  
SQ

Query Match 87.0%; Score 17.4; DB 3; Length 39;  
Best Local Similarity 94.7%; Pred. No. 4.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 AGGGGAGGGGAGGGAGGG 19  
Db 10 AGGGGAGGGGAGGGAGGG 28

RESULT 21  
AAZ39495  
ID AAZ39495 standard; DNA; 39 BP.  
XX AAZ39495;  
AC  
XX 07-MAR-2000 (first entry)  
XX  
XX Target sequence in a double stranded vector.  
XX  
XX Nucleic acid transport system; NTS; cell surface receptor; cytosol;  
KW nuclear membrane; lysis moiety; transgenic animal; human disease;  
KW nucleic acid delivery; cancer; ds.  
XX Synthetic.  
XX  
XX US5994109-A.  
XX  
XX 30-NOV-1999.  
XX  
XX 03-JUN-1995; 95US-00460890.  
XX  
XX 20-MAR-1992; 92US-00855389.  
XX 19-MAR-1993; 93WO-US0002725.  
XX 14-DEC-1993; 93US-00167641.  
XX  
XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX  
XX Woo SLC, Cristiano RJ, Gottchalk S, Sparrow J, Smith LC;  
XX WPI; 2000-038262/03.  
XX  
XX Nucleic acid transport system, useful for creating transgenic animals for  
PT assessing human disease such as cancer in an animal model.  
XX Disclosure; Fig 15A; 107pp; English.  
XX  
XX The invention relates to a nucleic acid transport system (NTS) for  
CC



Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 AGGGAGGGAGGGAGGG 19
Db	10 AAGGGAGGGAGGGAGGG 28
RESULT 24	
ID	ABK98155 standard; DNA; 39 BP.
XX	AC ABK98155;
XX	07-OCT-2002 (first entry)
DT	
XX	Triple helix forming associated DNA sequence #19.
DE	
XX	Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW	gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW	pathogenic bacteria; virus; replication; virulence; cancer;
KW	oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX	
OS	Synthetic.
XX	
XX	US6403302-B1.
XX	
PD	11-JUN-2002.
XX	
XX	
FF	16-DEC-1993; 93US-00168920.
XX	
XX	
PR	17-SEP-1992; 92US-00946976.
XX	
XX	
PA	(CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX	
PI	Dervan PB, Beal PA;
XX	
DR	WPI; 2002-536030/57.
XX	
XX	
PT	A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT	oligonucleotide which binds in parallel and antiparallel orientation,
PT	respectively, for targetting sequences on alternate strands of DHNA to
PT	control gene expression.
XX	
XX	
PS	Example 4; Fig 8B; 108pp; English.
XX	
CC	The present invention relates to methods and oligonucleotides for forming
CC	a triple-helix comprising a double helical nucleic acid comprising first
CC	and second substantially complementary strands, and an oligonucleotide
CC	bound to a purine-rich target sequence within the double helical nucleic
CC	acid, where the oligonucleotide binds in a parallel and antiparallel
CC	orientation, respectively, to target sequences on alternate strands of
CC	the double helical nucleic acid. The method has therapeutic applications,
CC	where gene expression is controlled by selective triple-helix formation
CC	within expression regulatory sequences of a target gene. The
CC	oligonucleotides can be used to form triple-helices, and are useful to
CC	detect the presence or absence of specific sequences within genomic DNA
CC	for diagnostic and therapeutic purposes. The oligonucleotides can be
CC	selected to specifically bind to pathogenic double-stranded DNA including
CC	specific sequences required by pathogenic bacteria or viruses for
CC	replication or virulence, reducing their pathogenicity. Alternatively,
CC	the oligonucleotide can be chosen to target a unique sequence of the
CC	pathogen which is not found in the genome of pathogen's host. The
CC	oligonucleotides can be used in cancer treatment by way of triple-helix
CC	suppression of specific oncogenes including those of endogenous or viral
CC	origin. Such therapeutic oligonucleotides are capable of forming triple-
CC	helices with such sequences in cancerous cells containing the activated
CC	oncogene, so preferentially killing or repressing the cancer causing
CC	cell. The present sequence represents a DNA sequence used in the methods
CC	of the present invention
XX	
XX	Sequence 39 BP; 13 A; 6 C; 14 G; 6 T; 0 U; 0 Other;
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	
XX	

Query Match	87.0%;	Score 17.4;	DB 6;	Length 39;	
Best Local Similarity	94.7%;	Pred. No. 4.1e+03;			
Matches	18;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
QY	1	AGGGGAGGGGAGGGGAGGG	19		
Db	30	AAGGGAGGGGAGGGGAGGG	12		
RESULT 26					
ABK98106					
ID	ABK98106	standard; DNA;	43 BP.		
XX					
AC	ABK98106;				
XX					
DT	07-OCT-2002	(first entry)			
XX					
DE	Triple helix forming associated oligonucleotide #3.				
XX					
KW	Triple-helix formation; purine-rich target sequence; double-helix DNA;				
KW	gene expression; regulatory sequence; pathogenic double-stranded DNA;				
KW	pathogenic bacteria; virus; replication; virulence; cancer;				
KW	oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.				
XX					
OS	Synthetic.				
XX					
PN	US6403302-B1.				
XX					
PD	11-JUN-2002.				
XX					
PF	16-DEC-1993;	93US-00168920.			
XX					
PR	17-SEP-1992;	92US-00946976.			
XX					
PA	(CALY ) CALIFORNIA INST OF TECHNOLOGY.				
XX					
PI	Dervan PB, Beal PA;				
XX					
DR	WPI; 2002-536030/57.				
XX					
PT	A triple-helix comprising a double helical nucleic acid (DHNA) and an				
PT	oligonucleotide which binds in parallel and antiparallel orientation,				
PT	respectively, for targeting sequences on alternate strands of DHNA to				
PT	control gene expression.				
XX					
PS	Example 4; Col 29; 108pp; English.				
XX					
CC	The present invention relates to methods and oligonucleotides for forming				
CC	a triple-helix comprising a double helical nucleic acid comprising first				
CC	and second substantially complementary strands, and an oligonucleotide				
CC	bound to a purine-rich target sequence within the double helical nucleic				
CC	acid, where the oligonucleotide binds in a parallel and antiparallel				
CC	orientation, respectively, to target sequences on alternate strands of				
CC	the double helical nucleic acid. The method has therapeutic applications,				
CC	where gene expression is controlled by selective triple-helix formation				
CC	within expression regulatory sequences of a target gene. The				
CC	oligonucleotides can be used to form triple-helices, and are useful to				
CC	detect the presence or absence of specific sequences within genomic DNA				
CC	for diagnostic and therapeutic purposes. The oligonucleotides can be				
CC	selected to specifically bind to pathogenic double-stranded DNA including				
CC	specific sequences required by pathogenic bacteria or viruses for				
CC	replication or virulence, reducing their pathogenicity. Alternatively,				
CC	the oligonucleotide can be chosen to target a unique sequence of the				
CC	pathogen which is not found in the genome of pathogen's host. The				
CC	oligonucleotides can be used in cancer treatment by way of triple-helix				
CC	suppression of specific oncogenes including those of endogenous or viral				
CC	origin. Such therapeutic oligonucleotides are capable of forming triple-				
CC	helices with such sequences in cancerous cells containing the activated				
CC	oncogene, so preferentially killing or repressing the cancer causing				
CC	cell. The present sequence represents an oligonucleotide used in the				
CC	methods of the present invention				
XX					
SO	Sequence 43 BP: 15 A: 6 C: 14 G: 8 T: 0 U: 0 Other:				

SQ Sequence 19 BP; 5 A; 0 C; 14 G; 0 T; 0 U; 0 Other;  
Query Match 85.0%; Score 17; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GGGAGGGGGGGGAGGG 19  
DB 2 GGGAGGGGGGGGAGGG 18  
RESULT 28  
ADH70505/c  
ID ADH70505 standard; DNA; 23 BP.  
XX AC ADH70505;  
XX DT 25-MAR-2004 (first entry)  
XX DE Human Vbeta gene repeat sequence #295.  
XX KW human; T-cell associated disease; Vbeta; autoimmune disease;  
KW degenerative nervous system disease; graft versus host disease;  
KW hypersensitivity disease; infectious disease; neoplastic disease;  
KW Addison's disease; atrophic gastritis;  
KW degenerative nervous system disease; multiple sclerosis;  
KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;  
KW allergy; type II hypersensitivity; Goodpasture's syndrome;  
KW type IV hypersensitivity; leprosy; infectious disease; viral infection;  
KW HIV; fungal infection; Candida; parasitic infection; schistosoma;  
KW filaria; bacterial infection; Mycobacterium; neoplastic disease;  
KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;  
KW breast cancer; ds.  
XX OS Homo sapiens.  
XX OS US2002150891-A1.  
XX FN 17-OCT-2002.  
XX PD 05-MAR-1999; 99US-00263959.  
XX PF 19-SEP-1994; 94US-00309335.  
XX PR 19-SEP-1995; 95US-00531241.  
XX XX (HOOD//) HOOD L E.  
XX FA (ROWE//) ROWEN L.  
XX PI Hood LE, Rowen L;  
XX WPI; 2004-059052/06.  
XX Kit for diagnosing and treating T-cell associated diseases e.g.  
XX autoimmune, degenerative nervous system and infectious disease, comprises  
XX nucleic acid primers specifically priming and allowing amplification of a  
XX Vbeta gene.  
XX Disclosure; SEQ ID NO 699; 164pp; English.  
XX The invention relates to a kit for diagnosing and treating T-cell  
XX associated diseases which comprises a panel of nucleic acid primers  
XX specifically priming and allowing amplification of each Vbeta gene,  
XX VbetatRNA or cDNA. The kit is useful for diagnosing organ transplant  
XX rejection and diagnosing and treating T-cell associated diseases  
XX including autoimmune diseases, degenerative nervous system diseases,  
XX graft versus host disease, hypersensitivity diseases, infectious diseases  
XX and neoplastic diseases. Autoimmune diseases include Addison's disease,  
XX atrophic gastritis. Degenerative nervous system diseases include multiple  
XX sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type  
XX I hypersensitivities such as contact with allergens that lead to  
XX allergies, type II hypersensitivities such as those present in  
XX Goodpasture's syndrome and Type IV hypersensitivities such as those  
XX manifested in leprosy. Infectious diseases include viral infections

CC caused by viruses such as HIV, fungal infections such as those caused by  
CC the yeast genus Candida, parasitic infections such as those caused by  
CC schistosomes, filaria and bacterial infections such as those caused by  
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases  
CC such as leukemias, lymphomas and cancers such as cancer of the brain,  
CC breast. The present sequence represents a Vbeta gene repeat sequence.  
XX SQ Sequence 23 BP; 1 A; 17 C; 1 G; 4 T; 0 U; 0 Other;  
Query Match 84.0%; Score 16.8; DB 12; Length 23;  
Best Local Similarity 90.0%; Pred. No. 6.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGGGAGGGGGGGGAGGGG 20  
DB 23 AGGGGGGGGGAGGTGAGGGG 4  
RESULT 29  
AAQ46253  
ID AAQ46253 standard; DNA; 43 BP.  
XX AC AAQ46253;  
XX DT 25-MAR-2003 (revised)  
XX DT 24-MAR-1994 (first entry)  
XX DE 39mer duplex forming DNA.  
XX KW Duplex; T4 polynucleotide kinase; nebularine; triple helix; triplex;  
KW detection; diagnosis; pathogen; bacteria; virus; virulence; cancer;  
KW oncogene; ss.  
XX OS Synthetic.  
XX OS Key Location/Qualifiers  
XX FT misc\_difference 19  
XX FT /\*tag= a  
XX FT /note= "A, G, C or T"  
XX FN W09318187-A1.  
XX PD 16-SEP-1993.  
XX PF 11-MAR-1993; 93WO-US002352.  
XX PR 13-MAR-1992; 92US-00850503.  
XX XX (CALY ) CALIFORNIA INST OF TECHN.  
XX XX Dervan PB;  
XX WPI; 1993-303498/38.  
XX Triple helix formation for diagnosis and therapy - by specific  
XX recognition by oligo:nucleotide probe of target sequence in double-  
XX stranded nucleic acid.  
XX Example 1; Page 18; 42pp; English.  
XX This sequence was used to form a 39mer duplex an example to illustrate  
XX the invention. Oligonucleotides conforming to this sequence were 5' and  
XX radioactively labeled using T4 polynucleotide kinase and gamma-32P ATP.  
XX The annealed oligomers form a purine-rich target sequence to which an  
XX oligonucleotide (TFO) containing a nebularine nucleotide binds, forming a  
XX triple helix. These triplex- forming oligomers may be used to detect the  
XX presence or absence of specific sequences within genomic DNA by the  
XX formation in situ or in vivo of triple helices for diagnostic and  
XX therapeutic purposes. TFO can be selected which specifically bind to  
XX pathogenic double-stranded DNA including specific sequences required by  
XX pathogenic bacteria or viruses for replication or virulence.  
XX Alternatively, TFO can be chosen to target a unique sequence of the  
XX pathogen which is not found in the genome of the host. It may include a

CC therapeutic agent to kill the pathogen or the cell containing it. Triple  
CC helix technology can also be used for cancer treatment by way of triple  
CC helix suppression of specific oncogenes including those of endogenous or  
CC viral origin. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;  
Query Match 82.0%; Score 16.4; DB 2; Length 43;  
Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGGGGAGGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 14 AAGGGGAGGGGAGGGAGGG 32  
RESULT 30  
AAQ46257/c  
ID AAQ46257 standard; DNA; 43 BP.  
XX  
AC AAQ46257;  
XX  
DT 25-MAR-2003 (revised)  
DT 24-MAR-1994 (first entry)  
XX  
DE Duplex forming DNA #2.  
XX  
KW Duplex; T4 polynucleotide kinase; nebularine; triple helix; triplex;  
KW detection; diagnosis; pathogen; bacteria; virus; virulence; cancer;  
KW oncogene; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 29 /\*tag= a  
FT misc\_difference 29 /\*tag= a  
FT /\*note= "A, G, C or T"  
XX  
PN WO9318187-A1.  
XX  
PD 16-SEP-1993.  
XX  
PF 11-MAR-1993; 93WO-US002352.  
XX  
PR 13-MAR-1992; 92US-00850503.  
XX  
PA (CALY ) CALIFORNIA INST OF TECHN.  
XX  
PI Dervan PB;  
XX  
WPI; 1993-303498/38.  
XX  
PT Triple helix formation for diagnosis and therapy - by specific  
PT recognition by oligo:nucleotide probe of target sequence in double-  
PT stranded nucleic acid.  
XX  
PS Example 1; Page 23; 42pp; English.  
XX  
The sequences given in AAQ46256-57 form a duplex which was used to  
CC evaluate the binding of triplex forming oligomers (TFO). The annealed  
CC oligomers form a purine-rich target sequence to which the TFO which  
CC contain a nebularine nucleotide binds, bind, forming a triple helix.  
CC These triplex-forming oligomers may be used to detect the presence or  
CC absence of specific sequences within genomic DNA by the formation in situ  
CC or in vivo of triple helices for diagnostic and therapeutic purposes. TFO  
CC can be selected which specifically bind to pathogenic double-stranded DNA  
CC including specific sequences required by pathogenic bacteria or viruses  
CC for replication or virulence. Alternatively, TFO can be chosen to target  
CC a unique sequence of the pathogen which is not found in the genome of the  
CC host. It may include a therapeutic agent to kill the pathogen or the cell  
CC containing it. Triple helix technology can also be used for cancer  
CC treatment by way of triple helix suppression of specific oncogenes  
CC including those of endogenous or viral origin. (Updated on 25-MAR-2003 to

CC correct PN field.)  
XX  
SQ Sequence 43 BP; 7 A; 15 C; 7 G; 13 T; 0 U; 1 Other;  
Query Match 82.0%; Score 16.4; DB 2; Length 43;  
Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGGGGAGGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 34 AAGGGGAGGGGAGGGAGGG 16  
RESULT 31  
AAQ46256  
ID AAQ46256 standard; DNA; 43 BP.  
XX  
AC AAQ46256;  
XX  
DT 21-OCT-2004 (revised)  
DT 25-MAR-2003 (revised)  
DT 24-MAR-1994 (first entry)  
XX  
DE Duplex forming DNA #1.  
XX  
KW Duplex; T4 polynucleotide kinase; nebularine; triple helix; triplex;  
KW detection; diagnosis; pathogen; bacteria; virus; virulence; cancer;  
KW oncogene; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /\*mod\_base= OTHER  
FT misc\_difference 19 /\*tag= b  
FT /\*note= "A, G, C or T"  
XX  
PN WO9318187-A1.  
XX  
PD 16-SEP-1993.  
XX  
PF 11-MAR-1993; 93WO-US002352.  
XX  
PR 13-MAR-1992; 92US-00850503.  
XX  
PA (CALY ) CALIFORNIA INST OF TECHN.  
XX  
PI Dervan PB;  
XX  
WPI; 1993-303498/38.  
XX  
PT Triple helix formation for diagnosis and therapy - by specific  
PT recognition by oligo:nucleotide probe of target sequence in double-  
PT stranded nucleic acid.  
XX  
PS Example 1; Page 23; 42pp; English.  
XX  
The sequences given in AAQ46256-57 form a duplex which was used to  
CC evaluate the binding of triplex forming oligomers (TFO). The annealed  
CC oligomers form a purine-rich target sequence to which the TFO which  
CC contain a nebularine nucleotide binds, bind, forming a triple helix.  
CC These triplex-forming oligomers may be used to detect the presence or  
CC absence of specific sequences within genomic DNA by the formation in situ  
CC or in vivo of triple helices for diagnostic and therapeutic purposes. TFO  
CC can be selected which specifically bind to pathogenic double-stranded DNA  
CC including specific sequences required by pathogenic bacteria or viruses  
CC for replication or virulence. Alternatively, TFO can be chosen to target  
CC a unique sequence of the pathogen which is not found in the genome of the  
CC host. It may include a therapeutic agent to kill the pathogen or the cell  
CC containing it. Triple helix technology can also be used for cancer

CC treatment by way of triple helix suppression of specific oncogenes  
CC including those of endogenous or viral origin. (Updated on 25-MAR-2003 to  
CC correct PN field.)

CC Revised record issued on 21-OCT-2004 : Correction to feature table key

XX  
XX  
SQ Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;

Query Match 82.0%; Score 16.4; DB 2; Length 43;  
Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 14 AAGGGGGGAGGGAGGG 32

RESULT 32  
ABK98158/c  
ID ABK98158 standard; DNA; 43 BP.

XX  
XX  
AC ABK98158;

XX  
XX  
DT 07-OCT-2002 (first entry)

XX  
XX  
DE Triple helix forming associated DNA sequence #21.

XX  
XX  
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
KW pathogenic bacteria; virus; replication; virulence; cancer;  
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX  
OS Synthetic.

XX  
FN US6403302-B1.

XX  
XX  
PD 11-JUN-2002.

XX  
XX  
PF 16-DEC-1993; 93US-00168920.

XX  
XX  
PF 17-SEP-1992; 92US-00946976.

XX  
XX  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.

XX  
XX  
PI Dervan PB, Beal PA;

XX  
XX  
DR WPI; 2002-536030/57.

XX  
XX  
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an  
PT oligonucleotide which binds in parallel and antiparallel orientation,  
PT respectively, for targetting sequences on alternate strands of DHNA to  
PT control gene expression.

XX  
PS Example 5; Fig 11; 108pp; English.

XX  
XX  
CC The present invention relates to methods and oligonucleotides for forming  
CC a triple-helix comprising a double helical nucleic acid comprising first  
CC and second substantially complementary strands, and an oligonucleotide  
CC bound to a purine-rich target sequence within the double helical nucleic  
CC acid, where the oligonucleotide binds in a parallel and antiparallel  
CC orientation, respectively, to target sequences on alternate strands of  
CC the double helical nucleic acid. The method has therapeutic applications,  
CC where gene expression is controlled by selective triple-helix formation,  
CC within expression regulatory sequences of a target gene. The  
CC oligonucleotides can be used to form triple-helices, and are useful to  
CC detect the presence or absence of specific sequences within genomic DNA  
CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
CC selected to specifically bind to pathogenic double-stranded DNA including  
CC specific sequences required by pathogenic bacteria or viruses for  
CC replication or virulence, reducing their pathogenicity. Alternatively,  
CC the oligonucleotide can be chosen to target a unique sequence of the  
CC pathogen which is not found in the genome of pathogen's host. The  
CC oligonucleotides can be used in cancer treatment by way of triple-helix

CC suppression of specific oncogenes including those of endogenous or viral  
CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
CC helices with such sequences in cancerous cells containing the activated  
CC oncogene, so preferentially killing or repressing the cancer causing  
CC cell. The present sequence represents a DNA sequence used in the methods  
CC of the present invention

SQ Sequence 43 BP; 7 A; 15 C; 7 G; 13 T; 0 U; 1 Other;

Query Match 82.0%; Score 16.4; DB 6; Length 43;  
Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 34 AAGGGGGGAGGGAGGG 16

RESULT 33  
ABK98112/c  
ID ABK98112 standard; DNA; 43 BP.

XX  
XX  
AC ABK98112;

XX  
XX  
DT 07-OCT-2002 (first entry)

XX  
XX  
DE Triple helix forming associated DNA sequence #3.

XX  
XX  
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
KW pathogenic bacteria; virus; replication; virulence; cancer;  
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX  
OS Synthetic.

XX  
FN US6403302-B1.

XX  
XX  
PD 11-JUN-2002.

XX  
XX  
PF 16-DEC-1993; 93US-00168920.

XX  
XX  
PF 17-SEP-1992; 92US-00946976.

XX  
XX  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.

XX  
XX  
PI Dervan PB, Beal PA;

XX  
XX  
DR WPI; 2002-536030/57.

XX  
XX  
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an  
PT oligonucleotide which binds in parallel and antiparallel orientation,  
PT respectively, for targetting sequences on alternate strands of DHNA to  
PT control gene expression.

XX  
PS Example 5; Col 35; 108pp; English.

XX  
XX  
CC The present invention relates to methods and oligonucleotides for forming  
CC a triple-helix comprising a double helical nucleic acid comprising first  
CC and second substantially complementary strands, and an oligonucleotide  
CC bound to a purine-rich target sequence within the double helical nucleic  
CC acid, where the oligonucleotide binds in a parallel and antiparallel  
CC orientation, respectively, to target sequences on alternate strands of  
CC the double helical nucleic acid. The method has therapeutic applications,  
CC where gene expression is controlled by selective triple-helix formation,  
CC within expression regulatory sequences of a target gene. The  
CC oligonucleotides can be used to form triple-helices, and are useful to  
CC detect the presence or absence of specific sequences within genomic DNA  
CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
CC selected to specifically bind to pathogenic double-stranded DNA including  
CC specific sequences required by pathogenic bacteria or viruses for  
CC replication or virulence, reducing their pathogenicity. Alternatively,  
CC the oligonucleotide can be chosen to target a unique sequence of the  
CC pathogen which is not found in the genome of pathogen's host. The



CC oligonucleotides can be used in cancer treatment by way of triple-helix  
 CC suppression of specific oncogenes including those of endogenous or viral  
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
 CC helices with such sequences in cancerous cells containing the activated  
 CC oncogene, so preferentially killing or repressing the cancer causing  
 CC cell. The present sequence represents a DNA sequence used in the methods  
 CC of the present invention

XX SQ Sequence 43 BP; 7 A; 15 C; 7 G; 13 T; 0 U; 1 Other;

Query Match 82.0%; Score 16.4; DB 6; Length 43;  
 Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGAGGGAGGG 19  
 |||||  
 Db 34 AAGGGGGAGGGAGGGAGG 16

RESULT 34  
 ABK98111  
 ID ABK98111 standard; DNA; 43 BP.

XX AC ABK98111;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated DNA sequence #2.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
 KW pathogenic bacteria; virus; replication; virulence; cancer;  
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX FN US6403302-B1.

XX PD 11-JUN-2002.

XX PF 16-DEC-1993; 93US-00168920.

XX PR 17-SEP-1992; 92US-00946976.

XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.

XX PI Dervan PB, Beal PA;

XX DR WPI; 2002-536030/57.

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an  
 PT oligonucleotide which binds in parallel and antiparallel orientation,  
 PT respectively, for targeting sequences on alternate strands of DHNA to  
 PT control gene expression.

XX Example 5; Col 35; 108pp; English.

XX The present invention relates to methods and oligonucleotides for forming  
 CC a triple-helix comprising a double helical nucleic acid comprising first  
 CC and second substantially complementary strands, and an oligonucleotide  
 CC bound to a purine-rich target sequence within the double helical nucleic  
 CC acid, where the oligonucleotide binds in a parallel and antiparallel  
 CC orientation, respectively, to target sequences on alternate strands of  
 CC the double helical nucleic acid. The method has therapeutic applications,  
 CC where gene expression is controlled by selective triple-helix formation  
 CC within expression regulatory sequences of a target gene. The  
 CC oligonucleotides can be used to form triple-helices, and are useful to  
 CC detect the presence or absence of specific sequences within genomic DNA  
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
 CC selected to specifically bind to pathogenic double-stranded DNA including  
 CC specific sequences required by pathogenic bacteria or viruses for  
 CC replication or virulence, reducing their pathogenicity. Alternatively,  
 CC the oligonucleotide can be chosen to target a unique sequence of the

CC pathogen which is not found in the genome of pathogen's host. The  
 CC oligonucleotides can be used in cancer treatment by way of triple-helix  
 CC suppression of specific oncogenes including those of endogenous or viral  
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
 CC helices with such sequences in cancerous cells containing the activated  
 CC oncogene, so preferentially killing or repressing the cancer causing  
 CC cell. The present sequence represents a DNA sequence used in the methods  
 CC of the present invention

XX SQ Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;

Query Match 82.0%; Score 16.4; DB 6; Length 43;  
 Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGAGGGAGGG 19  
 |||||  
 Db 14 AAGGGGGAGGGAGGGAGG 32

RESULT 35  
 ABK98107  
 ID ABK98107 standard; DNA; 43 BP.

XX AC ABK98107;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated oligonucleotide #4.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
 KW pathogenic bacteria; virus; replication; virulence; cancer;  
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX FN US6403302-B1.

XX PD 11-JUN-2002.

XX PF 16-DEC-1993; 93US-00168920.

XX PR 17-SEP-1992; 92US-00946976.

XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.

XX PI Dervan PB, Beal PA;

XX DR WPI; 2002-536030/57.

XX A triple-helix comprising a double helical nucleic acid (DHNA) and an  
 PT oligonucleotide which binds in parallel and antiparallel orientation,  
 PT respectively, for targeting sequences on alternate strands of DHNA to  
 PT control gene expression.

XX Example 5; Col 33; 108pp; English.

XX The present invention relates to methods and oligonucleotides for forming  
 CC a triple-helix comprising a double helical nucleic acid comprising first  
 CC and second substantially complementary strands, and an oligonucleotide  
 CC bound to a purine-rich target sequence within the double helical nucleic  
 CC acid, where the oligonucleotide binds in a parallel and antiparallel  
 CC orientation, respectively, to target sequences on alternate strands of  
 CC the double helical nucleic acid. The method has therapeutic applications,  
 CC where gene expression is controlled by selective triple-helix formation  
 CC within expression regulatory sequences of a target gene. The  
 CC oligonucleotides can be used to form triple-helices, and are useful to  
 CC detect the presence or absence of specific sequences within genomic DNA  
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be  
 CC selected to specifically bind to pathogenic double-stranded DNA including  
 CC specific sequences required by pathogenic bacteria or viruses for  
 CC replication or virulence, reducing their pathogenicity. Alternatively,

CC the oligonucleotide can be chosen to target a unique sequence of the  
CC pathogen which is not found in the genome of pathogen's host. The  
CC oligonucleotides can be used in cancer treatment by way of triple-helix  
CC suppression of specific oncogenes including those of endogenous or viral  
CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
CC helices with such sequences in cancerous cells containing the activated  
CC oncogene, so preferentially killing or repressing the cancer causing  
CC cell. The present sequence represents an oligonucleotide used in the  
CC methods of the present invention  
XX  
XX  
SQ Sequence 43 BP; 14 A; 6 C; 14 G; 8 T; 0 U; 1 Other;  
  
Query Match 82.0%; Score 16.4; DB 6; Length 43;  
Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 AGGGGAGGGGAGGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 14 AAGGGGGGGAGGGGAGGG 32  
  
RESULT 36  
ABK98157  
ID ABK98157 standard; DNA; 45 BP.  
XX  
AC ABK98157;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE Triple helix forming associated DNA sequence #20.  
XX  
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;  
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;  
KW pathogenic bacteria; virus; replication; virulence; cancer;  
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.  
XX  
OS Synthetic.  
XX  
XX US6403302-B1.  
XX  
XX 11-JUN-2002.  
XX  
XX 16-DEC-1993; 93US-00168920.  
XX  
XX 17-SEP-1992; 92US-00946976.  
XX  
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
XX  
XX Dervan PB, Beal PA;  
XX  
XX WPI; 2002-536030/57.  
XX  
XX A triple-helix comprising a double helical nucleic acid (DHNA) and an  
XX oligonucleotide which binds in parallel and antiparallel orientation,  
XX respectively, for targeting sequences on alternate strands of DHNA to  
XX control gene expression.  
XX  
XX Example 5; Fig 11; 108pp; English.  
XX  
XX The present invention relates to methods and oligonucleotides for forming  
XX a triple-helix comprising a double helical nucleic acid comprising first  
XX and second substantially complementary strands, and an oligonucleotide  
XX bound to a purine-rich target sequence within the double helical nucleic  
XX acid, where the oligonucleotide binds in a parallel and antiparallel  
XX orientation, respectively, to target sequences on alternate strands of  
XX the double helical nucleic acid. The method has therapeutic applications,  
XX where gene expression is controlled by selective triple-helix formation  
XX within expression regulatory sequences of a target gene. The  
XX oligonucleotides can be used to form triple-helices, and are useful to  
XX detect the presence or absence of specific sequences within genomic DNA  
XX for diagnostic and therapeutic purposes. The oligonucleotides can be  
XX selected to specifically bind to pathogenic double-stranded DNA including  
XX specific sequences required by pathogenic bacteria or viruses for

CC replication or virulence, reducing their pathogenicity. Alternatively,  
CC the oligonucleotide can be chosen to target a unique sequence of the  
CC pathogen which is not found in the genome of pathogen's host. The  
CC oligonucleotides can be used in cancer treatment by way of triple-helix  
CC suppression of specific oncogenes including those of endogenous or viral  
CC origin. Such therapeutic oligonucleotides are capable of forming triple-  
CC helices with such sequences in cancerous cells containing the activated  
CC oncogene, so preferentially killing or repressing the cancer causing  
CC cell. The present sequence represents a DNA sequence used in the methods  
CC of the present invention  
XX  
XX  
SQ Sequence 45 BP; 14 A; 7 C; 14 G; 9 T; 0 U; 1 Other;  
  
Query Match 82.0%; Score 16.4; DB 6; Length 45;  
Best Local Similarity 89.5%; Pred. No. 8.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 AGGGGAGGGGAGGGGAGGG 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 16 AAGGGGGGGAGGGGAGGG 34  
  
RESULT 37  
AAV76464/C  
ID AAV76464 standard; DNA; 50 BP.  
XX  
AC AAV76464;  
XX  
DT 16-MAR-1999 (first entry)  
XX  
DE Staphylococcus aureus contig SEQ ID #2153.  
XX  
KW Computer readable medium; vaccine; S.aureus infection; immunodetection;  
KW cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
KW skin infection; surgical wound infection; scalded skin syndrome;  
KW toxic shock syndrome; ds.  
XX  
XX Staphylococcus aureus.  
XX  
XX EP786519-A2.  
XX  
XX 30-JUL-1997.  
XX  
XX 07-JAN-1997; 97EP-00100117.  
XX  
XX 05-JAN-1996; 96US-0009861P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;  
XX  
XX WPI; 1997-374922/35.  
XX  
XX Polynucleotide(s) and proteins derived from Staphylococcus aureus -  
XX stored on computer readable medium and used in the production of anti-  
XX S.aureus vaccines.  
XX  
XX Claim 1; Page 2159; 3271pp; English.  
XX  
XX This sequence represents one of 5191 Staphylococcus aureus DNA sequences  
XX of the invention. The DNA sequences are recorded on a computer readable  
XX medium, preferably selected from a floppy or hard disk, random access  
XX memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using  
XX the S.aureus DNA sequences allows putative functions to be assigned so  
XX that protein-encoding or regulatory regions of commercial, therapeutic or  
XX industrial importance can be obtained. Specifically, sequences which are  
XX likely to encode antigens have been identified and these polypeptides can  
XX be used in a vaccine composition against S.aureus infection. The  
XX polypeptides can also be used in a kit for the immunodetection of  
XX S.aureus in a sample. S.aureus is implicated in numerous human diseases,  
XX including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
XX skin and surgical wound infections, scalded skin syndrome, toxic shock  
XX syndrome, etc. Organisms transformed with the DNA sequences can be used

CC for recombinant production of the polypeptides. The new DNA sequences  
 CC (and their fragments) are useful as primers or probes for isolating  
 CC homologues of any of the S.aureus DNA sequences contained on the computer  
 CC readable medium

XX Sequence 50 BP; 0 A; 46 C; 1 G; 2 T; 0 U; 1 Other;  
 SQ Query Match 82.0%; Score 16.4; DB 2; Length 50;  
 Best Local Similarity 89.5%; Pred. No. 8.5e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGAGGGGGGGGGGGG 20  
 ||||| ||||| ||||| |||||  
 Db 28 GGGGGGGGGGGGGGGG 10

RESULT 38  
 AAA22528/C  
 ID AAA22528 standard; RNA; 17 BP.

AC AAA22528;

XX 19-JUN-2000 (first entry)

XX Integrin subunit beta 3 substrate sequence SEQ ID NO:5754.

XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
 KW hammerhead ribozyme; angiogenic factor; cytotstatic; antidiabetic;  
 KW ophthalmologic; antiinflammatory; antiarthritis; antipsoriatic; ARMD;  
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
 KW age related macular degeneration; inflammation; neovascular glaucoma;  
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
 KW tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;  
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

OS WO9950403-A2.

PN 07-OCT-1999.

PD 24-MAR-1999; 98WO-US006507.

PF 27-MAR-1998; 98US-0079678P.

PR (RIBO-) RIBOZYME PHARM INC.

PA Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;

XX WPI; 1999-591315/50.

XX Novel ribozymes for modulating the synthesis, expression and/or stability  
 PT of an mRNA encoding an angiogenic factors.

PS Claim 54; Page 226; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA  
 CC cleaving activity, which specifically cleave RNA encoded by an aryl  
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
 CC AAA19194 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;  
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme  
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
 CC AAA21596 to AAA21688 represent their corresponding target sequences;  
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence  
 CC for integrin subunit beta 3, and AAA2476 to AAA23262, AAA23343 to  
 CC AAA23422 represent their corresponding target sequences. The ribozymes of  
 CC the invention are used for modulating the synthesis, expression and/or

CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are  
 CC especially used to treat cancer, diabetic retinopathy, age related  
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber  
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3

XX Sequence 17 BP; 0 A; 13 C; 1 G; 0 T; 3 U; 0 Other;

Query Match 80.0%; Score 16; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGAGGGGGGGGGG 18  
 ||||| ||||| ||||| |||||  
 Db 16 GGGAGGGGGGGGGG 1

RESULT 39

ADH70729

ID ADH70729 standard; DNA; 19 BP.

XX AC ADH70729;

XX 25-MAR-2004 (first entry)

XX Human Vbeta gene repeat sequence #519.

XX human; T-cell associated disease; Vbeta; autoimmune disease;  
 KW degenerative nervous system disease; graft versus host disease;  
 KW hypersensitivity disease; infectious disease; neoplastic disease;  
 KW Addison's disease; atrophic gastritis;  
 KW degenerative nervous system disease; multiple sclerosis;  
 KW Alzheimer's disease; hypersensitivity disease; type I hypersensitivity;  
 KW allergy; type II hypersensitivity; Goodpasture's syndrome;  
 KW type IV hypersensitivity; leprosy; infectious disease; viral infection;  
 KW HIV, fungal infection; Candida; parasitic infection; schistosoma;  
 KW filaria; bacterial infection; Mycobacterium; neoplastic disease;  
 KW lymphoproliferative disease; leukaemia; lymphoma; cancer; brain cancer;  
 KW breast cancer; ds.

XX Homo sapiens.

OS US2002150891-A1.

PN 17-OCT-2002.

PD 05-MAR-1999; 99US-00263959.

PF 19-SEP-1994; 94US-00309335.

PR 19-SEP-1995; 95US-00531241.

XX (HOOD/) HOOD L E.

XX (ROWE/) ROWEN L.

XX Hood LE, Rowen L;

XX WPI; 2004-059052/06.

XX Kit for diagnosing and treating T-cell associated diseases e.g.  
 PT autoimmune, degenerative nervous system and infectious disease, comprises  
 PT nucleic acid primers specifically priming and allowing amplification of a  
 PT Vbeta gene.

PS Disclosure; SEQ ID NO 923; 164pp; English.

XX The invention relates to a kit for diagnosing and treating T-cell  
 CC associated diseases which comprises a panel of nucleic acid primers  
 CC specifically priming and allowing amplification of each Vbeta gene,  
 CC VbetaRNA or cDNA. The kit is useful for diagnosing organ transplant

CC rejection and diagnosing and treating T-cell associated diseases  
CC including autoimmune diseases, degenerative nervous system diseases,  
CC graft versus host disease, hypersensitivity diseases, infectious diseases,  
CC and neoplastic diseases. Autoimmune diseases include Addison's disease,  
CC atrophic gastritis. Degenerative nervous system diseases include multiple  
CC sclerosis and Alzheimer's disease. Hypersensitivity diseases include Type  
CC I hypersensitivities such as contact with allergens that lead to  
CC allergies, Type II hypersensitivities such as those present in  
CC Goodpasture's syndrome and Type IV hypersensitivities such as those  
CC manifested in leprosy. Infectious diseases include viral infections  
CC caused by viruses such as HIV, fungal infections such as those caused by  
CC the yeast genus Candida, parasitic infections such as those caused by  
CC schistosomes, filaria and bacterial infections such as those caused by  
CC Mycobacterium. Neoplastic diseases include lymphoproliferative diseases  
CC such as leukemias, lymphomas and cancers such as cancer of the brain,  
CC breast. The present sequence represents a Vbeta gene repeat sequence.

XX  
SQ Sequence 19 BP; 1 A; 2 C; 16 G; 0 T; 0 U; 0 Other;  
Query Match 79.0%; Score 15.8; DB 12; Length 19;  
Best Local Similarity 89.5%; Pred. No. 1.5e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GGGGAGGGGAGGGGAGGGG 20  
Db 1 GGGCGGGGAGGGGCGGGG 19  
||||| ||||||| |||||

RESULT 40  
AAF99947  
ID AAF99947 standard; DNA; 20 BP.  
AC AAF99947;  
XX  
XX  
DT 12-JUL-2001 (first entry)  
XX  
DE Synthetic oligonucleotide #13.  
XX  
XX Oligonucleotide purification; liquid chromatography;  
KW hydrophobic protective group; deprotection; ds.  
XX  
OS Synthetic.  
XX  
XX JP2000342265-A.  
XX  
PD 12-DEC-2000.  
XX  
XX 02-JUN-1999; 99JP-00154974.  
XX  
XX 02-JUN-1999; 99JP-00154974.  
XX  
XX (TOAG ) TOA GOSEI CHEM IND LTD.  
FA  
DR WPI; 2001-268251/28.  
XX  
XX  
PT A process for purification of oligonucleotides using liquid  
PT chromatography.  
XX  
XX Example 1; Page 4; 13pp; Japanese.

XX The present sequence is an oligonucleotide provided in a specification  
XX relating to the simplified purification of oligonucleotides by liquid  
XX chromatography. The process comprises: (a) pouring oligonucleotides  
XX protected with a hydrophobic group and oligonucleotide with no protective  
XX group into a liquid chromatography column packed with an acid and alkali  
XX resistant packing agent, such as polystyrene resin; (b) pouring a mixed  
XX developing solvent composed of a buffer made from a volatile salt and a  
XX water soluble organic solvent at a suitable concentration gradient into  
XX the column; (c) pouring an acid, particularly 6-16 v/v% acetic acid, into  
XX the column to deprotect the oligonucleotides protected with the  
XX hydrophobic group; (d) pouring a mixed developing solvent composed of a  
XX buffer made from a volatile salt, particularly 0.05-0.5 N aqueous  
XX ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water

CC soluble organic solvent at a suitable concentration gradient to elute the  
CC deprotected oligonucleotides; and (e) removal of the solvent and the salt  
CC from the eluted oligonucleotides

XX  
SQ Sequence 20 BP; 1 A; 1 C; 17 G; 1 T; 0 U; 0 Other;  
Query Match 79.0%; Score 15.8; DB 4; Length 20;  
Best Local Similarity 89.5%; Pred. No. 1.5e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GGGGAGGGGAGGGGAGGGG 20  
Db 2 GGGCGGGGAGGGGAGGGG 20  
||||| ||||||| |||||||

RESULT 41  
AAX40753  
ID AAX40753 standard; DNA; 26 BP.  
AC AAX40753;  
XX  
XX  
DT 16-JUN-1999 (first entry)  
XX  
DE Oligonucleotide used for screening DCMTase binding discrimination.  
XX  
XX DNA cytosine methyltransferase; DCMTase; binding discrimination;  
KW C-5 methylcytosine; allosteric site; synthetic inhibitor; cancer cell;  
KW proliferation; development disorder; Huntington's disease;  
KW Down's syndrome; Hox gene; ss.  
XX  
OS Synthetic.  
XX  
XX WO9912027-A1.  
XX  
PD 11-MAR-1999.  
XX  
PF 12-JUN-1998; 98WO-US012351.  
XX  
PR 29-AUG-1997; 97US-0057411P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
FA  
XX Reich NO, Flynn J;  
PI  
XX WPI; 1999-205256/17.  
XX  
XX DNA cytosine methyltransferase modulator containing 5-C methylcytosine -  
XX used to inhibit methylation of DNA, and proliferation of cancer cells.  
XX  
XX Example 1; Fig 7; 114pp; English.

XX Oligonucleotides AAX40733-815 represent cloned and sequenced isolates  
XX from pooled generations used for screening DNA cytosine methyltransferase  
XX (DCMTase) binding discrimination. The oligonucleotides are double  
XX stranded, and the guanine containing strand is shown. The specification  
XX describes a synthetic oligonucleotide comprising a C-5 methylcytosine  
XX which recognizes and binds an allosteric site on DCMTase, thereby  
XX modulating DCMTase activity associated with the allosteric site. The  
XX synthetic inhibitor can be used to inhibit methylation of DNA. It can  
XX also be used to inhibit proliferation of cancer cells. The inhibitor can  
XX also be used to treat a disorder of development, which is linked to a  
XX genetic locus regulated by methylation, such as Huntington's disease,  
XX Down's syndrome, and disorders associated with a Hox gene

XX  
SQ Sequence 26 BP; 3 A; 1 C; 20 G; 2 T; 0 U; 0 Other;  
Query Match 79.0%; Score 15.8; DB 2; Length 26;  
Best Local Similarity 89.5%; Pred. No. 1.4e+04;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GGGGAGGGGAGGGGAGGGG 20  
Db 2 GGGGTGGGAGCGGAGGGG 20  
||||| ||||||| |||||||

```
RESULT 42
AAF28800/c
ID AAF28800 standard; DNA; 27 BP.
XX
AC AAF28800;
XX
DT 09-APR-2001 (first entry)
XX
DE Human GABA(b) receptor 1 promoter Plb primer 2057 PRLb CGVI Fwd.
XX
KW Neuroprotective; nootropic; antidepressant; tranquilizer; anticonvulsant;
KW cardiant; antiasthmatic; antiinflammatory; human; GABA; promoter; CNS;
KW gamma-amino butyric acid B receptor 1; splice isoform; spinal spasticity;
KW transcription modulator; central nervous system disorder; dementia;
KW muscle relaxation; Alzheimer's disease; depression; anxiety; epilepsy;
KW cardiovascular disorder; asthma; irritable bowel syndrome; emesis;
KW reflux disease; neurological disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200068268-A1.
XX
PD 16-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-SE000878.
XX
PR 06-MAY-1999; 99SE-00001659.
XX
PA (ASTR ) ASTRAZENECA AB.
XX
PI Ekstrand J, Edlund A, Johansson T, Leonardsson G;
XX WPI; 2001-024861/03.
XX
PT New nucleic acid molecules constituting the human gamma amino butyric
PT acid-B receptor 1 promoters, useful for screening modulators of the
PT receptors transcription or therapeutic agents regulating the expression
PT of its splice isoforms.
XX
PS Example 6; Page 21; 46pp; English.
XX
CC The invention relates to novel nucleic acid molecules constituting the
CC human gamma-amino butyric acid (GABA)B receptor 1 promoters PlA and/or
CC Plb (AAF28781 and AAF28782), or their functionally equivalent modified
CC forms or active fragments. PCR primers AAF28788-AAF28805 were used for
CC PCR mutagenesis of the GABA(b) promoter sequences for mutational analysis
CC of promoter element function. Nucleic acid molecules containing the human
CC GABAB receptor 1 promoters PlA and/or Plb are useful for screening
CC therapeutic agents that selectively regulate the expression of GABAB
CC receptor 1a- and 1b-type splice isoforms. These compounds, which are
CC modulators of GABAB receptor 1 transcription, are potentially useful in
CC the treatment of disorders that are related to neurally-controlled
CC physiological responses regulated by GABAB receptors such as central
CC nervous system (CNS) disorders, e.g. muscle relaxation in spinal
CC spasticity, Alzheimer's disease and other dementias, psychiatric and
CC neurological disorders, e.g. depression, anxiety or epilepsy,
CC cardiovascular disorders, asthma, gut motility disorders, e.g. irritable
CC bowel syndrome, emesis or reflux disease
XX
SQ Sequence 27 BP; 3 A; 16 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 79.0%; Score 15.8; DB 4; Length 27;
Best Local Similarity 89.5%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 AGGGGAGGGGAGGGAGGG 19
Db 19 AGGTTAGGGGAGGGAGGG 1
RESULT 43
AAF28801
ID AAF28801 standard; DNA; 27 BP.
XX
AC AAF28801;
XX
DT 09-APR-2001 (first entry)
XX
DE Human GABA(b) receptor 1 promoter Plb primer 2058 PRLb CGVI Rev.
XX
KW Neuroprotective; nootropic; antidepressant; tranquilizer; anticonvulsant;
KW cardiant; antiasthmatic; antiinflammatory; human; GABA; promoter; CNS;
KW gamma-amino butyric acid B receptor 1; splice isoform; spinal spasticity;
KW transcription modulator; central nervous system disorder; dementia;
KW muscle relaxation; Alzheimer's disease; depression; anxiety; epilepsy;
KW cardiovascular disorder; asthma; irritable bowel syndrome; emesis;
KW reflux disease; neurological disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200068268-A1.
XX
PD 16-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-SE000878.
XX
PR 06-MAY-1999; 99SE-00001659.
XX
PA (ASTR ) ASTRAZENECA AB.
XX
PI Ekstrand J, Edlund A, Johansson T, Leonardsson G;
XX WPI; 2001-024861/03.
XX
PT New nucleic acid molecules constituting the human gamma amino butyric
PT acid-B receptor 1 promoters, useful for screening modulators of the
PT receptors transcription or therapeutic agents regulating the expression
PT of its splice isoforms.
XX
PS Example 6; Page 21; 46pp; English.
XX
CC The invention relates to novel nucleic acid molecules constituting the
CC human gamma-amino butyric acid (GABA)B receptor 1 promoters PlA and/or
CC Plb (AAF28781 and AAF28782), or their functionally equivalent modified
CC forms or active fragments. PCR primers AAF28788-AAF28805 were used for
CC PCR mutagenesis of the GABA(b) promoter sequences for mutational analysis
CC of promoter element function. Nucleic acid molecules containing the human
CC GABAB receptor 1 promoters PlA and/or Plb are useful for screening
CC therapeutic agents that selectively regulate the expression of GABAB
CC receptor 1a- and 1b-type splice isoforms. These compounds, which are
CC modulators of GABAB receptor 1 transcription, are potentially useful in
CC the treatment of disorders that are related to neurally-controlled
CC physiological responses regulated by GABAB receptors such as central
CC nervous system (CNS) disorders, e.g. muscle relaxation in spinal
CC spasticity, Alzheimer's disease and other dementias, psychiatric and
CC neurological disorders, e.g. depression, anxiety or epilepsy,
CC cardiovascular disorders, asthma, gut motility disorders, e.g. irritable
CC bowel syndrome, emesis or reflux disease
XX
SQ Sequence 27 BP; 6 A; 2 C; 16 G; 3 T; 0 U; 0 Other;
Query Match 79.0%; Score 15.8; DB 4; Length 27;
Best Local Similarity 89.5%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 AGGGGAGGGGAGGGAGGG 19
Db 9 AGGTTAGGGGAGGGAGGG 27
RESULT 44
AAL28918/c
ID AAL28918 standard; DNA; 50 BP.
XX
```

```

AC AAL28918;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #2126.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
FN 05-JUL-2001.
XX
PD 28-DEC-2000; 2000WO-US035498.
XX
PF 28-DEC-1999; 99US-0173419P.
XX
PR 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
PA Shimkets RA, Leach M;
XX
PI WPI; 2001-465210/50.
XX
DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
PT
XX Claim 1; Page 1990; 4143pp; English.
PS
XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 50 BP; 9 A; 26 C; 3 G; 12 T; 0 U; 0 Other;
Query Match 79.0%; Score 15.8; DB 4; Length 50;
Best Local Similarity 89.5%; Pred. No. 1.3e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGGAGGGGGAGGGAGGGG 20
| | | | | | | | | | | | | | | | | | | |
DB 44 GGGGAGGGGAGGGAGGGG 26
| | | | | | | | | | | | | | | | | | | |

RESULT 45
AAL32132
ID AAL32132 standard; DNA; 50 BP.
XX
AC AAL32132;
XX
DT 24-JAN-2002 (first entry)
XX

```

---

```

XX DE Human SNP oligonucleotide #5340.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
FN 05-JUL-2001.
XX
PD 28-DEC-2000; 2000WO-US035498.
XX
PF 28-DEC-1999; 99US-0173419P.
XX
PR 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
PA Shimkets RA, Leach M;
XX
PI WPI; 2001-465210/50.
XX
DR Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
PT
XX Claim 1; Page 2224; 4143pp; English.
PS
XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC protein coupled receptors and thioesterases. The present sequence is one
CC such oligonucleotide. The oligonucleotides and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of the proteins listed above.
CC Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms
XX
SQ Sequence 50 BP; 11 A; 12 C; 22 G; 5 T; 0 U; 0 Other;
Query Match 79.0%; Score 15.8; DB 4; Length 50;
Best Local Similarity 89.5%; Pred. No. 1.3e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGGAGGGGGAGGGAGGGG 19
| | | | | | | | | | | | | | | | | | | |
DB 7 AGAGGAGGGAGGGAGGGG 25
| | | | | | | | | | | | | | | | | | | |

RESULT 46
AAL32131
ID AAL32131 standard; DNA; 50 BP.
XX
AC AAL32131;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #5339.
XX

```

KW	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW	neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW	amyloid protein; angiotensinogen; apoptosis related protein; cadherin;
KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW	complement related protein; cytochrome; kinesin; cytokine; interferon;
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW	multifactorial disease; autoimmune disease; infection;
KW	nervous system disease; ss.
XX	Homo sapiens.
OS	
XX	
PN	WO200147944-A2.
XX	
PD	05-JUL-2001.
XX	
PF	28-DEC-2000; 2000WO-US035498.
XX	
PR	28-DEC-1999; 99US-0173419P.
PR	27-DEC-2000; 2000US-00173419.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shinkets RA, Leach M;
PI	
DR	WPI; 2001-465210/50.
XX	
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT	oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT	autoimmune diseases and infections.
XX	
PS	Claim 1; Page 2923; 4143pp; English.
XX	
CC	The present invention relates to oligonucleotides encoding polymorphic
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC	histones, kinases, colony stimulating factors, complement related
CC	proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC	protein coupled receptors and thioesterases. The present sequence is one
CC	such oligonucleotide. The oligonucleotides and the peptides encoded by
CC	them may be used in the prevention, diagnosis and treatment of diseases
CC	associated with inappropriate expression of the proteins listed above.
CC	Disorders that may be prevented, diagnosed and/or treated include
CC	multifactorial diseases with a genetic component, such as autoimmune
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,
CC	leukaemia), diseases of the nervous system and an infection of pathogenic
CC	organisms
XX	
SQ	Sequence 50 BP; 11 A; 12 C; 23 G; 4 T; 0 U; 0 Other;
	Query Match            79.0%; Score 15.8; DB 4; Length 50;
	Best Local Similarity   89.5%; Pred. No. 1.3e+04;
	Matches   17; Conservative   0; Mismatches   2; Indels   0; Gaps   0
QY	1 AGCGGAGGGGAGGGGAGGG 19
DB	10 AGAGGAGGAGGGGAGGG 28
RESULT 47	
AAL28919/c	
ID AAL28919 standard; DNA; 50 BP.	
XX	
AC AAL28919;	
XX	
DT 24-JAN-2002 (first entry)	
XX	
DE Human SNP oligonucleotide #2127.	
XX	
XX	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX	neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW	amyloid protein; angiotensinogen; apoptosis related protein; cadherin;
KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW	complement related protein; cytochrome; kinesin; cytokine; interferon;
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW	multifactorial disease; autoimmune disease; infection;
KW	nervous system disease; ss.

KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW	complement related protein; cytochrome; kinesin; cytokine; interferon;
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW	multifactorial disease; autoimmune disease; infection;
KW	nervous system disease; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200147944-A2.
XX	
PD	05-JUL-2001.
XX	
PF	28-DEC-2000; 200WO-US035498.
XX	
PR	28-DEC-1999; 99US-0173419P.
PR	27-DEC-2000; 2000US-00173419.
XX	
PA	(CURA-) CUPAGEN CORP.
XX	
PI	Shimkets RA, Leach M;
XX	
DR	WPI; 2001-465210/50.
XX	
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT	oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT	autoimmune diseases and infections.
XX	
PS	Claim 1; Page 1990; 4143pp; English.
XX	
CC	The present invention relates to oligonucleotides encoding polymorphic
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC	histones, kinases, colony stimulating factors, complement related
CC	proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC	protein coupled receptors and thioesterases. The present sequence is one
CC	such oligonucleotide. The oligonucleotides and the peptides encoded by
CC	them may be used in the prevention, diagnosis and treatment of diseases
CC	associated with inappropriate expression of the proteins listed above.
CC	Disorders that may be prevented, diagnosed and/or treated include
CC	multifactorial diseases with a genetic component, such as autoimmune
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,
CC	leukaemia), diseases of the nervous system and an infection of pathogenic
CC	organisms
XX	
SQ	Sequence 50 BP; 7 A; 31 C; 2 G; 10 T; 0 U; 0 Other;
Query Match	79.0%; Score 15.8; DB 4; Length 50;
Best Local Similarity	89.5%; Pred. No. 1.3e+04;
Matches 17; Conservative	0; Mismatches 2; Indels 0; Gaps 0
Qy	2 GGGAGGGGGGGGGGGGGG 20
Db	36 GGGAGGGGGGAAGGGGGGG 18
RESULT 48	
AAA22527/C	
ID	AAA22527 standard; RNA; 17 BP.
XX	
AC	AAA22527;
XX	
DT	19-JUN-2000 (first entry)
XX	
DE	Integrin subunit beta 3 substrate sequence SEQ ID NO:5753.
XX	
KW	Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW	integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW	hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW	ophthalmologic; antiinflammatory; antiarthritic; aniposiatric; ARMD;
KW	dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW	age related macular degeneration; inflammation; neovascular glaucoma;

KW	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW	neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW	amyloid protein; angiotensinogen; apoptosis related protein; cadherin;
KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW	complement related protein; cytochrome; kinesin; cytokine; interferon;
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW	mucopolysaccharide; autoimmunity disease; infection;
KW	nervous system disease; ss.
XX	Homo sapiens.
OS	
XX	
PN	WO200147944-A2.
PD	
XX	
PP	05-JUL-2001.
XX	
PP	28-DEC-2000; 2000WO-US035498.
XX	
PR	28-DEC-1999; 99US-01734119P.
PR	27-DEC-2000; 2000US-00173419.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shinkets RA, Leach M;
PI	
DR	WI; 2001-465210/50.
XX	
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT	oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT	autoimmune diseases and infections.
XX	
PS	Claim 1; Page 2923; 4143pp; English.
XX	
CC	The present invention relates to oligonucleotides encoding polymorphic
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC	histones, kinases, colony stimulating factors, complement related
CC	proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC	protein coupled receptors and thioesterases. The present sequence is one
CC	such oligonucleotide. The oligonucleotides and the peptides encoded by
CC	them may be used in the prevention, diagnosis and treatment of diseases
CC	associated with inappropriate expression of the proteins listed above.
CC	Disorders that may be prevented, diagnosed and/or treated include
CC	multifactorial diseases with a genetic component, such as autoimmune
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,
CC	leukaemia), diseases of the nervous system and an infection of pathogenic
CC	organisms
XX	
SQ	Sequence 50 BP; 11 A; 12 C; 23 G; 4 T; 0 U; 0 Other;
	Query Match 79.0%; Score 15.8; DB 4; Length 50;
	Best Local Similarity 89.5%; Pred. No. 1.3e+04;
	Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY	1 AGCGGAGGGGAGGGAGGG 19
DB	10 AGAGGAGGAGGGAGGG 28
RESULT 47	
AAL28919/c	
ID AAL28919 standard; DNA; 50 BP.	
XX	
AC AAL28919;	
XX	
DT 24-JAN-2002 (first entry)	
XX	
DE Human SNP oligonucleotide #2127.	
XX	
XX	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX	neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW	amyloid protein; angiotensinogen; apoptosis related protein; cadherin;
KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW	complement related protein; cytochrome; kinesin; cytokine; interferon;
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW	mucopolysaccharide; autoimmunity disease; infection;
KW	nervous system disease; ss.

KW	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW	neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW	amyloid protein; angiotensinogen; apoptosis related protein; cadherin;
KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW	complement related protein; cytochrome; kinesin; cytokine; interferon;
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW	mucopolysaccharide; autoimmunity disease; infection;
KW	nervous system disease; ss.
XX	Homo sapiens.
OS	
XX	
PN	WO200147944-A2.
PD	
XX	
PP	05-JUL-2001.
XX	
PP	28-DEC-2000; 2000WO-US035498.
XX	
PR	28-DEC-1999; 99US-01734119P.
PR	27-DEC-2000; 2000US-00173419.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shinkets RA, Leach M;
PI	
DR	WI; 2001-465210/50.
XX	
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT	oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT	autoimmune diseases and infections.
XX	
XX	Claim 1; Page 2923; 4143pp; English.
PS	
CC	The present invention relates to oligonucleotides encoding polymorphic
CC	variants of proteins related to amylases, amyloid proteins, angiotensin,
CC	apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC	histones, kinases, colony stimulating factors, complement related
CC	proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC	protein coupled receptors and thioesterases. The present sequence is one
CC	such oligonucleotide. The oligonucleotides and the peptides encoded by
CC	them may be used in the prevention, diagnosis and treatment of diseases
CC	associated with inappropriate expression of the proteins listed above.
CC	Disorders that may be prevented, diagnosed and/or treated include
CC	multifactorial diseases with a genetic component, such as autoimmune
CC	diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC	systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC	(e.g. cancers of the bladder, brain, breast, colon and kidney,
CC	leukaemia), diseases of the nervous system and an infection of pathogenic
CC	organisms
XX	
SQ	Sequence 50 BP; 11 A; 12 C; 23 G; 4 T; 0 U; 0 Other;
	Query Match 79.0%; Score 15.8; DB 4; Length 50;
	Best Local Similarity 89.5%; Pred. No. 1.3e+04;
	Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY	1 AGCGGAGGGGAGGGGAGGG 19
DB	10 AGAGGAGGAGGGGAGGG 28
RESULT 47	
AAL28919/c	
ID AAL28919 standard; DNA; 50 BP.	
XX	
AC AAL28919;	
XX	
DT 24-JAN-2002 (first entry)	
XX	
DE Human SNP oligonucleotide #2127.	
XX	
XX	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX	neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW	amyloid protein; angiotensinogen; apoptosis related protein; cadherin;
KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW	complement related protein; cytochrome; kinesin; cytokine; interferon;
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW	mucopolysaccharide; autoimmunity disease; infection;
KW	nervous system disease; ss.

KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
 KW tuberos sclerosi; pot-wine stain; Sturge Weber syndrome;  
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9950403-A2.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PF 24-MAR-1999; 93WO-US006507.  
 XX  
 PR 27-MAR-1998; 98US-0079678P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;  
 XX WPI; 1999-591315/50.  
 DR  
 XX Novel ribozymes for modulating the synthesis, expression and/or stability  
 PT of an mRNA encoding an angiogenic factors.  
 XX  
 PS Claim 54; Page 226; 305pp; English.

XX The present invention describes enzymatic cleave RNA molecules with RNA  
 CC cleaving activity, which specifically cleave RNA encoded by an aryl  
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to  
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,  
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;  
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme  
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
 CC AAA21596 to AAA21688 represent their corresponding target sequences;  
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence  
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
 CC AAA23422 represent their corresponding target sequences. The ribozymes of  
 CC the invention are used for modulating the synthesis, expression and/or  
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are  
 CC especially used to treat cancer, diabetic retinopathy, age related  
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiofibroma of tuberos sclerosi, pot-wine stains, Sturge Weber  
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3

XX Sequence 17 BP; 0 A; 13 C; 1 G; 0 T; 3 U; 0 Other;

Query Match 77.0%; Score 15.4; DB 2; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 2e+04;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGG 18

DB 17 GGGGAGGGGAGGGAGG 1

RESULT 49

AB244397

ID AB244397 standard; DNA; 41 BP.

XX AC AB244397;

XX DT 26-JUN-2003 (first entry)

XX DE Human catechol-O-methyltransferase COMT gene polymorphic site, #1181.

XX KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;

KW polymorphic site; drug evaluation; drug screening; genotyping;  
 KW genetic profiling; therapeutic customisation; adverse reaction;  
 KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT variation replace(21,A)  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism (SNP)"

PN WO200252044-A2.

PD 04-JUL-2002.

XX 27-DEC-2001; 2001WO-JP011592.

PF 27-DEC-2000; 2000JP-00399443.

XX 02-MAY-2001; 2001JP-00135256.

PR 27-AUG-2001; 2001JP-00256862.

XX (RIKE ) RIKEN KK.

PA Nakamura Y, Sekine A, Iida A, Saito S;

XX WPI; 2002-583571/62.

DR Identifying individuals having a polymorphism, useful for determining the

XX effectiveness or side effect of a drug or treatment protocol, comprises  
 FT detecting at least one polymorphism in the drug metabolizing enzyme  
 PT nucleic acid.  
 XX  
 PS Claim 23; Page 83; 2785pp; English.

XX Sequences AB243217-AB250887 represent polymorphic sites within genes

CC encoding enzymes associated with drug metabolism. The invention relates  
 CC to methods and compositions for identifying individuals who have at least  
 CC one polymorphism in such drug metabolising enzyme-encoding genes. The  
 CC polymorphisms may be identified in a nucleic acid sample using probes or  
 CC primers specific for a sequence selected from AB243217-AB250887 using a  
 CC variety of detection assays, including hybridisation assays, nucleic acid  
 CC arrays and PCR-based methods. The invention also encompasses methods of  
 CC evaluating and screening drugs using genetic polymorphism data. Genetic  
 CC polymorphism data, particularly that relating to single nucleotide  
 CC polymorphisms (SNPs), may be used in studying the relationship between  
 CC DNA sequence variations and human diseases, conditions, and responses to  
 CC drugs. SNPs are also useful as polymorphism markers for discovering genes  
 CC that cause or exacerbate certain diseases. SNPs are particularly useful  
 CC in the above respects as they are stable in populations, occur  
 CC frequently, and have lower mutation rates than other genome variations  
 CC such as repeating sequences. The detection and analysis of polymorphisms  
 CC in genes encoding drug metabolising enzymes allows the customisation of  
 CC drug therapies based upon the genetic profile of individual patients.

CC This would not only take the guesswork out of selecting the drug with the  
 CC greatest therapeutic effect for a particular patient, but would also  
 CC reduce the likelihood of adverse reactions, thereby increasing safety.  
 CC Methods of the invention are also useful in the drug discovery and  
 CC approval processes. For example, individuals could be selected for  
 CC clinical trials only if their genetic profiles indicate that they are  
 CC capable of responding to a particular drug or drug class, and previously  
 CC failed drug candidates could be revived if they were matched with more  
 CC appropriate patient populations. The methods, data and compositions of  
 CC the invention may therefore lead to an increase in the range of  
 CC possible drug targets and decreases in the number of adverse drug  
 CC reactions, failed drug trials, the time taken for a drug to be approved,  
 CC the length of time patients are on medication and the number of different  
 CC medications a patient needs to take before finding an effective therapy

XX Sequence 41 BP; 7 A; 11 C; 21 G; 2 T; 0 U; 0 Other;

Query Match 77.0%; Score 15.4; DB 6; Length 41;

Best Local Similarity 94.1%; Pred. No. 1.8e+04;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 4 GGAGGGGAGGGGAGGGG 20  
DB 10 GGAAGGGAGGGGAGGGG 26

RESULT 50  
ID ABZ48593  
XX ABZ48593 standard; DNA; 41 BP.  
AC ABZ48593;  
XX 26-JUN-2003 (first entry)  
XX Human catechol-O-methyltransferase COMT gene polymorphic site, #5376.  
DE Human; drug metabolising enzyme; gene; drug metabolism; chromosome 22;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT variation replace(21,A)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX WO200252044-A2.  
XX 04-JUL-2002.  
XX 27-DEC-2001; 2001WO-JP011592.  
XX 27-DEC-2000; 2000JP-00399443.  
XX 02-MAY-2001; 2001JP-00135256.  
XX 27-AUG-2001; 2001JP-00256862.  
XX (RIKE ) RIKEN KK.  
XX Nakamura Y, Sekine A, Iida A, Saito S;  
XX WPI; 2002-583571/62.

Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.

Claim 23; Page 169; 2785pp; English.

Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety.

CC Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy

XX SQ Sequence 41 BP; 7 A; 11 C; 21 G; 2 T; 0 U; 0 Other;

Query Match 77.0%; Score 15.4; DB 6; Length 41;  
Best Local Similarity 94.1%; Pred. No. 1.8e+04;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 4 GGAGGGGAGGGGAGGGG 20  
DB 10 GGAAGGGAGGGGAGGGG 26

Search completed: February 15, 2006, 18:07:23  
Job time : 157.744 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:07:43 ; Search time 1330.25 Seconds  
(without alignments)  
703.434 Million cell updates/sec

Title: US-09-669-187A-906  
Perfect score: 20  
Sequence: 1 agggaggaggaggaggagg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues  
Total number of hits satisfying chosen parameters: 179606

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database :

EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_est3:\*
- 4: gb\_hic:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_est7:\*
- 9: gb\_gss1:\*
- 10: gb\_gss2:\*
- 11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	9	AZ867169
2	20	100.0	35	9	AZ359724
3	18.4	92.0	22	9	AZ958287
C 4	17.4	87.0	26	9	AZ462959
5	17.4	87.0	28	10	CL661180
6	17.4	87.0	32	9	AZ971404
7	17.4	87.0	33	9	AZ800326
8	17.4	87.0	38	10	EX004665
C 9	17.4	87.0	43	9	AZ820833
C 10	17.4	87.0	45	9	AZ375586
C 11	17.4	87.0	47	1	AJ793526
12	17.4	87.0	50	9	AZ800436
C 13	16.8	84.0	25	9	AZ780325
C 14	16.8	84.0	30	10	AL935924
C 15	16.8	84.0	33	9	AZ652279
C 16	16.8	84.0	38	9	AZ424085
C 17	16.8	84.0	39	9	AZ825536
C 18	16.8	84.0	43	9	AZ877472
19	16.4	82.0	37	1	AL800153
20	16.4	82.0	46	1	AL597960
C 21	15.8	79.0	19	9	AZ447248
C 22	15.8	79.0	20	9	AZ512326

c 96	15.8	79.0	41	9	AZ871797	AZ871797 2M0184C24	169	15.2	76.0	47	10	CZ910062	CZ910062 4012001B0
c 97	15.8	79.0	41	10	CW956912	CW956912 TcB51.4_C	c 170	15.2	76.0	48	9	AZ652813	AZ652813 1M0526M08
c 98	15.8	79.0	41	10	EX001342	EX001342 Arabidops	c 171	15.2	76.0	48	10	CZ258850	CZ258850 AH0165 Sa
c 99	15.8	79.0	42	9	AZ499950	AZ499950 1M0338101	c 172	15.2	76.0	49	3	B1762841	B1762841 603048373
c 100	15.8	79.0	42	9	AZ764537	AZ764537 1M0560M21	c 173	15.2	76.0	50	11	AU256770	AU256770 AU256770
c 101	15.8	79.0	42	9	AZ801055	AZ801055 2M0059C22	c 174	15.2	76.0	50	11	CR041958	CR041958 Forward s
c 102	15.8	79.0	43	1	A1811876	A1811876 tw45g01.x	c 175	15.2	76.0	50	11	CR166872	CR166872 Forward s
c 103	15.8	79.0	43	9	AZ345493	AZ345493 1M0080E05	c 176	14.8	74.0	19	9	AZ760597	AZ760597 1M0554N21
c 104	15.8	79.0	43	9	AZ488464	AZ488464 1M0318F17	c 177	14.8	74.0	20	9	AZ969440	AZ969440 2M0242012
c 105	15.8	79.0	43	9	AZ864816	AZ864816 2M0174A11	c 178	14.8	74.0	21	9	AZ476392	AZ476392 1M0295F12
c 106	15.8	79.0	44	1	AM046897	AM046897 AM046897	c 179	14.8	74.0	22	1	A1582080	A1582080 ar96b07.x
c 107	15.8	79.0	44	9	AZ860493	AZ860493 2M0166F01	c 180	14.8	74.0	22	5	BQ585098	BQ585098 E011826-0
c 108	15.8	79.0	45	9	AZ366532	AZ366532 1M0115F18	c 181	14.8	74.0	22	5	AQ2611419	AQ2611419 1M0437D15
c 109	15.8	79.0	45	9	AZ442112	AZ442112 1M0234K08	c 182	14.8	74.0	22	9	AZ871408	AZ871408 2M0184E16
c 110	15.8	79.0	45	9	AZ473613	AZ473613 1M0289O03	c 183	14.8	74.0	23	9	AZ618720	AZ618720 1M0450O19
c 111	15.8	79.0	45	9	AZ776609	AZ776609 2M0010J20	c 184	14.8	74.0	25	1	A1363940	A1363940 qw43b12.x
c 112	15.8	79.0	45	10	AL7533618	AL7533618 Arabidops	c 185	14.8	74.0	25	11	TA185B02Q	TA185B02Q
c 113	15.8	79.0	45	10	AL763837	AL763837 Arabidops	c 186	14.8	74.0	26	9	AZ816353	AZ816353 2M0085K06
c 114	15.8	79.0	46	9	AZ325773	AZ325773 1M0048J12	c 187	14.8	74.0	30	5	BX624507	BX624507 BX624507
c 115	15.8	79.0	46	10	CZ906361	CZ906361 BGB236 Ba	c 188	14.8	74.0	30	9	AZ875577	AZ875577 2M0190G06
c 116	15.8	79.0	47	9	AZ769421	AZ769421 1M0570O01	c 189	14.8	74.0	33	11	TA95A01P	TA95A01P
c 117	15.8	79.0	48	5	BQ591368	BQ591368 E012714-0	c 190	14.8	74.0	34	1	A1224571	A1224571 qw36a07.x
c 118	15.8	79.0	48	9	AZ650456	AZ650456 1M0520G09	c 191	14.8	74.0	34	9	AZ432435	AZ432435 1M0217B21
c 119	15.8	79.0	48	9	AZ860712	AZ860712 2M0166P18	c 192	14.8	74.0	34	10	AL759611	AL759611 Arabidops
c 120	15.8	79.0	49	1	A1189618	A1189618 qd32h02.x	c 193	14.8	74.0	34	11	TA128E02Q	TA128E02Q
c 121	15.8	79.0	49	5	CX033453	CX033453 pw54h05.y	c 194	14.8	74.0	39	11	DR41D12S	DR41D12S
c 122	15.8	79.0	49	5	AZ506149	AZ506149 1M0347U05	c 195	14.8	74.0	39	11	TA200E07Q	TA200E07Q
c 123	15.8	79.0	50	9	AZ456166	AZ456166 1M0258B20	c 196	14.8	74.0	48	10	AL752522	AL752522 Arabidops
c 124	15.8	79.0	50	9	AZ776242	AZ776242 2M0009P12	c 197	14.8	74.0	50	11	CR025955	CR025955 Reverse s
c 125	15.8	79.0	50	9	AZ787456	AZ787456 2M0033O06	c 198	14.8	74.0	50	11	CR042155	CR042155 Reverse s
c 126	15.8	79.0	50	10	BX987794	BX987794 Reverse s	c 199	14.4	72.0	36	10	AL763948	AL763948 Arabidops
c 127	15.8	79.0	50	11	CR117295	CR117295 Reverse s	c 200	14.4	72.0	47	10	AG220079	AG220079 Lotus cor
c 128	15.8	79.0	50	11	CR138789	CR138789 Forward s	c 201	14.4	72.0	49	11	TA33D12P	TA33D12P
c 129	15.8	79.0	50	11	CR165643	CR165643 Reverse s	c 202	14.2	71.0	49	11	AJ659543	AJ659543
c 130	15.4	77.0	49	1	A1687811	A1687811 tp39a10.x	c 203	14.2	71.0	19	1	AJ747090	AJ747090 AJ747090
c 131	15.2	76.0	22	9	AZ656873	AZ656873 1M0532M09	c 204	14.2	71.0	19	6	CF280692	CF280692 14ETL--07
c 132	15.2	76.0	22	9	AZ305188	AZ305188 1M0005C17	c 205	14.2	71.0	19	6	CF282249	CF282249 14ETL--09
c 133	15.2	76.0	23	9	AZ968672	AZ968672 2M0241B09	c 206	14.2	71.0	19	6	CF295184	CF295184 30DGS--05
c 134	15.2	76.0	24	9	AZ642567	AZ642567 1M0505H12	c 207	14.2	71.0	19	6	CF312583	CF312583 ABF--08-G
c 135	15.2	76.0	26	10	CZ906862	CZ906862 4011003E0	c 208	14.2	71.0	19	6	CF323353	CF323353 HDN--03-K
c 136	15.2	76.0	27	1	AM047386	AM047386 AM047386	c 209	14.2	71.0	19	8	CK007735	CK007735 HDN--07-F
c 137	15.2	76.0	27	9	AZ776617	AZ776617 2M0010D23	c 210	14.2	71.0	19	8	CK007735	CK007735
c 138	15.2	76.0	27	11	TA289G07Q	TA289G07Q	c 211	14.2	71.0	19	8	DN953961	DN953961 1030B01.9
c 139	15.2	76.0	29	6	CF295257	CF295257 30DGS--05	c 212	14.2	71.0	19	8	DN953961	DN953961 1030B01.9
c 140	15.2	76.0	29	9	AZ642459	AZ642459 1M0505P06	c 213	14.2	71.0	19	8	DR062674	DR062674 iq20d11.9
c 141	15.2	76.0	31	9	AZ648445	AZ648445 1M0517A02	c 214	14.2	71.0	19	8	DR072910	DR072910 ik79a02.9
c 142	15.2	76.0	31	9	AZ761993	AZ761993 1M0556D11	c 215	14.2	71.0	19	8	DR074124	DR074124 ik98d12.9
c 143	15.2	76.0	32	9	AZ758290	AZ758290 1M0550A16	c 216	14.2	71.0	19	9	AZ328696	AZ328696 1M0030B22
c 144	15.2	76.0	32	10	CZ910279	CZ910279 4012001H1	c 217	14.2	71.0	19	9	AZ328727	AZ328727 1M0052F10
c 145	15.2	76.0	32	10	CZ918374	CZ918374 4021009B0	c 218	14.2	71.0	19	9	AZ330766	AZ330766 1M0056N07
c 146	15.2	76.0	34	1	A1521590	A1521590 to65b11.x	c 219	14.2	71.0	19	9	AZ338927	AZ338927 1M0070N07
c 147	15.2	76.0	34	1	AM047178	AM047178 AM047178	c 220	14.2	71.0	19	9	AZ342171	AZ342171 1M0075P01
c 148	15.2	76.0	34	9	AZ776846	AZ776846 2M0010A20	c 221	14.2	71.0	19	9	AZ345792	AZ345792 1M0080G12
c 149	15.2	76.0	34	11	TA367E10Q	TA367E10Q	c 222	14.2	71.0	19	9	AZ390115	AZ390115 1M0151U15
c 150	15.2	76.0	35	9	AZ807171	AZ807171 2M0069H18	c 223	14.2	71.0	19	9	AZ412494	AZ412494 1M0186A09
c 151	15.2	76.0	35	10	CZ916366	CZ916366 4021001B0	c 224	14.2	71.0	19	9	AZ423757	AZ423757 1M0203D19
c 152	15.2	76.0	36	9	AZ462645	AZ462645 1M0269M12	c 225	14.2	71.0	19	9	AZ439205	AZ439205 1M0229B15
c 153	15.2	76.0	36	10	CZ906811	CZ906811 4011003B0	c 226	14.2	71.0	19	9	AZ447234	AZ447234 1M0224L16
c 154	15.2	76.0	37	10	CZ917576	CZ917576 4021006B1	c 227	14.2	71.0	19	9	AZ466785	AZ466785 1M0277A16
c 155	15.2	76.0	37	1	A1433088	A1433088 th41c06.x	c 228	14.2	71.0	19	9	AZ468226	AZ468226 1M0287D10
c 156	15.2	76.0	37	9	AZ784558	AZ784558 2M0027G15	c 229	14.2	71.0	19	9	AZ481469	AZ481469 1M0303B15
c 157	15.2	76.0	38	2	B788802	B788802 601475711	c 230	14.2	71.0	19	9	AZ499200	AZ499200 1M0336O22
c 158	15.2	76.0	38	6	CF291715	CF291715 14ROOT--0	c 231	14.2	71.0	19	9	AZ499200	AZ499200 1M0336O22
c 159	15.2	76.0	38	9	AZ314682	AZ314682 1M0031B07	c 232	14.2	71.0	19	9	AZ587841	AZ587841 1M0395J14
c 160	15.2	76.0	39	2	B878080	B878080 601487463	c 233	14.2	71.0	19	9	AZ611179	AZ611179 1M0436B01
c 161	15.2	76.0	39	2	AZ949370	AZ949370 2M0212O18	c 234	14.2	71.0	19	9	AZ611509	AZ611509 1M0437B21
c 162	15.2	76.0	39	10	AL947253	AL947253 Arabidops	c 235	14.2	71.0	19	9	AZ615843	AZ615843 1M0445E23
c 163	15.2	76.0	39	10	CG724099	CG724099 1119079F0	c 236	14.2	71.0	19	9	AZ618258	AZ618258 1M0449G23
c 164	15.2	76.0	40	1	A1205954	A1205954 gg26f01.x	c 237	14.2	71.0	19	9	AZ625211	AZ625211 1M0464P22
c 165	15.2	76.0	40	1	EX185628	EX185628 Danio rer	c 238	14.2	71.0	19	9	AZ625605	AZ625605 1M0465D17
c 166	15.2	76.0	41	1	AJ806745	AJ806745 AJ806745	c 239	14.2	71.0	19	9	AZ634205	AZ634205 1M0489D19
c 167	15.2	76.0	41	8	CW998414	CW998414 iv49a12.b	c 240	14.2	71.0	19	9	AZ648703	AZ648703 1M0517A20
c 168	15.2	76.0	43	10	EX001839	EX001839 Arabidops	c 241	14.2	71.0	19	9	AZ649856	AZ649856 1M0519O07

C 242	14.2	71.0	19	9	AZ654733	AZ654733	1M0529A09
C 243	14.2	71.0	19	9	AZ654842	AZ654842	1M0529A20
C 244	14.2	71.0	19	9	AZ657564	AZ657564	1M0533P18
C 245	14.2	71.0	19	9	AZ764500	AZ764500	1M0560K06
246	14.2	71.0	19	9	AZ764526	AZ764526	1M0560J15
C 247	14.2	71.0	19	9	AZ769239	AZ769239	1M0569K09
C 248	14.2	71.0	19	9	AZ786434	AZ786434	1M0531M24
C 249	14.2	71.0	19	9	AZ795057	AZ795057	2M0049B08
C 250	14.2	71.0	19	9	AZ798934	AZ798934	2M0056F01
C 251	14.2	71.0	19	9	AZ799886	AZ799886	2M0057C12
C 252	14.2	71.0	19	9	AZ802234	AZ802234	2M0060M21
C 253	14.2	71.0	19	9	AZ808113	AZ808113	2M0071A01
C 254	14.2	71.0	19	9	AZ820788	AZ820788	2M0093A16
C 255	14.2	71.0	19	9	AZ843215	AZ843215	2M0142B06
C 256	14.2	71.0	19	9	AZ8545178	AZ8545178	2M0144P16
C 257	14.2	71.0	19	9	AZ861541	AZ861541	2M0168F19
C 258	14.2	71.0	19	9	AZ941561	AZ941561	2M0201B19
C 259	14.2	71.0	19	9	AZ969354	AZ969354	2M0242A07
C 260	14.2	71.0	19	10	CL657666	CL657666	PR1012a.H
C 261	14.2	71.0	19	10	CL665369	CL665369	PR10149C
C 262	14.2	71.0	20	6	CF279207	CF279207	14ETL--05
C 263	14.2	71.0	20	6	CF309954	CF309954	ABF--04.F
C 264	14.2	71.0	20	6	CF311285	CF311285	ABF--06-H
C 265	14.2	71.0	20	6	CF312611	CF312611	ABF--08-H
C 266	14.2	71.0	20	6	CF317375	CF317375	HD--07-A1
C 267	14.2	71.0	20	6	CF337475	CF337475	JMT--07-O
C 268	14.2	71.0	20	8	DN955107	DN955107	it82b01.g
C 269	14.2	71.0	20	8	DR073134	DR073134	ik86109.9
C 270	14.2	71.0	20	9	AZ328703	AZ328703	1M0052A07
C 271	14.2	71.0	20	9	AZ335199	AZ335199	1M0064K22
C 272	14.2	71.0	20	9	AZ342269	AZ342269	1M0075F13
C 273	14.2	71.0	20	9	AZ358156	AZ358156	1M0100M22
C 274	14.2	71.0	20	9	AZ360709	AZ360709	1M0100A05
C 275	14.2	71.0	20	9	AZ435223	AZ435223	1M0233B21
C 276	14.2	71.0	20	9	AZ437804	AZ437804	1M0236F18
C 277	14.2	71.0	20	9	AZ441557	AZ441557	1M0233G21
C 278	14.2	71.0	20	9	AZ445158	AZ445158	1M0240H15
C 279	14.2	71.0	20	9	AZ447205	AZ447205	1M0244I07
C 280	14.2	71.0	20	9	AZ448206	AZ448206	1M0245E15
C 281	14.2	71.0	20	9	AZ464607	AZ464607	1M0274L03
C 282	14.2	71.0	20	9	AZ465233	AZ465233	1M0275G04
C 283	14.2	71.0	20	9	AZ466043	AZ466043	1M0276K24
C 284	14.2	71.0	20	9	AZ470070	AZ470070	1M0283P24
C 285	14.2	71.0	20	9	AZ473415	AZ473415	1M0289K14
C 286	14.2	71.0	20	9	AZ486866	AZ486866	1M0315P24
C 287	14.2	71.0	20	9	AZ500172	AZ500172	1M0338F24
C 288	14.2	71.0	20	9	AZ500347	AZ500347	1M0338I07
C 289	14.2	71.0	20	9	AZ508103	AZ508103	1M0350B10
C 290	14.2	71.0	20	9	AZ519524	AZ519524	1M0367G14
C 291	14.2	71.0	20	9	AZ596645	AZ596645	1M0410I04
C 292	14.						

## ALIGNMENTS

RESULT 1	AZ867169	20 bp	DNA	linear	GSS 21-FEB-2001
LOCUS	AZ867169				
DEFINITION	2M0177120R Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM2M0177120 R, genomic survey sequence.				
ACCESSION	AZ867169				
VERSION	AZ867169.1				
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				

**ORGANISM**  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
**REFERENCE**  
**AUTHORS**  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
**JOURNAL**  
Unpublished (2000)  
**COMMENT**  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0177 row: 1 column: 20  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
**FEATURES**  
source  
1. .20  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0177120"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/motus="Vector; PWD42n; Purified genomic DNA from M.  
musculus C57BL/6J (male); was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match	100.0%	Score 20;	DB 9;	Length 20;
Best Local Similarity	100.0%;	Pred. No.	6.3e+03;	
Matches	20;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	AGGGGAGGGGAGGGGAGGGG	20	
Dd	1	AGGGGAGGGGAGGGGAGGGG	20	

RESULT 2	AZ359724	35 bp	DNA	linear	GSS 02-OCT-2000
LOCUS	AZ359724	1M0102M11R	Mouse 10kb plasmid	UUGCIM library	Mus musculus genomic
DEFINITION	AZ359724	clone UUGCIM0102M11 R,	genomic survey	sequence.	
ACCESSION	AZ359724				
VERSION	AZ359724.1	GI:10473424			
KEYWORDS	GSS.				

**SOURCE**  
**ORGANISM** Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 35)

**REFERENCE**  
**AUTHORS** Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
**JOURNAL**  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0102 row: M column: 11  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 35.

**FEATURES**  
 source  
 1..35  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0102M11"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

**ORIGIN**  
 Query Match 100.0%; Score 20; DB 9; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 AGGGGAGGGAGGGAGGGG 20  
 |||||  
 Db 4 AGGGGAGGGAGGGAGGGG 23  
 |||||  
 RESULT 3  
 AZ958287  
 LOCUS  
 DEFINITION 2M0225G02R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0225G02 R, genomic survey sequence.  
 ACCSSION AZ958287  
 VERSION AZ958287.1 GI:13829514

**KEYWORDS**  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 22)

**REFERENCE**  
**AUTHORS** Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
**JOURNAL**  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0225 row: G column: 02  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 22.

**FEATURES**  
 source  
 1..22  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0225G02"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

**ORIGIN**  
 Query Match 92.0%; Score 18.4; DB 9; Length 22;  
 Best Local Similarity 95.0%; Pred. No. 2.1e+04;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 AGGGGAGGGAGGGAGGGG 20  
 |||||  
 Db 3 AGGGGAGGGAGGGAGGGG 22  
 |||||  
 RESULT 4  
 AZ462959/c  
 LOCUS  
 DEFINITION 1M0271G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0271G04 R, genomic survey sequence.  
 ACCSSION AZ462959

```

VERSION AZ462959.1 GI:10621084
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
          1 (bases 1 to 26)
          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
        plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0271 row: G column: 04
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 26.
FEATURES
source
          Location/Qualifiers
          1..26
          /organism="Mus musculus"
          /mol_type="genomic DNA"
          /strain="C57BL/6J"
          /db_xref="taxon:10090"
          /clone="UUC1M0271G04"
          /sex="Male"
          /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
          /clone_lib="Mouse 10kb plasmid UUC1M library"
          /note="Vector: PWD42nv; Purified genomic DNA from M.
          musculus C57BL/6J (male) was obtained from the Jackson
          Laboratory Mouse DNA Resource
          (http://www.jax.org/resources/documents/dnares/). The DNA
          was hydrodynamically sheared by repeated passage through a
          0.005 inch orifice at constant velocity. The sheared DNA
          was blunt end-repaired with T4 DNA polymerase and T4
          polynucleotide kinase. Adaptor oligonucleotides were
          ligated to the blunt ends in high molar excess. The
          adaptor DNA was purified and size-selected for a 9.5 to
          10.5 kb range using preparative agarose gel
          electrophoresis. Vector DNA was prepared from a derivative
          of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
          inducible derivative of plasmid R1. The vector was ligated
          with adaptors complementary to the insert adaptors and
          purified. The sheared, adaptor mouse DNA was annealed to
          adaptor vector DNA, and transformed into
          chemically-competent E. coli XL10-Gold (Stratagene) cells
          and selected for ampicillin resistance."
ORIGIN
          Query Match 87.0%; Score 17.4; DB 9; Length 26;
          Best Local Similarity 94.7%; Pred. NO. 4.3e+04;
          Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

          Qy 2 GGGGAGGGGAGGGGAGGGG 20
          Db 25 GGGGAGGGGAGGGGAGGGG 7
          |||||||||||||||||||
          |||||||||||||||||||

RESULT 5
CL661180
LOCUS CL661180 28 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0139a.F07 - PRI0139a.B21 (28) Mixed stage fosmid library of P.
          pacificus var. California Pristionchus pacificus genomic, genomic
          pacificus var. California Pristionchus pacificus genomic, genomic

```

```

survey sequence.
ACCESSION CL661180
VERSION CL661180.1 GI:50147339
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
          Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
          Neodiplogasteridae; Pristionchus.
          1 (bases 1 to 28)
          Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
          AppaDB: an AcedB database for the nematode satellite organism
          Pristionchus pacificus
          Nucleic Acids Res. 32 (1), D421-D422 (2004)
          14681447
          Contact: Sommer RJ
          Evolutionary Biology
          Max-Planck-Institute for Developmental Biology
          Spemannstr. 37-39, Tuebingen D-72076, Germany
          Tel: 00497071601371
          Fax: 00497071601498
          Email: ralf.sommer@tuebingen.mpg.de
          This library was generated at Caltech, Pasadena, USA and end
          sequenced at Vancouver, Canada.
          Seq primer: T7
          Class: fosmid ends.
FEATURES
source
          Location/Qualifiers
          1..28
          /organism="Pristionchus pacificus"
          /mol_type="genomic DNA"
          /strain="California"
          /db_xref="taxon:54126"
          /clone_lib="Mixed stage fosmid library of P. pacificus
          var. California"
          /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN
          Query Match 87.0%; Score 17.4; DB 10; Length 28;
          Best Local Similarity 94.7%; Pred. NO. 4.3e+04;
          Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

          Qy 2 GGGGAGGGGAGGGGAGGGG 20
          Db 8 GGGGAGTGGAGGGGAGGGG 26
          |||||||||||||||||||
          |||||||||||||||||||

RESULT 6
LOCUS AZ9711404 32 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0244G20R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
          clone UUGC2M0244G20 R, genomic survey sequence.
ACCESSION AZ9711404
VERSION AZ9711404.1 GI:13842631
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Muroidea; Muridae; Murinae; Mus.
          1 (bases 1 to 32)
          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
          Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177

```

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0244 row: G column: 20  
 Seq primer: CACACAGGAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 32.

# FEATURES

Location/Qualifiers

1..32  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0244G20"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 32;  
 Best Local Similarity 94.7%; Pred. No. 4.3e+04;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGGGAGGGAGGGG 20  
 |||||  
 Db 7 GGGGAGGGGGGAGGGAGGGG 25

RESULT 7  
 AZ802326/c  
 LOCUS  
 DEFINITION 2M0061L09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 Clone UUGC2M0061L09 F, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 33)

# REFERENCE

AUTHORS  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

# JOURNAL

COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center

Unpublished (2000)  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0061 row: L column: 09  
 Seq primer: CGTTGTAATAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 33.

# FEATURES

Location/Qualifiers

1..33  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0061L09"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

# ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 33;  
 Best Local Similarity 94.7%; Pred. No. 4.3e+04;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGGGAGGGAGGGG 20  
 |||||  
 Db 20 GGAGAGGGGGGAGGGAGGGG 2

# RESULT 8

BX004665

LOCUS

DEFINITION

Arabidopsis thaliana T-DNA flanking sequence

genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

REFERENCE

AUTHORS

TITLE

JOURNAL

Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for  
 flanking sequence tag-based reverse genetics  
 Plant Mol. Biol. 53 (1-2), 247-259 (2003)



PUBMED 14756321  
 REFERENCE 3  
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveper, P., Dekker, K.A. and Weishaar, B.  
 TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
 JOURNAL Biotechniques 35 (6), 1164-1168 (2003)  
 PUBMED 14682050  
 REFERENCE 4  
 AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weishaar, B.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 COMMENT This sequence has been recovered from the left border of the T-DNA. Details on the protocols used for generation of the sequence are described in References 1-3. Re-examination of the source from which this sequence has been produced indicates that the sequence is of low reliability. Therefore, no information on a potential insertion site is deduced. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES  
 source  
 1..38  
 Location/Qualifiers  
 /organism="Arabidopsis thaliana"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3702"  
 /clone="GK-400A12-017894"  
 /clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
 /ecotype="Col-0"  
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN  
 Query Match 87.0%; Score 17.4; DB 10; Length 38;  
 Best Local Similarity 94.7%; Fred. No. 4.3e+04;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GGGGAGGGGAGGGAGGGG 20  
 |||||  
 Db 1 GGGGAGGGGAGGGAGGGG 19  
 |||||

RESULT 9  
 A2820833/c  
 LOCUS A2820833 43 bp DNA linear GSS 20-FEB-2001  
 DEFINITION clone UUGC2M00931b6 F, genomic survey sequence.  
 ACCESSION A2820833  
 VERSION A2820833.1 GI:12990741  
 GSS.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 43)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0093 row: L column: 16  
 Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 43.  
 Location/Qualifiers  
 1..43  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0093L16"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN  
 Query Match 87.0%; Score 17.4; DB 9; Length 43;  
 Best Local Similarity 94.7%; Fred. No. 4.3e+04;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 GGGGAGGGGAGGGAGGGG 20  
 |||||  
 Db 38 GGGGAGGGGAGGGAGGGG 20  
 |||||

RESULT 10  
 A2375586/c  
 LOCUS A2375586 45 bp DNA linear GSS 02-OCT-2000  
 DEFINITION 1M0129G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0129G03 F, genomic survey sequence.  
 ACCESSION A2375586  
 VERSION A2375586.1 GI:10489286  
 GSS.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 45)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0129 row: G column: 03  
Seq primer: CGTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 45.  
Location/Qualifiers

FEATURES  
source

1. .45  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UUGC1M0129G03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 45;  
Best Local Similarity 94.7%; Pred. No. 4.3e+04;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
|||||  
Db 39 GGGGAGGGGAGGGAGGGG 21

RESULT 11  
AJ793526/c

LOCUS  
DEFINITION  
AJ793526 Antirrhinum majus whole plant Antirrhinum majus cDNA clone  
018 3 02 k18, mRNA sequence.

ACCESSION  
AJ793526  
EST.

KEYWORDS  
SOURCE  
ORGANISM

Antirrhinum majus (snapdragon)  
Antirrhinum majus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamids; Lamiales; Plantaginaceae; Antirrhineae;  
Antirrhinum.

REFERENCE  
1 (bases 1 to 47)  
Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H.,  
Siedler, H. and Zachgo, S.

TITLE  
Characterization of Antirrhinum Petal Development and  
Identification of Target Genes of the Class B MADS Box Gene  
DEFICIENS

JOURNAL  
Plant Cell 16 (12), 3197-3215 (2004)

PUBMED  
15539471

COMMENT

Contact: Schwarz-Sommer Z  
Molekulare Pflanzen-genetik  
MPI fuer Zuechtungsforschung  
Carl-von-Linne Weg 10, D-50829, Germany.

FEATURES  
source

1. .47  
/organism="Antirrhinum majus"  
/mol\_type="mRNA"  
/db\_xref="taxon:4151"  
/clone="018\_3\_02\_k18"  
/tissue\_type="whole plant"  
/clone\_lib="Antirrhinum majus whole plant"

ORIGIN

Query Match 87.0%; Score 17.4; DB 1; Length 47;  
Best Local Similarity 94.7%; Pred. No. 4.3e+04;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
|||||  
Db 29 GGGGAGGGGAGGGAGGGG 11

RESULT 12  
AZ800436

LOCUS  
DEFINITION  
AZ800436 Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0058L20 F, genomic survey sequence.

ACCESSION  
AZ800436  
VERSION  
AZ800436.1 GI:12952548

KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1 (bases 1 to 50)

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0058 row: L column: 20

Seq primer: CGTGTAAACGACGGCCAGT  
Class: plasmid ends

High quality sequence stop: 50.  
Location/Qualifiers

FEATURES  
source

1. .50  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0058L20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 50;  
 Best Local Similarity 94.7%; Pred. No. 4.2e+04;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGGAGGG 19  
 |||||  
 Db 32 AGAGGAGGGGAGGGGAGGG 50

## RESULT 13

## AZ780325/c

## LOCUS

DEFINITION 25 bp DNA linear GSS 16-FEB-2001  
 clone UUGC2M0017N06 R, genomic survey sequence.

## ACCESSION

## AZ780325

## VERSION

## AZ780325.1

## KEYWORDS

## GSS.

## SOURCE

## Mus musculus

## ORGANISM

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

## Sciurognathi; Muridae; Murinae; Mus.

## 1 (bases 1 to 25)

## Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

## Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

## Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

## Niederhausern, A. and Wright, D., Weiss, R.

## Mouse whole genome scaffolding with paired end reads from 10kb

## plasmid inserts

## Unpublished (2000)

## Contact: Robert B. Weiss

## University of Utah

## Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

## 84112, USA

## Tel: 801 585 5606

## Fax: 801 585 7177

## Email: ddunne@genetics.utah.edu

## Insert Length: 10000 Std Error: 0.00

## Plate: 0017 row: N column: 06

## Seq primer: CACACGGAACAGCTATGACC

## Class: plasmid ends

## High quality sequence stop: 25.

## Location/Qualifiers

## 1..25

## /organism="Mus musculus"

## /mol\_type="genomic DNA"

## /strain="C57BL/6J"

## /db\_xref="taxon:10090"

## /clone="UUGC2M0017N06"

## /sex="Male"

## /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

## /clone\_lib="Mouse 10kb plasmid UUGC1M library"

## /note="Vector: pWD42nv; Purified genomic DNA from M.

## musculus C57BL/6J (male) was obtained from the Jackson

## Laboratory Mouse DNA Resource

## (http://www.jax.org/resources/documents/dnares/). The DNA

## was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 25;  
 Best Local Similarity 90.0%; Pred. No. 6.8e+04;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGGAGGGG 20  
 |||||  
 Db 23 AGGGGAGGGGAGGGGAGGGG 4

## RESULT 14

## AL935924/c

## LOCUS

DEFINITION 30 bp DNA linear GSS 31-MAR-2004  
 Arabidopsis thaliana T-DNA flanking sequence GK-009H02-016930,  
 genomic survey sequence.

## ACCESSION

## AL935924

## VERSION

## AL935924.1

## KEYWORDS

## GSS.

## SOURCE

## Arabidopsis thaliana (thale cress)

## Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

## rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

## 1

## Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.

## GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for

## the identification of T-DNA insertion mutants in Arabidopsis

## thaliana

## Bioinformatics 19 (11), 1441-1442 (2003)

## 2

## Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and

## Weisshaar, B.

## An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for

## flanking sequence tag-based reverse genetics

## Plant Mol. Biol. 53 (1-2), 247-259 (2003)

## 3

## Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and

## Weisshaar, B.

## High-throughput generation of sequence indexes from T-DNA

## mutagenized Arabidopsis thaliana lines

## BioTechniques 35 (6), 1164-1168 (2003)

## 4

## Li, Y., Strizhov, N., Rosso, M.G. and Weisshaar, B.

## Direct Submission

## Submitted (31-MAR-2004)

## Weisshaar, B., Max-Planck-Institut fuer

## Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

## This sequence has been recovered from the left border of the T-DNA.

## Details on the protocols used for generation of the sequence are

## described in References 1-3. Re-examination of the source from

## which this sequence has been produced indicates that the sequence

## is of low reliability. Therefore, no information on a potential

## insertion site is deduced. The sequences are generated at the MPI

## for Plant Breeding Research in the context of the GABI-Kat project.

## GABI-Kat is part of the German Plant Genomics program designated

## 'GABI'. Information on line availability can be found at:

```

http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES
  source
    Location/Qualifiers
      1..30
        /organism="Arabidopsis thaliana"
        /mol_type="genomic DNA"
        /db_xref="taxon:3702"
        /clone="GK-009H02-016930"
        /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
        /ecotype="Col-0"
        /note="PCR was performed on DNA from Arabidopsis thaliana
        plants (TI) which were transformed with the T-DNA from
        vector pAC106 (GenBank accession number: AJ537513). The
        lines contain one or more T-DNA insertions. The DNA
        fragment(s) resulting from the PCR were directly sequenced
        to determine the genomic sequence flanking the insertion.
        T-DNA derived sequences were removed."
ORIGIN
  Query Match      84.0%; Score 16.8; DB 10; Length 30;
  Best Local Similarity 90.0%; Pred. No. 6.8e+04;
  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 23 AGGGGGGGGGGGGGAGGGG 4

RESULT 15
AZ652279/c
LOCUS
DEFINITION
  1M0525K06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0525K06 R, genomic survey sequence.
ACCESSION
  AZ652279
VERSION
  AZ652279.1 GI:11788802
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 33)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0525 row: K column: 06
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 33.
  Location/Qualifiers
    1..33
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0525K06"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson

FEATURES
  source
    Location/Qualifiers
      1..38
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0203B05"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pW42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
ORIGIN
  Query Match      84.0%; Score 16.8; DB 9; Length 33;
  Best Local Similarity 90.0%; Pred. No. 6.7e+04;
  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 31 AGGGAGAGGAGGGAGGGAG 12

RESULT 16
AZ424085/c
LOCUS
DEFINITION
  1M0203B05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0203B05 R, genomic survey sequence.
ACCESSION
  AZ424085
VERSION
  AZ424085.1 GI:10548098
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 38)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0203 row: B column: 05
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 38.
  Location/Qualifiers
    1..38
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0203B05"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.

```



/clone\_lib="Mouse 10kb plasmid UUC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4731114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 43;  
 Best Local Similarity 90.0%; Pred. No. 6.7e+04;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20

Db 41 AGGGAGGGGAGAGGAGG 22

## RESULT 19

AI800153

LOCUS

DEFINITION

tr23a06.x1 NCI CGAP OV23 Homo sapiens cDNA clone IMAGE:2219122 3', similar to SW:PRPB\_HUMAN P02814 PROLINE-RICH PEPTIDE P-B. ;contains element MSR1 repetitive element ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 37)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..37

/organism="Homo sapiens"

/mol\_type="mrna"

/db\_xref="taxon:9606"

/clone="IMAGE:2219122"

/tissue\_type="tumor, 5 pooled (see description)"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Ov23"

## FEATURES

source

Query Match 82.0%; Score 16.4; DB 1; Length 46;  
 Best Local Similarity 94.4%; Pred. No. 9e+04;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGAGGGGAGGGAGGGG 20

Db 16 GGGAGGGGAGGGAGGGG 33

/note="Organ: ovary; Vector: pCMV-SPORT6; Site.1: SalI;  
 Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.35 kb. tumor types include: mixed  
 Mullerian tumor, papillary serous, clear cell, spindle  
 cell. All are primary tumors, metastasis positive. Life  
 Technologies catalog #: 11534-013"

## ORIGIN

Query Match 82.0%; Score 16.4; DB 1; Length 37;  
 Best Local Similarity 94.4%; Pred. No. 9e+04;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGGAGGGGAGGGAGGGG 20

Db 17 GGGAGGGGAGGGAGGGG 34

## RESULT 20

AI597960

LOCUS

DEFINITION

t804f05.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2227617 3', similar to SW:PRPB\_HUMAN P02814 PROLINE-RICH PEPTIDE P-B. ;contains TARI.t2 MSR1 repetitive element ;, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 46)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 3675 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

FEATURES

source

1..46

/organism="Homo sapiens"

/mol\_type="mrna"

/db\_xref="taxon:9606"

/clone="IMAGE:2227617"

/tissue\_type="adenocarcinoma"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Panl"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site.1: SalI;  
 Site.2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.72 kb. Life Technologies catalog #:  
 11548-013"

```

RESULT 21
AZ447248/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: H column: 23
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0244H23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
ORIGIN
Query Match 79.0%; Score 15.8; DB 9; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGGAGGGG 20
| | | | |
Db 19 GGGGAGGGGAGGGGAGGGG 1
| | | | |

```

```
Db      19 GGGGAGGGGGGGGGGGGGG 1

RESULT 24
LOCUS   AZ772707/c
DEFINITION 1M0583L18R Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0583L18 R, genomic survey sequence.
ACCESSION  AZ772707
VERSION     AZ772707.1
KEYWORDS    GI:12896303
SOURCE      GSS.
ORGANISM    Mus musculus (house mouse)
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Islam,H., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0583 row: L column: 18
            Seq primer: CACACAGGAACACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.

FEATURES             Location/Qualifiers
     source            1..20
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="UGCLM0583L18"
                        /sex="Male"
                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                        /clone_lib="Mouse 10kb plasmid UGCLM library"
                        /notes="Vector: PWD42nv; Purified genomic DNA from M.
                        musculus C57BL/6J (male) was obtained from the Jackson
                        Laboratory Mouse DNA Resource
                        (http://www.jax.org/resources/documents/dnares/). The DNA
                        was hydrodynamically sheared by repeated passage through a
                        0.005 inch orifice at constant velocity. The sheared DNA
                        was blunt end-repaired with T4 DNA polymerase and T4
                        polynucleotide kinase. Adaptor oligonucleotides were
                        ligated to the blunt ends in high molar excess. The
                        adaptored DNA was purified and size-selected for a 9.5 to
                        10.5 kb range using preparative agarose gel
                        electrophoresis. Vector DNA was prepared from a derivative
                        of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
                        inducible derivative of plasmid R1. The vector was ligated
                        with adaptors complementary to the insert adaptors and
                        purified. The sheared, adaptored mouse DNA was annealed to
                        adaptored vector DNA, and transformed into
                        chemically-competent E. coli XL10-Gold (Stratagene) cells
                        and selected for ampicillin resistance."

ORIGIN
Query Match      79.0%; Score 15.8; DB 9; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GGGGAGGGGGGGGGGGGGG 20
        ||||||| ||||| |||||
```

```
Db      19 GGGGAGGGGGGGGGGGGGG 1

RESULT 24
LOCUS   AZ772707/c
DEFINITION 1M0583L18R Mouse 10kb plasmid UGCLM library Mus musculus genomic
clone UGCLM0583L18 R, genomic survey sequence.
ACCESSION  AZ772707
VERSION     AZ772707.1
KEYWORDS    GI:12896303
SOURCE      GSS.
ORGANISM    Mus musculus (house mouse)
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Islam,H., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0583 row: L column: 18
            Seq primer: CACACAGGAACACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.

FEATURES             Location/Qualifiers
     source            1..20
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="UGCLM0583L18"
                        /sex="Male"
                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                        /clone_lib="Mouse 10kb plasmid UGCLM library"
                        /notes="Vector: PWD42nv; Purified genomic DNA from M.
                        musculus C57BL/6J (male) was obtained from the Jackson
                        Laboratory Mouse DNA Resource
                        (http://www.jax.org/resources/documents/dnares/). The DNA
                        was hydrodynamically sheared by repeated passage through a
                        0.005 inch orifice at constant velocity. The sheared DNA
                        was blunt end-repaired with T4 DNA polymerase and T4
                        polynucleotide kinase. Adaptor oligonucleotides were
                        ligated to the blunt ends in high molar excess. The
                        adaptored DNA was purified and size-selected for a 9.5 to
                        10.5 kb range using preparative agarose gel
                        electrophoresis. Vector DNA was prepared from a derivative
                        of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
                        inducible derivative of plasmid R1. The vector was ligated
                        with adaptors complementary to the insert adaptors and
                        purified. The sheared, adaptored mouse DNA was annealed to
                        adaptored vector DNA, and transformed into
                        chemically-competent E. coli XL10-Gold (Stratagene) cells
                        and selected for ampicillin resistance."

ORIGIN
Query Match      79.0%; Score 15.8; DB 9; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GGGGAGGGGGGGGGGGGGG 20
        ||||||| ||||| |||||
```



```

Db      20 GGGGGGGGGAGGGGGGGG 2
||||| ||||| ||||| ||||| |||||
RESULT 25
LOCUS   AZ583408
DEFINITION 21 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0378N23 F, genomic survey sequence.
ACCESSION AZ583408
VERSION   1
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0378 row: N column: 23
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0378N23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Db      20 GGGGGGGGGAGGGGGGGG 2
||||| ||||| ||||| ||||| |||||
RESULT 26
LOCUS   AZ653464
DEFINITION 21 bp DNA linear GSS 14-DEC-2000
clone UUGC1M0527G11 F, genomic survey sequence.
ACCESSION AZ653464
VERSION   1
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0527 row: G column: 11
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0527G11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0527G11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 79.0%; Score 15.8; DB 9; Length 21;
Best Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ORIGIN
Query Match 79.0%; Score 15.8; DB 9; Length 21;
Best Local Similarity 89.5%; Pred. No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```
QY      2 GGGGAGGGGAGGGGAGGGG 20
      |||||
Db      21 GGGGGGGGAGGGGGGGGG 3

RESULT 28
AZ871715      21 bp      DNA      linear      GSS 21-FEB-2001
LOCUS      AZ871715
DEFINITION      2M0184B13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0184B13 R, genomic survey sequence.
ACCESSION      AZ871715
VERSION      AZ871715.1 GI:13078192
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0184 row: B column: 13
Seq primer: CACACAGGAAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0184B13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
QY      2 GGGGAGGGGAGGGGAGGGG 20
      |||||
Db      21 GGGGGGGGAGGGGGGGGG 3

RESULT 28
AZ331988      22 bp      DNA      linear      GSS 29-SEP-2000
LOCUS      AZ331988
DEFINITION      IM0060B11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0060B11 F, genomic survey sequence.
ACCESSION      AZ331988
VERSION      AZ331988.1 GI:10395213
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0060 row: B column: 11
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0060B11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
FEATURES
source
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0060B11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
ORIGIN
Query Match      79.0%; Score 15.8; DB 9; Length 22;
Best Local Similarity      89.5%; Pred. No. 1.4e+05;
```



Query Match 79.0%; Score 15.8; DB 9; Length 22;  
 Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
 |||||  
 Db 22 GGGGGGGGGAGGGGGGGG 4

RESULT 31  
 AZ645874/c 22 bp DNA linear GSS 14-DEC-2000  
 LOCUS  
 DEFINITION IM0511C07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0511C07 R, genomic survey sequence.

ACCESSION AZ645874  
 VERSION AZ645874.1 GI:11775791  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0511 row: C column: 07

Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends

High quality sequence stop: 22.  
 Location/Qualifiers

FEATURES  
 source

1. .22  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clones="UUGC1M0511C07"  
 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 22;  
 Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
 |||||  
 Db 19 GGGGAGGGGGGGGGGGGG 1

RESULT 32

AZ488138/c

LOCUS

DEFINITION IM0318E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0318E13 F, genomic survey sequence.

ACCESSION AZ488138

VERSION AZ488138.1 GI:10656541

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0318 row: E column: 13

Seq primer: CGTTGTAAACGACGCCAGT  
 Class: plasmid ends

High quality sequence stop: 23.  
 Location/Qualifiers

FEATURES  
 source

1. .23  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clones="UUGC1M0318E13"  
 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

# ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 23;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GGGGAGGGGAGGGGAGGGG 20  
|||||  
Db 22 GGGGGGGGAGGGGGGGGG 4

# RESULT 33

AZ581259/c  
LOCUS  
DEFINITION 1M0369N11R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC1M0369N11 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ581259 23 bp DNA linear GSS 13-DEC-2000  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

# REFERENCE

AUTHORS  
1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

# JOURNAL

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0369 row: N column: 11  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends

High quality sequence stop: 23.

# FEATURES

Location/Qualifiers  
1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC1M0369N11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

# ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 23;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GGGGAGGGGAGGGGAGGGG 20  
|||||  
Db 23 GGGGGGGGAGGGGGGGGG 5

# RESULT 34

AZ800632/c  
LOCUS  
DEFINITION 2M0058E17R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUC2M0058E17 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ800632 23 bp DNA linear GSS 16-FEB-2001  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

# REFERENCE

AUTHORS  
1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

# JOURNAL

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0058 row: E column: 17  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends

High quality sequence stop: 23.

# FEATURES

Location/Qualifiers  
1..23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUC2M0058E17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
purified. The sheared, adapted mouse DNA was annealed to

adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 23;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGAGGGGAGGGAGGGG 20  
||||| ||||| |||||  
Db 19 GGGAGGGGAGGGAGGGG 1

## RESULT 35

AZ404465  
LOCUS  
DEFINITION  
1M0172P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0172P09 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

AZ404465.1 GI:10528394  
GSS.

Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0172 row: P column: 09

Seq primer: CACACGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 24.

## FEATURES

source

1..24

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0172P09"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 24;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGAGGGGAGGGAGGGG 20  
||||| ||||| |||||  
Db 4 GGGGGGGGAGGAGAGGGG 22

## RESULT 36

AZ640795/c

LOCUS

DEFINITION  
1M0503D04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0503D04 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

AZ640795.1 GI:11764195  
GSS.

Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Muridae; Murinae; Mus.

1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0503 row: D column: 04

Seq primer: CGTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

## FEATURES

source

1..24

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0503D04"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 24;  
 Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGGAGGGG 20  
 ||||| ||||| ||||| |||||  
 Db 23 GGGGAGGGGAGGGGAGGGG 5

RESULT 37  
 AZ789161/c  
 LOCUS  
 DEFINITION 2M0036A15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0036A15 R, genomic survey sequence.

ACCESSION AZ789161  
 VERSION AZ789161.1 GI:12929693  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 24)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
 COMMENT Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0036 row: A column: 15  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 24.

## FEATURES

Location/Qualifiers  
 1..24  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0036A15"  
 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 24;  
 Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGGAGGGG 20  
 ||||| ||||| ||||| |||||  
 Db 20 GGGGAGGGGAGGGGAGGGG 2

RESULT 38  
 AZ823931  
 LOCUS  
 DEFINITION 2M0098F17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0098F17 F, genomic survey sequence.

ACCESSION AZ823931  
 VERSION AZ823931.1 GI:12993839  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 24)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
 COMMENT Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0098 row: F column: 17  
 Seq primer: CGTTGTAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 24.

## FEATURES

Location/Qualifiers  
 1..24  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0098F17"  
 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pMDA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 24;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GGGGAGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 5 GGGGAGGGGAGGGGAGGGG 23

## RESULT 19

AZ468549/c  
LOCUS  
DEFINITION  
IM0281D10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0281D10 R, genomic survey sequence.

ACCESSION  
AZ468549  
VERSION  
AZ468549.1 GI:10626674

KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 25)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0281 row: D column: 10

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

## FEATURES

source

1. .25

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0281D10"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 GGGGAGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 23 GGGGGGGGGGGGAGGGG 5

## RESULT 40

AZ602480/c

LOCUS

DEFINITION

IM0421F16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0421F16 F, genomic survey sequence.

ACCESSION

AZ602480

VERSION

AZ602480.1 GI:11724670

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 25)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0421 row: F column: 16

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1. .25

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0421F16"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."



10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* Xl10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
|||||

Db 25 GGGGGGGGAGGGGAGGGGG 7  
|||||

RESULT 41  
TA33E11P/c

LOCUS TA33E11P 25 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 33e11, forward sequence,  
genomic survey sequence.

ACCESSION AL453376  
VERSION AL453376.1 GI:11854702

KEYWORDS GSS.

## SOURCE

ORGANISM Trypanosoma brucei  
Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

REFERENCE 1 (bases 1 to 25)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, W.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

## COMMENT

Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

source

1..25  
Location/Qualifiers  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="33e11"

## ORIGIN

Query Match 79.0%; Score 15.8; DB 11; Length 25;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
|||||

Db 20 GGGGGGGGAGGGGAGGGGG 2  
|||||

## RESULT 42

EX626114

LOCUS BX626114 26 bp mRNA linear EST 08-AUG-2003  
DEFINITION NAP1 Anopheles gambiae cDNA clone ANGNP1181G08T7, mRNA  
sequence.

ACCESSION BX626114

VERSION BX626114.1 GI:33552251

KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae

REFERENCE 1 (bases 1 to 26)  
AUTHORS Lobo, N.L., Gardner, M., Romans, P. and Collins, P.H.  
TITLE Anopheles gambiae EST, Center for Tropical Disease Research and  
Training

JOURNAL Unpublished (2003)

COMMENT Contact: Frank H. Collins  
Center for Tropical Disease Research and Training  
University of Notre Dame  
Notre Dame, IN 46556, USA  
Tel: 574-631-9245  
Fax: 574-631-3996  
Email: frank.h.collins.75@nd.edu.

## FEATURES

source

1..26  
Location/Qualifiers  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/db\_xref="taxon:7165"  
/clone="ANGNP1181G08T7"  
/lab\_host="E. coli DH10B"  
/clone\_lib="NAP1"  
/note="Vector: pT7T3D-Pac (Pharmacia); Site 1: NotI;  
Site 2: EcoRI; ESTs sequenced from the T7 priming site  
that reads from the 5' end of cDNA. The NAP1 is a  
directionally cloned and normalized, oligo-T primed cDNA  
library constructed from a mixture of Anopheles gambiae  
developmental stages according to: Bonaldo, Lennon &  
Soares (1996): Normalization and Subtraction: Two  
Approaches To Facilitate Gene Discovery, Genome Research  
6, 791-806."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 5; Length 26;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
|||||

Db 1 GGGGAGGGGAGGGGAGGGG 19  
|||||

## RESULT 43

AZ307654/c

LOCUS AZ307654 26 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0009F22R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
clone UUGC1M0009F22 R, genomic survey sequence.

ACCESSION AZ307654

VERSION AZ307654.1 GI:10346867

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mus whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

Unpublished (2000)  
Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0009 row: F column: 22  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.  
Location/Qualifiers

## FEATURES

source

1..26  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0009F22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 26;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
|||||  
Db 22 GGGGGGGGGAGGGGGGGG 4  
|||||

RESULT 44  
AZ447254/c  
LOCUS  
DEFINITION  
1M0244020F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0244020 F, genomic survey sequence.

ACCESSION  
AZ447254  
VERSION  
AZ447254.1 GI:10599055  
GSS.  
SOURCE  
Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1 (bases 1 to 26)

## REFERENCE

## AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

Unpublished (2000)

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0244 row: O column: 20  
Seq primer: CGTTGTAACAGCGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 26.  
Location/Qualifiers

## FEATURES

source

1..26  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0244020"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 26;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20  
|||||  
Db 24 GGGGGGGGGAGGGGGGGG 6  
|||||

## RESULT 45

AZ810458/c

## LOCUS

DEFINITION  
2M0076C02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0076C02 F, genomic survey sequence.

ACCESSION

AZ810458

## VERSION

AZ810458.1

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus

## REFERENCE

## AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## TITLE

Unpublished (2000)

## JOURNAL

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0076 row: C column: 02  
Seq primer: CTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 26.

## FEATURES

source

1. 26  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0076C02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 26;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20

Db 26 GGGGAGGGGAGGGAGGGG 8

## RESULT 46

AZ861534/c

## LOCUS

AZ861534 26 bp DNA linear GSS 21-FEB-2001  
DEFINITION 2M0168K19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0168K19 F, genomic survey sequence.

## ACCESSION

AZ861534

## VERSION

AZ861534.1

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 26)

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

## JOURNAL

## COMMENT

plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0168 row: K column: 19  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 26.

## FEATURES

source

1. 26  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0168K19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 26;  
Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20

Db 23 GGGGAGGGGAGGGAGGGG 5

## RESULT 47

AZ604434/c

## LOCUS

AZ604434 27 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0425I19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0425I18 F, genomic survey sequence.

## ACCESSION

AZ604434

## VERSION

AZ604434.1

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 27)

## AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

TITLE	Niederhausem,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plats: 0519 row: P column: 18 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends

```

FEATURES
source
High quality sequence stop. 27.
Location/Qualifiers
1. 27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="JUGC1M0519P18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells

```

```

ORIGIN
Query Match          79.0%; Score 15.8; DB 9; Length 27;
Best Local Similarity 89.8%; Pred.No. 1.4e+05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  GCGGAGGGAGGGAGGG 20
      |||||

```

RESULT 49  
AZ327022  
LOCUS  
DEFINITION  
AZ327022 28 bp DNA linear GSS 29-SEP-2000  
1M0050112F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0050112 F, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 28)  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0050 row: 1 column: 12  
 Seq primer: CGTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 28.  
 Location/Qualifiers  
 1..28  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0050112"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### FEATURES

source

1..28  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0315G02"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 28;  
 Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AGGGAGGGGAGGGAGGG 19  
 |||||  
 Db 9 AGGGAAGTGGAGGGAGGG 27

#### RESULT 50

AZ486749/c  
 LOCUS  
 DEFINITION  
 AZ486749 28 bp DNA linear GSS 05-OCT-2000  
 1M0315G02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315G02 F, genomic survey sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 28)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0315 row: G column: 02  
 Seq primer: CGTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 28.  
 Location/Qualifiers  
 1..28  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0315G02"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### FEATURES

1..28  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0315G02"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

#### ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 28;  
 Best Local Similarity 89.5%; Pred. No. 1.4e+05;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GGGGAGGGGAGGGAGGGG 20  
 |||||  
 Db 26 GGGGAGGGGAGGGAGGGG 8

Search completed: February 15, 2006, 21:10:50  
 Job time : 1343.25 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 18:56:18 ; Search time 44.9587 Seconds  
(without alignments)  
790.754 Million cell updates/sec

Title: US-09-669-187A-906  
Perfect score: 20  
Sequence: 1 aggggaggggaggggagggg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1299706

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Issued Patents\_NA.\*

- 1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/PCRTUS COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.4	87.0	27	2	US-08-460-890A-14
C 2	17.4	87.0	27	2	US-08-460-890A-15
C 3	17.4	87.0	27	3	US-08-167-641C-14
C 4	17.4	87.0	27	3	US-08-167-641C-15
C 5	17.4	87.0	27	3	US-08-460-971A-14
C 6	17.4	87.0	27	3	US-08-460-971A-15
C 7	17.4	87.0	27	3	US-08-462-040-14
C 8	17.4	87.0	27	3	US-08-462-040-15
C 9	17.4	87.0	39	2	US-08-460-890A-13
C 10	17.4	87.0	39	3	US-08-167-641C-13
C 11	17.4	87.0	39	3	US-08-460-971A-13
C 12	17.4	87.0	39	3	US-08-462-040-13
C 13	16.4	82.0	43	6	PCT-US93-02352-2
C 14	16.4	82.0	43	6	PCT-US93-02352-3
C 15	16.4	82.0	50	3	US-08-956-171E-2153
C 16	16.4	82.0	50	3	US-08-781-986A-2153
C 17	15.8	79.0	27	3	US-09-622-745B-20
C 18	15.8	79.0	27	3	US-09-622-745B-21
C 19	15.8	79.0	42	9	5182196-21
C 20	15.2	76.0	37	3	US-09-118-752-2
C 21	15.2	76.0	38	2	US-08-324-001-2
C 22	14.8	74.0	30	3	US-09-230-222-18
C 23	14.8	74.0	30	3	US-09-230-225B-25
C 24	14.8	74.0	31	3	US-09-254-352B-31

c 98	13.8	69.0	37	3	US-09-280-270A-1	Sequence 1, Appli	c 171	13.2	66.0	30	3	US-08-976-427-17	Sequence 17, Appl
99	13.8	69.0	45	2	US-08-872-446-9	Sequence 9, Appli	c 172	13.2	66.0	30	3	US-08-976-427-19	Sequence 19, Appl
100	13.8	69.0	47	3	US-09-280-270A-9	Sequence 9, Appli	c 173	13.2	66.0	30	3	US-09-648-312-12	Sequence 12, Appl
101	13.8	69.0	45	3	US-09-641-638-679	Sequence 679, App	c 174	13.2	66.0	30	3	US-09-648-312-13	Sequence 13, Appl
102	13.8	69.0	47	3	US-09-422-978-285	Sequence 285, App	c 175	13.2	66.0	30	3	US-09-648-312-15	Sequence 15, Appl
c 103	13.8	69.0	47	3	US-09-422-978-3218	Sequence 3218, Ap	c 176	13.2	66.0	30	3	US-09-648-312-17	Sequence 17, Appl
c 104	13.8	69.0	47	3	US-10-170-097-679	Sequence 679, App	c 177	13.2	66.0	30	3	US-09-648-312-19	Sequence 19, Appl
c 105	13.8	69.0	50	3	US-10-131-827-5327	Sequence 5327, Ap	c 178	13.2	66.0	30	3	US-09-896-650C-12	Sequence 12, Appl
106	13.6	68.0	21	2	US-08-424-663-2	Sequence 2, Appli	c 179	13.2	66.0	30	3	US-09-896-650C-13	Sequence 13, Appl
107	13.6	68.0	21	2	US-08-872-446-2	Sequence 2, Appli	c 180	13.2	66.0	30	3	US-09-896-650C-15	Sequence 15, Appl
108	13.6	68.0	21	3	US-09-280-270A-2	Sequence 2, Appli	c 181	13.2	66.0	30	3	US-09-896-650C-17	Sequence 17, Appl
109	13.6	68.0	24	3	US-08-729-598-7	Sequence 7, Appli	c 182	13.2	66.0	30	3	US-09-896-650C-19	Sequence 19, Appl
110	13.6	68.0	24	3	US-09-894-799-21	Sequence 21, Appl	c 183	13.2	66.0	31	3	US-08-976-427-2	Sequence 2, Appli
c 111	13.6	68.0	25	3	US-09-863-049B-67	Sequence 67, Appl	c 184	13.2	66.0	31	3	US-08-976-427-3	Sequence 3, Appli
c 112	13.6	68.0	30	2	US-08-802-547-14	Sequence 14, Appl	c 185	13.2	66.0	31	3	US-08-976-427-4	Sequence 4, Appli
c 113	13.6	68.0	39	3	US-09-679-971-3	Sequence 3, Appli	c 186	13.2	66.0	31	3	US-08-976-427-5	Sequence 5, Appli
c 114	13.6	68.0	45	3	US-08-931-220-36	Sequence 36, Appl	c 187	13.2	66.0	31	3	US-08-976-427-6	Sequence 6, Appli
c 115	13.6	68.0	45	6	PCT-US95-11723-36	Sequence 36, Appl	c 188	13.2	66.0	31	3	US-08-976-427-7	Sequence 7, Appli
c 116	13.6	68.0	45	6	PCT-US96-05997-36	Sequence 36, Appl	c 189	13.2	66.0	31	3	US-08-976-427-8	Sequence 8, Appli
c 117	13.6	68.0	47	3	US-09-671-317-679	Sequence 679, App	c 190	13.2	66.0	31	3	US-08-976-427-9	Sequence 9, Appli
c 118	13.6	68.0	48	2	US-08-872-446-12	Sequence 12, Appl	c 191	13.2	66.0	31	3	US-08-976-427-10	Sequence 10, Appl
c 119	13.6	68.0	48	3	US-09-280-270A-12	Sequence 12, Appl	c 192	13.2	66.0	31	3	US-08-976-427-11	Sequence 11, Appl
c 120	13.6	68.0	50	3	US-10-131-827-3003	Sequence 3003, Ap	c 193	13.2	66.0	31	3	US-08-976-427-14	Sequence 14, Appl
121	13.4	67.0	22	3	US-10-131-792A-3	Sequence 3, Appli	c 194	13.2	66.0	31	3	US-08-976-427-21	Sequence 21, Appl
122	13.4	67.0	34	2	US-07-743-245-2	Sequence 3, Appli	c 195	13.2	66.0	31	3	US-08-976-427-22	Sequence 22, Appl
c 123	13.4	67.0	47	3	US-09-422-978-523	Sequence 523, App	c 196	13.2	66.0	31	3	US-08-976-427-23	Sequence 23, Appl
c 124	13.4	67.0	50	3	US-10-131-827-1882	Sequence 1882, Ap	c 197	13.2	66.0	31	3	US-08-976-427-24	Sequence 24, Appl
c 125	13.2	66.0	18	2	US-08-145-704-42	Sequence 42, Appl	c 198	13.2	66.0	31	3	US-09-648-312-2	Sequence 2, Appli
c 126	13.2	66.0	18	2	US-08-145-704-43	Sequence 43, Appl	c 199	13.2	66.0	31	3	US-09-648-312-3	Sequence 3, Appli
c 127	13.2	66.0	18	2	US-08-358-556A-24	Sequence 24, Appl	c 200	13.2	66.0	31	3	US-09-648-312-4	Sequence 4, Appli
c 128	13.2	66.0	18	3	US-08-987-574-42	Sequence 42, Appl	c 201	13.2	66.0	31	3	US-09-648-312-5	Sequence 5, Appli
c 129	13.2	66.0	18	3	US-08-987-574-43	Sequence 43, Appl	c 202	13.2	66.0	31	3	US-09-648-312-6	Sequence 6, Appli
c 130	13.2	66.0	18	3	US-08-535-168-42	Sequence 42, Appl	c 203	13.2	66.0	31	3	US-09-648-312-7	Sequence 7, Appli
c 131	13.2	66.0	18	3	US-08-535-168-43	Sequence 43, Appl	c 204	13.2	66.0	31	3	US-09-648-312-8	Sequence 8, Appli
c 132	13.2	66.0	18	3	US-09-437-076-3	Sequence 3, Appli	c 205	13.2	66.0	31	3	US-09-648-312-9	Sequence 9, Appli
c 133	13.2	66.0	18	3	US-09-017-974-42	Sequence 42, Appl	c 206	13.2	66.0	31	3	US-09-648-312-10	Sequence 10, Appl
c 134	13.2	66.0	18	3	US-09-017-974-43	Sequence 43, Appl	c 207	13.2	66.0	31	3	US-09-648-312-11	Sequence 11, Appl
c 135	13.2	66.0	18	3	US-08-682-255A-42	Sequence 42, Appl	c 208	13.2	66.0	31	3	US-09-648-312-14	Sequence 14, Appl
c 136	13.2	66.0	18	3	US-08-682-255A-43	Sequence 43, Appl	c 209	13.2	66.0	31	3	US-09-648-312-21	Sequence 21, Appl
c 137	13.2	66.0	18	3	US-09-429-130-42	Sequence 42, Appl	c 210	13.2	66.0	31	3	US-09-648-312-22	Sequence 22, Appl
c 138	13.2	66.0	18	3	US-09-429-130-43	Sequence 43, Appl	c 211	13.2	66.0	31	3	US-09-648-312-23	Sequence 23, Appl
c 139	13.2	66.0	18	3	US-10-352-704-24	Sequence 24, Appl	c 212	13.2	66.0	31	3	US-09-896-650C-2	Sequence 2, Appli
140	13.2	66.0	18	3	US-09-904-744-3	Sequence 3, Appli	c 213	13.2	66.0	31	3	US-09-896-650C-3	Sequence 3, Appli
c 141	13.2	66.0	18	3	US-09-097-791D-4	Sequence 4, Appli	c 214	13.2	66.0	31	3	US-09-896-650C-4	Sequence 4, Appli
c 142	13.2	66.0	18	6	PCT-US96-11786-42	Sequence 42, Appl	c 215	13.2	66.0	31	3	US-09-896-650C-5	Sequence 5, Appli
c 143	13.2	66.0	18	6	PCT-US96-11786-43	Sequence 43, Appl	c 216	13.2	66.0	31	3	US-09-896-650C-6	Sequence 6, Appli
c 144	13.2	66.0	19	3	US-09-109-663-31	Sequence 31, Appl	c 217	13.2	66.0	31	3	US-09-896-650C-7	Sequence 7, Appli
c 145	13.2	66.0	19	3	US-09-230-652-117	Sequence 117, App	c 218	13.2	66.0	31	3	US-09-896-650C-8	Sequence 8, Appli
146	13.2	66.0	21	2	US-08-424-663-3	Sequence 3, Appli	c 219	13.2	66.0	31	3	US-09-896-650C-9	Sequence 9, Appli
147	13.2	66.0	21	2	US-08-424-663-4	Sequence 4, Appli	c 220	13.2	66.0	31	3	US-09-896-650C-10	Sequence 10, Appl
148	13.2	66.0	21	2	US-08-424-663-5	Sequence 5, Appli	c 221	13.2	66.0	31	3	US-09-896-650C-11	Sequence 11, Appl
149	13.2	66.0	21	2	US-08-872-446-3	Sequence 3, Appli	c 222	13.2	66.0	31	3	US-09-896-650C-14	Sequence 14, Appl
150	13.2	66.0	21	2	US-08-872-446-4	Sequence 4, Appli	c 223	13.2	66.0	31	3	US-09-896-650C-21	Sequence 21, Appl
151	13.2	66.0	21	2	US-08-872-446-5	Sequence 5, Appli	c 224	13.2	66.0	31	3	US-09-896-650C-22	Sequence 22, Appl
c 152	13.2	66.0	21	3	US-09-109-663-23	Sequence 23, Appl	c 225	13.2	66.0	31	3	US-09-896-650C-23	Sequence 23, Appl
c 153	13.2	66.0	21	3	US-09-280-270A-3	Sequence 3, Appli	c 226	13.2	66.0	31	3	US-09-896-650C-24	Sequence 24, Appl
154	13.2	66.0	21	3	US-09-280-270A-4	Sequence 4, Appli	c 227	13.2	66.0	31	3	US-09-896-650C-24	Sequence 24, Appl
c 155	13.2	66.0	21	3	US-09-280-270A-5	Sequence 5, Appli	c 228	13.2	66.0	32	3	US-08-976-427-18	Sequence 18, Appl
c 156	13.2	66.0	24	3	US-09-894-799-22	Sequence 22, Appl	c 229	13.2	66.0	32	3	US-08-976-427-20	Sequence 20, Appl
157	13.2	66.0	24	9	5245022-8	Patent No. 5245022	c 230	13.2	66.0	32	3	US-09-648-312-18	Sequence 18, Appl
c 158	13.2	66.0	25	2	US-08-068-945A-48	Sequence 48, Appl	c 231	13.2	66.0	32	3	US-09-648-312-20	Sequence 20, Appl
c 159	13.2	66.0	25	2	US-08-442-806-48	Sequence 48, Appl	c 232	13.2	66.0	32	3	US-09-896-650C-18	Sequence 18, Appl
160	13.2	66.0	25	3	US-09-097-791D-3	Sequence 3, Appli	c 233	13.2	66.0	32	3	US-09-896-650C-20	Sequence 20, Appl
161	13.2	66.0	26	2	US-08-145-704-18	Sequence 18, Appl	c 234	13.2	66.0	33	2	US-08-238-163-11	Sequence 11, Appl
162	13.2	66.0	26	3	US-08-987-574-18	Sequence 18, Appl	c 235	13.2	66.0	33	3	US-08-976-427-31	Sequence 31, Appl
163	13.2	66.0	26	3	US-08-535-168-18	Sequence 18, Appl	c 236	13.2	66.0	33	3	US-09-648-312-31	Sequence 31, Appl
164	13.2	66.0	26	3	US-09-017-974-18	Sequence 18, Appl	c 237	13.2	66.0	33	3	US-09-896-650C-31	Sequence 31, Appl
165	13.2	66.0	26	3	US-08-682-255A-18	Sequence 18, Appl	c 238	13.2	66.0	38	2	US-08-145-704-1	Sequence 1, Appli
166	13.2	66.0	26	3	US-09-429-130-18	Sequence 18, Appl	c 239	13.2	66.0	38	2	US-08-987-574-1	Sequence 1, Appli
c 167	13.2	66.0	26	6	PCT-US96-11786-18	Sequence 18, Appl	240	13.2	66.0	38	3	US-08-987-574-2	Sequence 2, Appli
c 168	13.2	66.0	30	3	US-08-976-427-12	Sequence 12, Appl	241	13.2	66.0	38	3	US-08-987-574-2	Sequence 2, Appli
c 169	13.2	66.0	30	3	US-08-976-427-13	Sequence 13, Appl	242	13.2	66.0	38	3	US-08-535-168-1	Sequence 1, Appli
c 170	13.2	66.0	30	3	US-08-976-427-15	Sequence 15, Appl	243	13.2	66.0	38	3	US-08-535-168-2	Sequence 2, Appli



244	13.2	66.0	38	3	US-09-017-974-1	Sequence 1, Appli
245	13.2	66.0	38	3	US-09-017-974-2	Sequence 2, Appli
246	13.2	66.0	38	3	US-08-682-255A-1	Sequence 1, Appli
247	13.2	66.0	38	3	US-08-682-255A-2	Sequence 2, Appli
248	13.2	66.0	38	3	US-09-429-130-1	Sequence 1, Appli
249	13.2	66.0	38	3	US-09-429-130-2	Sequence 2, Appli
250	13.2	66.0	38	6	PCT-US92-09202-10	Sequence 10, Appli
251	13.2	66.0	38	6	PCT-US93-07743-1	Sequence 1, Appli
252	13.2	66.0	38	6	PCT-US93-07743-6	Sequence 6, Appli
253	13.2	66.0	38	6	PCT-US93-07743-15	Sequence 15, Appli
254	13.2	66.0	38	6	PCT-US93-08329-11	Sequence 11, Appli
255	13.2	66.0	38	6	PCT-US96-11786-1	Sequence 1, Appli
256	13.2	66.0	38	6	PCT-US96-11786-2	Sequence 2, Appli
257	13.2	66.0	39	3	US-09-052-995-7	Sequence 7, Appli
258	13.2	66.0	40	2	US-08-199-507B-48	Sequence 48, Appli
259	13.2	66.0	40	2	US-08-441-828-48	Sequence 48, Appli
260	13.2	66.0	44	2	US-07-931-473B-44	Sequence 44, Appli
261	13.2	66.0	44	2	US-07-714-131C-44	Sequence 44, Appli
262	13.2	66.0	44	2	US-08-412-110-44	Sequence 44, Appli
263	13.2	66.0	44	2	US-08-409-442A-44	Sequence 44, Appli
264	13.2	66.0	44	2	US-08-469-609A-44	Sequence 44, Appli
265	13.2	66.0	44	3	US-09-143-190-44	Sequence 44, Appli
266	13.2	66.0	44	3	US-09-502-344-44	Sequence 44, Appli
267	13.2	66.0	44	3	US-10-037-986-44	Sequence 44, Appli
c 268	13.2	66.0	47	2	US-08-171-389-59	Sequence 59, Appli
c 269	13.2	66.0	47	2	US-08-123-936-59	Sequence 59, Appli
c 270	13.2	66.0	47	2	US-08-475-228A-59	Sequence 59, Appli
c 271	13.2	66.0	47	3	US-08-482-080A-59	Sequence 59, Appli
c 272	13.2	66.0	47	3	US-09-354-947-59	Sequence 59, Appli
c 273	13.2	66.0	47	3	US-09-423-978-2397	Sequence 2397, Ap
c 274	13.2	66.0	47	3	US-09-993-346-59	Sequence 59, Appli
c 275	13.2	66.0	47	6	PCT-US93-12388-59	Sequence 59, Appli
c 276	13.2	66.0	48	3	US-09-896-650C-32	Sequence 32, Appli
c 277	13.2	66.0	50	3	US-10-131-827-5223	Sequence 5223, Ap
c 278	13.2	66.0	50	3	US-10-131-827-5224	Sequence 5224, Ap
c 279	13.2	66.0	50	3	US-10-131-827-7271	Sequence 7271, Ap
c 280	12.8	64.0	17	2	US-08-173-489C-95	Sequence 95, Appli
c 281	12.8	64.0	17	2	US-08-173-489C-96	Sequence 96, Appli
c 282	12.8	64.0	17	3	US-09-495-140-26	Sequence 26, Appli
c 283	12.8	64.0	17	3	US-10-058-877-26	Sequence 26, Appli
c 284	12.8	64.0	18	2	US-08-758-308-1351	Sequence 1351, Ap
c 285	12.8	64.0	20	3	US-09-400-046-10	Sequence 10, Appli
c 286	12.8	64.0	20	3	US-09-509-595B-25	Sequence 25, Appli
c 287	12.8	64.0	21	2	US-08-424-663-8	Sequence 8, Appli
c 288	12.8	64.0	21	2	US-08-872-446-8	Sequence 8, Appli
c 289	12.8	64.0	21	3	US-09-109-663-22	Sequence 22, Appli
c 290	12.8	64.0	21	3	US-09-280-270A-8	Sequence 8, Appli
c 291	12.8	64.0	22	3	US-09-425-804-27	Sequence 27, Appli
c 292	12.8	64.0	23	3	US-09-400-046-9	Sequence 9, Appli
c 293	12.8	64.0	28	3	US-09-400-046-8	Sequence 8, Appli
c 294	12.8	64.0	29	3	US-09-400-046-3	Sequence 3, Appli
c 295	12.8	64.0	29	3	US-09-400-046-4	Sequence 4, Appli
c 296	12.8	64.0	29	3	US-09-400-046-5	Sequence 5, Appli
c 297	12.8	64.0	30	3	US-09-342-681C-41	Sequence 41, Appli
c 298	12.8	64.0	30			

## ALIGNMENTS

RESULT 1  
 US-08-460-890A-14/c  
 ; Sequence 14, Application US/08450890A  
 ; Patent No. 5994109  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Woo, Savio L.C.  
 ; APPLICANT: Smith, Louis C.  
 ; APPLICANT: Cristiano, Richard J.  
 ; APPLICANT: Gottchalk, Stephen  
 ; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
 ; TITLE OF INVENTION: METHODS OF USE  
 ; APPLICANT: Gottchalk, Stephen  
 ; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
 ; TITLE OF INVENTION: METHODS OF USE  
 ; NUMBER OF SEQUENCES: 65  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.

```
;
;
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,890A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167,641
; FILING DATE: December 14, 1993
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-460-890A-15

Query Match 87.0%; Score 17.4; DB 2; Length 27;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19
Db 4 AAGGGAGGGAGGGAGGG 22

RESULT 3
US-08-167-641C-14/c
; Sequence 14, Application US/08167641C
; Patent No. 6033884
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,641C
; FILING DATE: December 14, 1993
```

```
;
;
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992/02725
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; FEATURE:
; OTHER INFORMATION: "C" stands for 5-methylcytosine
; US-08-167-641C-14

Query Match 87.0%; Score 17.4; DB 3; Length 27;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19
Db 24 AAGGGAGGGAGGGAGGG 6

RESULT 4
US-08-167-641C-15
; Sequence 15, Application US/08167641C
; Patent No. 6033884
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,641C
; FILING DATE: December 14, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/012
```

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-167-641C-15

Query Match 87.0%; Score 17.4; DB 3; Length 27;  
Best Local Similarity 94.7%; Pred. No. 4.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGGAGGGAGGG 19  
DB 4 AAGGGAGGGGAGGGAGGG 22

## RESULT 5

US-08-460-971A-14/c  
; Sequence 14, Application US/08460971A  
; Patent No. 6150168

; GENERAL INFORMATION:  
; APPLICANT: Woo, Savio L.C.  
; APPLICANT: Smith, Louis C.  
; APPLICANT: Cristiano, Richard J.  
; APPLICANT: Gottchalk, Stephen  
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
; TITLE OF INVENTION: METHODS OF USE  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,971A  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167,641  
; FILING DATE: December 14, 1993  
; APPLICATION NUMBER: 07/855,389  
; FILING DATE: March 20, 1992  
; APPLICATION NUMBER: PCT/US93/02725  
; FILING DATE: March 19, 1993

; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 212/063  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: Other nucleic acid  
; FEATURE:  
; OTHER INFORMATION: "C" stands for 5-methylcytosine  
US-08-460-971A-14

Query Match 87.0%; Score 17.4; DB 3; Length 27;  
Best Local Similarity 94.7%; Pred. No. 4.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGGAGGGAGGG 19  
DB 24 AAGGGAGGGGAGGGAGGG 6

## RESULT 6

US-08-460-971A-15  
; Sequence 15, Application US/08460971A  
; Patent No. 6150168

; GENERAL INFORMATION:  
; APPLICANT: Woo, Savio L.C.  
; APPLICANT: Smith, Louis C.  
; APPLICANT: Cristiano, Richard J.  
; APPLICANT: Gottchalk, Stephen  
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
; TITLE OF INVENTION: METHODS OF USE  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,971A  
; FILING DATE: June 5, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/167,641  
; FILING DATE: December 14, 1993  
; APPLICATION NUMBER: 07/855,389  
; FILING DATE: March 20, 1992  
; APPLICATION NUMBER: PCT/US93/02725  
; FILING DATE: March 19, 1993

; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 212/063  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 27 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
US-08-460-971A-15

Query Match 87.0%; Score 17.4; DB 3; Length 27;  
Best Local Similarity 94.7%; Pred. No. 4.3e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGGAGGGAGGG 19



```

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-460-890A-13

Query Match 87.0%; Score 17.4
Best Local Similarity 94.7%; Pred. No.
Matches 18; Conservative 0; Mismatch

QY 1 AGGGAGGGAGGGAGGGAGGG 19
    |||||
DB 10 AAGGAGGGAGGGAGGGAGGG 28

RESULT 10
US-08-167-641C-13
Sequence 13, Application US/08167641C
Patent No. 6033884
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANS-
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible

```

```

/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq For Windows 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/167,641C
/ FILING DATE: December 14, 1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/855,389
/ FILING DATE: March 20, 1992
/ APPLICATION NUMBER: PCT/US93/02725
/ FILING DATE: March 19, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 205/012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 39 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-167-641C-13

Query Match 87.0% Score 17.4; DB 3; Length 39;
Best Local Similarity 94.7%; Pred.No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels

QY 1 AGGGGAGGGGAGGGGAGGG 19
   | | | | | | | | | |
Db 10 AAGGGAGGGGAGGGGAGGG 28

RESULT 11
US-08-460-971A-13
/ Sequence 13, Application US/08460971A
/ Patent No. 6150168
/ GENERAL INFORMATION:
/ APPLICANT: Woo, Savio L.C.
/ APPLICANT: Smith, Louis C.
/ APPLICANT: Cristiano, Richard J.
/ APPLICANT: Gottchalk, Stephen
/ TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
/ METHOD OF INVENTION: METHODS OF USE
/ NUMBER OF SEQUENCES: 65
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq for Windows 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/460,971A
/ FILING DATE: June 5, 1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/167,641
/ FILING DATE: December 14, 1993
/ APPLICATION NUMBER: 07/855,389
/ FILING DATE: March 20, 1992
/ APPLICATION NUMBER: PCT/US93/02725

```

```

; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-460-971A-13

Query Match      87.0%; Score 17.4; DB 3; Length 39;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19
   | ||||| ||||| |||||
Db 10 AAGGGAGGGAGGGAGGG 28

RESULT 12
US-08-462-040-13
; Sequence 13, Application US/08462040
; Patent No. 6177554
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462.040
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167,641
; FILING DATE: December 14, 1993
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 13:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-462-040-13

Query Match      87.0%; Score 17.4; DB 3; Length 39;
Best Local Similarity 94.7%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19
   | ||||| ||||| |||||
Db 10 AAGGGAGGGAGGGAGGG 28

RESULT 13
PCT-US93-02352-2
; Sequence 2, Application PC/TUS9302352
; GENERAL INFORMATION:
; APPLICANT: California Institute of Technology,
; APPLICANT: Pasadena, California 91125, U.S.A.
; TITLE OF INVENTION: Triple helix recognition of DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02352
; FILING DATE: 19930311
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/850,503
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: FP-56557/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 5..43
; OTHER INFORMATION: /note= "Sticky single-stranded end
; OTHER INFORMATION: from base 1 to 4. Double stranded from base 5 to
; OTHER INFORMATION: 43 to complementary strand, SEQ ID NO:3."
; PCT-US93-02352-2

Query Match      82.0%; Score 16.4; DB 6; Length 43;
Best Local Similarity 89.5%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGG 19
   | ||||| ||||| |||||
Db 14 AAGGGAGGGAGGGAGGG 32

```

```
RESULT 14
PCT-US93-02352-3/c
; Sequence 3, Application PC/TUS9302352
; GENERAL INFORMATION:
; APPLICANT: California Institute of Technology,
; APPLICANT: Pasadena, California 91125, U.S.A.
; TITLE OF INVENTION: Triple helix recognition of DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02352
; FILING DATE: 19930311
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 07/850,503
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: FP-56557/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: 5..43
; OTHER INFORMATION: /note= "sticky single-stranded end
; OTHER INFORMATION: from base 1 to 4. Double-stranded from base 5 to
; OTHER INFORMATION: 37 to complementary strand, SEQ ID NO:2."
PCT-US93-02352-3

Query Match 82.0%; Score 16.4; DB 6; Length 43;
Best Local Similarity 89.5%; Fred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

PCT-US93-02352-3
QY 1 AGGGGAGGGGAGGGAGGG 19
Db 34 AAGGGGAGGGGAGGGAGGG 16

RESULT 15
US-08-956-171E-2153/c
; Sequence 2153, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2153:
US-08-956-171E-2153

Query Match 82.0%; Score 16.4; DB 3; Length 50;
Best Local Similarity 89.5%; Fred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20
Db 28 GGGGGGGGGGGAGGGGG 10

RESULT 16
US-08-781-986A-2153/c
; Sequence 2153, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-2153

Query Match      82.0%; Score 16.4; DB 3; Length 50;
Best Local Similarity 89.5%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  28 GGGGGGGGGGGGGGGGG 10

RESULT 17
US-09-622-745B-20/c
; Sequence 20, Application US/09622745B
; Patent No. 6933124
; GENERAL INFORMATION:
; APPLICANT: AstraZeneca AB
; APPLICANT: Edlund, Anders
; APPLICANT: Ekstrand, Jonas
; APPLICANT: Johansson, Thore
; APPLICANT: Leonardsson, Goran
; TITLE OF INVENTION: HUMAN GABA B RECEPTOR 1 PROMOTERS
; FILE REFERENCE: 1103326-0633
; CURRENT APPLICATION NUMBER: US/09/622,745B
; CURRENT FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/SE00/00878
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: P R 1b GCVI Fwd
US-09-622-745B-20

Query Match      79.0%; Score 15.8; DB 3; Length 27;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 AGGGAGGGGAGGGAGGGG 19
    ||| ||||| ||||| |||||
Db  19 AGGTTAGGGAGGGAGGGG 1

RESULT 18
US-09-622-745B-21
; Sequence 21, Application US/09622745B
; Patent No. 6933124
; GENERAL INFORMATION:
; APPLICANT: AstraZeneca AB
; APPLICANT: Edlund, Anders
; APPLICANT: Ekstrand, Jonas
; APPLICANT: Johansson, Thore
; APPLICANT: Leonardsson, Goran
; TITLE OF INVENTION: HUMAN GABA B RECEPTOR 1 PROMOTERS
; FILE REFERENCE: 1103326-0633
; CURRENT APPLICATION NUMBER: US/09/622,745B
; CURRENT FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: PCT/SE00/00878
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: P R 1b GCVI Rev
US-09-622-745B-21

Query Match      79.0%; Score 15.8; DB 3; Length 27;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 AGGGAGGGGAGGGAGGGG 19
    ||| ||||| ||||| |||||
Db  9 AGGTTAGGGAGGGAGGGG 27

RESULT 19
5182196-21
; Patent No. 5182196
; APPLICANT: ALLET, BERNARD; KAWASHIMA, ERIC H.
; TITLE OF INVENTION: EXPRESSION SYSTEMS FOR OVERPRODUCTION OF
; DESIRED PROTEINS
; NUMBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,281
; FILING DATE: 27-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 53,398
; FILING DATE: 18-MAY-1987
; APPLICATION NUMBER: 785,847
; FILING DATE: 09-OCT-1985
; SEQ ID NO:21
; LENGTH: 42
5182196-21

Query Match      79.0%; Score 15.8; DB 9; Length 42;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  17 GGGGGGGGGGGGGGGGG 35

RESULT 20
US-09-118-752-2
; Sequence 2, Application US/09118752
; Patent No. 6114154
; GENERAL INFORMATION:
; APPLICANT: Li, Huiwu
; TITLE OF INVENTION: Direct Construction and Isolation Full Length Target
; FILE REFERENCE: 12660-0100
; CURRENT APPLICATION NUMBER: US/09/118,752
; CURRENT FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 37
; TYPE: DNA
; ORGANISM: murine
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: primer_bind
; LOCATION: (1)...(22)
US-09-118-752-2
```



```

; APPLICANT: KONO, TOSHIAKI
; TITLE OF INVENTION: ENZYME ENDOGLUCANASE AND CELLULOSE PREPARATIONS
; TITLE OF INVENTION: CONTAINING THE SAME
; FILE REFERENCE: 99-0055*/LC(WMC)/144
; CURRENT APPLICATION NUMBER: US/09/230,222A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PRIMER
US-09-230-222-18

Query Match          74.0%; Score 14.8; DB 3; Length 30;
Best Local Similarity 88.9%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCGGAGGGAGGGAGG 18
    ||||| |||||
Db 25 AGCGGAGGAGGGAGG 8

RESULT 23
US-09-230-225B-25/c
; Sequence 25, Application US/09230225B
; Patent No. 6403362
; GENERAL INFORMATION:
; APPLICANT: Meiiji Seika Kaisha, Ltd.
; APPLICANT: Moriya, Tatsuki
; TITLE OF INVENTION: Systems for the Mass Production of Proteins or Peptides
; TITLE OF INVENTION: of the Genus Humicola
; FILE REFERENCE: VX990054
; CURRENT APPLICATION NUMBER: US/09/230,225B
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Humicola insolens
US-09-230-225B-25

Query Match          74.0%; Score 14.8; DB 3; Length 30;
Best Local Similarity 88.9%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGCGGAGGGAGGGAGG 18
    ||||| |||||
Db 25 AGCGGAGGAGGGAGG 8

RESULT 24
US-09-254-352B-31
; Sequence 31, Application US/09254352B
; Patent No. 6365350
; GENERAL INFORMATION:
; APPLICANT: HAYASHIZAKI, Yoshihide
; TITLE OF INVENTION: METHOD OF DNA SEQUENCING
; FILE REFERENCE: 024705-080
; CURRENT APPLICATION NUMBER: US/09/254,352B
; CURRENT FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/JP98/03039
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: JP 10-155847
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: JP 9-196478
; PRIOR FILING DATE: 1997-07-07
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31

```

```
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T7 RNA polymerase (WT)
; NAME/KEY: misc feature
; LOCATION: (25)
; OTHER INFORMATION: Nucleotide 25 is n wherein n = any nucleotide.
US-09-254-352B-31

Query Match          74.0%; Score 14.8; DB 3; Length 31;
Best Local Similarity 88.9%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  3 GGGAGGGGGGGGGGGG 20
Db  1 GGGAGGGGGGGGGGGG 18

RESULT 25
US-09-254-344-17
; Sequence 17, Application US/09254344
; Patent No. 6867027
; GENERAL INFORMATION:
; APPLICANT: HAYASHIZAKI, Yoshihide
; APPLICANT: WATAHIKI, Masanori
; TITLE OF INVENTION: RNA Polymerase
; FILE REFERENCE: 024705-077
; CURRENT APPLICATION NUMBER: US/09/254,344
; CURRENT FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/JP98/03037
; PRIOR FILING DATE: 1998-07-06
; PRIOR APPLICATION NUMBER: JP 9/180883
; PRIOR FILING DATE: 1997-07-07
; PRIOR APPLICATION NUMBER: JP 10/155759
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Bacteriophage T7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(31)
; OTHER INFORMATION: Mutant T7 RNA polymerase wild type.
; NAME/KEY: misc feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: Nucleotide 25 is "n" wherein "n" = any nucleotide.
US-09-254-344-17

Query Match          74.0%; Score 14.8; DB 3; Length 31;
Best Local Similarity 88.9%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  3 GGGAGGGGGGGGGGGG 20
Db  1 GGGAGGGGGGGGGGGG 18

RESULT 26
US-08-777-708C-16/c
; Sequence 16, Application US/08777708C
; Patent No. 6159334
; GENERAL INFORMATION:
; APPLICANT: Pescovitz, Ora H.
; TITLE OF INVENTION: USE OF GHRH-RP TO STIMULATE STEM CELL FACTOR PRODUCTION
; FILE REFERENCE: 7037-175/1U-62
; CURRENT APPLICATION NUMBER: US/08/777,708C
; CURRENT FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: US 60/008,933
; PRIOR FILING DATE: 1995-12-20
; NUMBER OF SEQ ID NOS: 23
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-08-777-708C-16

Query Match          72.0%; Score 14.4; DB 3; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5 GAGGGGAGGGGAGGGG 20
Db  20 GAGGGGAGGTGAGGGG 5

RESULT 27
US-09-875-453B-66
; Sequence 66, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453B-66

Query Match          72.0%; Score 14.4; DB 3; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGGAG 17
Db  1 GGTGAGGGGAGGGGAG 16

RESULT 28
US-09-197-951-2/c
; Sequence 2, Application US/09197951
; Patent No. 6197554
; GENERAL INFORMATION:
; APPLICANT: LIN, SHI-LUNG
; APPLICANT: CHUNG, CHENG-MING
; APPLICANT: YING, SHAO-YAO
; TITLE OF INVENTION: Method for Generating Full-Length cDNA
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David & Raymond Patent Firm
; STREET: 108 N. Ynez Ave., Suite 128
; CITY: Monterey Park
; STATE: CA
; COUNTRY: USA
```

ZIP: 91754  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/197,951  
FILING DATE: 20-NO. 6197554-1998  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Chan, Raymond Y.C.  
REGISTRATION NUMBER: 37,484  
REFERENCE/DOCKET NUMBER: USP8462A-SL(3)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 571-9812  
TELEFAX: (626) 571-9813  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic"  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-197-951-2

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 20 GGGGGGGGGGGGGGGGGG 20

## RESULT 29

US-09-082-649B-55/c  
Sequence 55, Application US/09082649B  
Patent No. 6339068  
GENERAL INFORMATION:  
APPLICANT: Davis, Heather L.  
APPLICANT: Krieg, Arthur M.  
APPLICANT: Schorr, Joachim  
APPLICANT: Wu, Tong  
TITLE OF INVENTION: Vectors and Methods for Immunization or  
FILE REFERENCE: C1039/7009  
CURRENT APPLICATION NUMBER: US/09/082,649B  
CURRENT FILING DATE: 1998-05-20  
PRIOR APPLICATION NUMBER: US 60/047,233  
PRIOR FILING DATE: 1997-05-20  
PRIOR APPLICATION NUMBER: US 60/047,209  
PRIOR FILING DATE: 1997-05-20  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 55  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic oligonucleotide  
US-09-082-649B-55

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||

Db 20 GGGGGGGGGGGGGGGGGG 20

## RESULT 30

US-09-965-101-55/c  
Sequence 55, Application US/09965101  
Patent No. 6821957  
GENERAL INFORMATION:  
APPLICANT: Davis, Heather L.  
APPLICANT: Krieg, Arthur M.  
APPLICANT: Schorr, Joachim  
APPLICANT: Wu, Tong  
TITLE OF INVENTION: Vectors and Methods for Immunization or  
FILE REFERENCE: C1039/7057 (HCL/MAT)  
CURRENT APPLICATION NUMBER: US/09/965,101  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 09/082,649  
PRIOR FILING DATE: 1998-05-20  
PRIOR APPLICATION NUMBER: US 60/047,233  
PRIOR FILING DATE: 1997-05-20  
PRIOR APPLICATION NUMBER: US 60/047,209  
PRIOR FILING DATE: 1997-05-20  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 55  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic oligonucleotide  
US-09-965-101-55

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 20 GGGGGGGGGGGGGGGGGG 20

## RESULT 31

US-09-672-126B-134  
Sequence 134, Application US/09672126B  
Patent No. 6949520  
GENERAL INFORMATION:  
APPLICANT: Hartmann, Gunther L.  
APPLICANT: Bratzler, Robert L.  
APPLICANT: Krieg, Arthur  
TITLE OF INVENTION: Methods Related to Immunostimulatory  
FILE REFERENCE: C1039/7044  
CURRENT APPLICATION NUMBER: US/09/672,126B  
CURRENT FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: 60/156,147  
PRIOR FILING DATE: 1999-09-29  
NUMBER OF SEQ ID NOS: 169  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 134  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-672-126B-134

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||



REFERENCE/DOCKET NUMBER: ISIS-1229  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-403-888A-42

Query Match 71.0%; Score 14.2; DB 2; Length 21;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
Db 1 GGGGCGGGCGGGCGGGG 19

## RESULT 35

US-08-863-639A-11/C  
Sequence 11, Application US/08863639A  
Patent No. 5981185  
GENERAL INFORMATION:  
APPLICANT: Matson, Robert S.  
APPLICANT: Coassin, Peter J.  
APPLICANT: Rampal, Jang B.  
APPLICANT: Caskey, C. T.  
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, 9th Floor  
CITY: Pasadena  
STATE: CA  
COUNTRY: USA  
ZIP: 91101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Corel WordPerfect 8 version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/863,639A  
FILING DATE: May 28, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph E. Mueth  
REGISTRATION NUMBER: 20,532  
REFERENCE/DOCKET NUMBER: 11859-1  
TELEPHONE: (626) 796-4000  
TELEFAX: (626) 795-6321  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-08-863-639A-11

Query Match 71.0%; Score 14.2; DB 2; Length 21;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
Db 21 GGGGGGGGGGGGGGGGGG 3

RESULT 36  
US-08-863-639A-12  
Sequence 12, Application US/08863639A  
Patent No. 5981185  
GENERAL INFORMATION:  
APPLICANT: Matson, Robert S.  
APPLICANT: Coassin, Peter J.  
APPLICANT: Rampal, Jang B.  
APPLICANT: Caskey, C. T.  
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, 9th Floor  
CITY: Pasadena  
STATE: CA  
COUNTRY: USA  
ZIP: 91101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Corel WordPerfect 8 version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/863,639A  
FILING DATE: May 28, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph E. Mueth  
REGISTRATION NUMBER: 20,532  
REFERENCE/DOCKET NUMBER: 11859-1  
TELEPHONE: (626) 796-4000  
TELEFAX: (626) 795-6321  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
US-08-863-639A-12

Query Match 71.0%; Score 14.2; DB 2; Length 21;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
Db 1 GGGGGGGGGGGGGGGGGG 19

## RESULT 17

US-09-696-791-4484/C  
Sequence 4484, Application US/09696791  
Patent No. 6770633  
GENERAL INFORMATION:  
APPLICANT: Robbins, Joan M.  
APPLICANT: Tritz, Richard  
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE  
DISEASES  
FILE REFERENCE: 480124.407  
CURRENT APPLICATION NUMBER: US/09/696,791  
CURRENT FILING DATE: 2000-10-25  
NUMBER OF SEQ ID NOS: 4523  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4484  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
OTHER INFORMATION: PDGF A ribozyme recognition site  
US-09-696-791-4484

Query Match 71.0%; Score 14.2; DB 3; Length 21;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
Db 19 GGGGTGGGACGGAAGGG 1

RESULT 38  
US-07-808-452-15  
Sequence 15, Application US/07808452  
Patent No. 6063612  
GENERAL INFORMATION:  
APPLICANT: Jayasena, Suredha D.  
APPLICANT: Johnston, Brian H.  
TITLE OF INVENTION: Antiviral Reagents Based on  
RNA-Binding Proteins  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/808,452  
FILING DATE: 19911213  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 8255-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: SINGLE STRAND OLIGONUCLEOTIDE,  
INDIVIDUAL ISOLATE: 12/C-1  
US-07-808-452-15

Query Match 71.0%; Score 14.2; DB 3; Length 23;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
Db 5 GGAGAGGGGAGAGGGGGG 23

RESULT 39  
PCT-US92-10770-15  
Sequence 15, Application PC/TUS9210770  
GENERAL INFORMATION:  
APPLICANT: Jayasena, Suredha D.  
APPLICANT: Johnston, Brian H.  
TITLE OF INVENTION: Antiviral Reagents Based on  
RNA-Binding Proteins

NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SRI International  
STREET: 333 Ravenswood Avenue  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10770  
FILING DATE: 19921211  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/808,452  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: P-2962  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 859-4550  
TELEFAX: (415) 859-3880  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: SINGLE STRAND OLIGONUCLEOTIDE,  
INDIVIDUAL ISOLATE: 12/C-1  
PCT-US92-10770-15

Query Match 71.0%; Score 14.2; DB 6; Length 23;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGAGGGG 20  
Db 5 GGAGAGGGGAGAGGGGGG 23

RESULT 40  
PCT-US92-10792-13  
Sequence 13, Application PC/TUS9210792  
GENERAL INFORMATION:  
APPLICANT: Jayasena, Suredha D.  
APPLICANT: Johnston, Brian H.  
TITLE OF INVENTION: Triple Helix Formation at  
PunPun - (PunPun) - (PunPun) Tracts  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SRI International  
STREET: 333 Ravenswood Avenue  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10792  
FILING DATE: 19921211

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/826,934
; FILING DATE: 21-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,452
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: P-3141
; TELEPHONE: (415) 859-4550
; TELEFAX: (415) 859-3880
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: FIGURE 10, C-1
; PCT-US92-10792-13

Query Match 71.0%; Score 14.2; DB 6; Length 23;
Best Local Similarity 84.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGAGGGGGAGGGGGGGG 20
DB 5 GGAGAGGGGAGAGGGGGG 23

RESULT 41
US-08-014-943A-7
; Sequence 7, Application US/08014943A
; Patent No. 5545551
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: Cloning And Expression Of Pur Protein
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,943A
; FILING DATE: 02-FEB-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-014-943A-7

Query Match 71.0%; Score 14.2; DB 2; Length 24;
Best Local Similarity 84.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGAGGGGGAGGGGGGGG 20
DB 1 GGGGGGGGGGGGGGGGGG 19

RESULT 42
US-08-486-421-49
; Sequence 49, Application US/08486421
; Patent No. 5672479
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,421
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-486-421-49

Query Match 71.0%; Score 14.2; DB 2; Length 24;
Best Local Similarity 84.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGAGGGGGAGGGGGGGG 20
DB 1 GGGGGGGGGGGGGGGGGG 19

RESULT 43
US-08-470-911-49
; Sequence 49, Application US/08470911
; Patent No. 5756684
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.

```

```
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,911
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-470-911-49

Query Match 71.0%; Score 14.2; DB 2; Length 24;
Best Local Similarity 84.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20
    |||||
Db 1 GGGGGGGGGGGGGGGGG 19

RESULT 44
US-08-486-809-49
; Sequence 49, Application US/08486809
; Patent No. 5869622
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,809
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-486-809-49

Query Match 71.0%; Score 14.2; DB 2; Length 24;
Best Local Similarity 84.2%; Pred. No. 6.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20
    |||||
Db 1 GGGGGGGGGGGGGGGGG 19

RESULT 45
US-08-960-190A-31
; Sequence 31, Application US/08960190A
; Patent No. 6232445
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Acevedo, Jorge
; APPLICANT: Burkhardt, Martin
; APPLICANT: Jiao, Jin-an
; APPLICANT: Wong, Hing C.
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: usa
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,190A
; FILING DATE: 29-OCT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 48002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-960-190A-31
```



Query Match 71.0%; Score 14.2; DB 3; Length 24;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 3 GGGGGGGGGGGGGGGGG 21

RESULT 46  
US-08-976-427-26/c  
; Sequence 26, Application US/08976427A  
; Patent No. 6322968  
; GENERAL INFORMATION:  
; APPLICANT: Head, Steven R.  
; APPLICANT: Geolet, Philip  
; APPLICANT: Karn, Jonathan  
; APPLICANT: Boyce-Jacino, Michael  
; TITLE OF INVENTION: De No. 6322968 or "Universal" Sequencing Array  
; FILE REFERENCE: 04990.0049  
; CURRENT APPLICATION NUMBER: US/08/976,427A  
; CURRENT FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 26  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic primer  
US-08-976-427-26

Query Match 71.0%; Score 14.2; DB 3; Length 25;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 25 GGGGGGGGGGGGGGGGG 7

RESULT 47  
US-09-648-312-26/c  
; Sequence 26, Application US/09648312  
; Patent No. 6337188  
; GENERAL INFORMATION:  
; APPLICANT: Head, Steven R.  
; APPLICANT: Geolet, Philip  
; APPLICANT: Karn, Jonathan  
; APPLICANT: Boyce-Jacino, Michael  
; TITLE OF INVENTION: De No. 6337188 or "Universal" Sequencing Array  
; FILE REFERENCE: 04990.0049  
; CURRENT APPLICATION NUMBER: US/09/648,312  
; CURRENT FILING DATE: 2000-08-25  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 26  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic primer  
US-09-648-312-26

Query Match 71.0%; Score 14.2; DB 3; Length 25;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 25 GGGGGGGGGGGGGGGGG 7

RESULT 48  
US-09-896-650C-26/c  
; Sequence 26, Application US/09896650C  
; Patent No. 6946249  
; GENERAL INFORMATION:  
; APPLICANT: Head, Steven R.  
; APPLICANT: Geolet, Philip  
; APPLICANT: Karn, Jonathan  
; APPLICANT: Boyce-Jacino, Michael  
; TITLE OF INVENTION: De No. 6946249 or Universal Sequencing Array  
; FILE REFERENCE: 13019-2  
; CURRENT APPLICATION NUMBER: US/09/896,650C  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: 08/976,427  
; PRIOR FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Primer  
US-09-896-650C-26

Query Match 71.0%; Score 14.2; DB 3; Length 25;  
Best Local Similarity 84.2%; Pred. No. 6.1e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 25 GGGGGGGGGGGGGGGGG 7

RESULT 49  
US-08-208-486-80/c  
; Sequence 80, Application US/08208486  
; Patent No. 5389531  
; GENERAL INFORMATION:  
; APPLICANT: Ito, Junetsu  
; APPLICANT: Yoo, Seung-Ku  
; TITLE OF INVENTION: METHODS TO REPLICATE DNA IN VITRO USING  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cahill, Sutton & Thomas  
; STREET: 155 Park One, 2141 E. Highland Ave.  
; CITY: Phoenix  
; STATE: Arizona  
; COUNTRY: U.S.A.  
; ZIP: 85016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb  
; COMPUTER: Packard Bell (IBM PC/AT compatible)  
; OPERATING SYSTEM: MS-Dos, Version 5.0  
; SOFTWARE: WordPerfect Version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/208,486  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/869,916  
; FILING DATE: April 14, 1992  
; APPLICATION NUMBER: Japan 240525/91  
; FILING DATE: August 26, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janelle Faunce Raupp  
; REGISTRATION NUMBER: 30,485  
; REFERENCE/DOCKET NUMBER: #3954-A-7  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (602) 956-7000  
; TELEFAX: (602) 495-9475





c 97	14.2	71.0	20	8	US-10-831-778-531	Sequence 531, App	c 170	14.2	71.0	40	7	US-10-661-355-22	Sequence 22, Appl
c 98	14.2	71.0	20	8	US-10-831-778-811	Sequence 811, App	c 171	14.2	71.0	40	7	US-10-661-099-21	Sequence 21, Appl
c 99	14.2	71.0	20	8	US-10-831-778-987	Sequence 987, App	c 172	14.2	71.0	40	7	US-10-661-099-22	Sequence 21, Appl
c 100	14.2	71.0	20	8	US-10-838-659-55	Sequence 55, Appl	c 173	14.2	71.0	40	8	US-10-661-415-21	Sequence 21, Appl
c 101	14.2	71.0	20	9	US-10-661-402-13	Sequence 13, Appl	c 174	14.2	71.0	40	8	US-10-661-415-22	Sequence 21, Appl
c 102	14.2	71.0	20	9	US-10-661-402-14	Sequence 14, Appl	c 175	14.2	71.0	40	9	US-10-661-402-21	Sequence 21, Appl
c 103	14.2	71.0	20	9	US-10-661-403-13	Sequence 13, Appl	c 176	14.2	71.0	40	9	US-10-661-402-22	Sequence 21, Appl
c 104	14.2	71.0	20	9	US-10-661-403-14	Sequence 14, Appl	c 177	14.2	71.0	40	9	US-10-661-403-21	Sequence 21, Appl
c 105	14.2	71.0	20	9	US-10-969-812A-12	Sequence 12, Appl	c 178	14.2	71.0	40	9	US-10-661-403-22	Sequence 21, Appl
c 106	14.2	71.0	20	9	US-10-969-812A-13	Sequence 13, Appl	c 179	14.2	71.0	40	9	US-10-969-812A-20	Sequence 20, Appl
c 107	14.2	71.0	20	9	US-10-969-812A-21	Sequence 21, Appl	c 180	14.2	71.0	40	9	US-10-969-812A-21	Sequence 21, Appl
c 108	14.2	71.0	20	10	US-11-056-463-134	Sequence 134, App	c 181	14.2	71.0	40	9	US-09-896-650A-1	Sequence 29, Appl
c 109	14.2	71.0	22	9	US-10-487-869-12	Sequence 12, Appl	c 182	14.2	71.0	50	3	US-09-896-650A-29	Sequence 29, Appl
c 110	14.2	71.0	24	3	US-09-766-378A-31	Sequence 31, Appl	c 183	14.2	71.0	50	3	US-09-993-346-522	Sequence 522, App
c 111	14.2	71.0	24	3	US-09-888-326-170	Sequence 170, App	c 184	14.2	71.0	50	6	US-10-131-827-2115	Sequence 2115, App
c 112	14.2	71.0	24	3	US-09-776-479-428	Sequence 428, App	c 185	14.2	71.0	50	6	US-10-131-827-4165	Sequence 4165, App
c 113	14.2	71.0	24	3	US-09-776-479-963	Sequence 963, App	c 186	14	70.0	14	3	US-08-283-359-632	Sequence 632, App
c 114	14.2	71.0	24	3	US-09-776-479-963	Sequence 428, App	c 187	14	70.0	14	3	US-10-131-827-4819	Sequence 4819, App
c 115	14.2	71.0	24	3	US-09-776-479-963	Sequence 963, App	c 188	14	70.0	50	6	US-10-131-827-4820	Sequence 4820, App
c 116	14.2	71.0	24	5	US-10-112-653-410	Sequence 410, App	c 189	13.8	69.0	19	9	US-10-923-115-73	Sequence 73, Appl
c 117	14.2	71.0	24	5	US-10-112-653-921	Sequence 921, App	c 190	13.8	69.0	19	9	US-10-923-115-189	Sequence 189, App
c 118	14.2	71.0	24	5	US-10-017-995-428	Sequence 428, App	c 191	13.8	69.0	25	8	US-10-719-900-630483	Sequence 630483, App
c 119	14.2	71.0	24	5	US-10-017-995-963	Sequence 963, App	c 192	13.8	69.0	25	9	US-10-956-157-261648	Sequence 261648, App
c 120	14.2	71.0	24	6	US-10-314-578-428	Sequence 428, App	c 193	13.8	69.0	25	10	US-11-060-756-254379	Sequence 254379, App
c 121	14.2	71.0	24	6	US-10-314-578-963	Sequence 963, App	c 194	13.8	69.0	29	3	US-09-847-232-13	Sequence 13, Appl
c 122	14.2	71.0	24	7	US-10-374-307-14	Sequence 14, Appl	c 195	13.8	69.0	29	3	US-10-623-810A-69	Sequence 69, Appl
c 123	14.2	71.0	24	7	US-10-374-307-15	Sequence 15, Appl	c 196	13.8	69.0	29	10	US-11-083-617-13	Sequence 13, Appl
c 124	14.2	71.0	24	8	US-10-831-778-428	Sequence 428, App	c 197	13.8	69.0	30	7	US-10-676-248B-204	Sequence 204, App
c 125	14.2	71.0	24	8	US-10-831-778-963	Sequence 963, App	c 198	13.8	69.0	36	8	US-10-466-894-1864	Sequence 1864, App
c 126	14.2	71.0	25	3	US-09-828-034-13	Sequence 13, Appl	c 199	13.8	69.0	36	8	US-10-035-833A-6319	Sequence 6319, App
c 127	14.2	71.0	25	3	US-09-896-650A-26	Sequence 26, Appl	c 200	13.8	69.0	41	7	US-10-035-833A-145	Sequence 145, App
c 128	14.2	71.0	25	8	US-10-719-900-145261	Sequence 145261, App	c 201	13.8	69.0	41	7	US-10-035-833A-658	Sequence 658, App
c 129	14.2	71.0	25	9	US-10-956-157-133269	Sequence 133269, App	c 202	13.8	69.0	41	7	US-10-035-833A-1954	Sequence 1954, App
c 130	14.2	71.0	25	9	US-10-956-157-261874	Sequence 261874, App	c 203	13.8	69.0	41	7	US-10-035-833A-4549	Sequence 4549, App
c 131	14.2	71.0	25	10	US-11-060-756-168206	Sequence 168206, App	c 204	13.8	69.0	41	7	US-10-035-833A-5484	Sequence 5484, App
c 132	14.2	71.0	25	10	US-11-060-756-168207	Sequence 168207, App	c 205	13.8	69.0	47	6	US-10-170-097-679	Sequence 679, App
c 133	14.2	71.0	25	10	US-11-060-756-249632	Sequence 249632, App	c 206	13.8	69.0	47	6	US-10-349-143-285	Sequence 285, App
c 134	14.2	71.0	25	10	US-11-060-756-249632	Sequence 249632, App	c 207	13.8	69.0	47	6	US-10-349-143-3218	Sequence 3218, App
c 135	14.2	71.0	26	5	US-10-117-108A-11	Sequence 11, Appl	c 208	13.8	69.0	47	6	US-10-926-684-679	Sequence 679, App
c 136	14.2	71.0	26	5	US-10-010-476-40	Sequence 40, Appl	c 209	13.8	69.0	50	6	US-10-131-827-5327	Sequence 5327, App
c 137	14.2	71.0	27	9	US-10-931-077-27	Sequence 27, Appl	c 210	13.6	68.0	21	9	US-10-708-204-3690	Sequence 3690, App
c 138	14.2	71.0	28	3	US-09-888-326-171	Sequence 171, App	c 211	13.6	68.0	24	3	US-09-894-799-21	Sequence 21, Appl
c 139	14.2	71.0	28	3	US-09-776-479-770	Sequence 770, App	c 212	13.6	68.0	24	7	US-10-648-984-21	Sequence 21, Appl
c 140	14.2	71.0	28	3	US-09-776-479-770	Sequence 770, App	c 213	13.6	68.0	25	3	US-09-863-049A-67	Sequence 67, Appl
c 141	14.2	71.0	28	5	US-10-112-653-743	Sequence 743, App	c 214	13.6	68.0	25	6	US-10-088-256-4	Sequence 4, Appl
c 142	14.2	71.0	28	5	US-10-017-995-770	Sequence 770, App	c 215	13.6	68.0	25	6	US-10-088-256-9	Sequence 9, Appl
c 143	14.2	71.0	28	6	US-10-314-578-770	Sequence 770, App	c 216	13.6	68.0	25	10	US-11-060-756-175501	Sequence 175501, App
c 144	14.2	71.0	29	5	US-10-831-778-770	Sequence 770, App	c 217	13.6	68.0	25	10	US-11-060-756-217870	Sequence 217870, App
c 145	14.2	71.0	30	6	US-10-085-906-105	Sequence 105, App	c 218	13.6	68.0	25	10	US-11-060-756-217871	Sequence 217871, App
c 146	14.2	71.0	30	7	US-10-314-578-1096	Sequence 1096, App	c 219	13.6	68.0	26	5	US-10-010-476-84	Sequence 84, Appl
c 147	14.2	71.0	30	7	US-10-433-899-9	Sequence 9, Appl	c 220	13.6	68.0	26	5	US-10-407-449-4	Sequence 4, Appl
c 148	14.2	71.0	30	9	US-10-688-745-55	Sequence 55, Appl	c 221	13.6	68.0	28	7	US-10-660-897-4	Sequence 4, Appl
c 149	14.2	71.0	32	9	US-10-849-491-4	Sequence 4, Appl	c 222	13.6	68.0	28	8	US-10-820-487-4	Sequence 4, Appl
c 150	14.2	71.0	32	9	US-10-849-491-5	Sequence 5, Appl	c 223	13.6	68.0	28	9	US-10-903-975-4	Sequence 4, Appl
c 151	14.2	71.0	33	3	US-09-888-326-172	Sequence 172, App	c 224	13.6	68.0	30	3	US-09-978-333B-7	Sequence 7, Appl
c 152	14.2	71.0	35	3	US-09-776-479-771	Sequence 771, App	c 225	13.6	68.0	32	9	US-10-495-629A-5	Sequence 5, Appl
c 153	14.2	71.0	35	3	US-09-776-479-771	Sequence 771, App	c 226	13.6	68.0	32	9	US-10-294-934-679	Sequence 679, App
c 154	14.2	71.0	35	5	US-10-027-632-53376	Sequence 53376, A	c 227	13.6	68.0	47	7	US-10-035-833A-2350	Sequence 2350, App
c 155	14.2	71.0	35	5	US-10-112-653-744	Sequence 744, App	c 228	13.6	68.0	47	7	US-10-035-833A-3753	Sequence 3753, App
c 156	14.2	71.0	35	5	US-10-017-995-771	Sequence 771, App	c 229	13.6	68.0	50	6	US-10-131-827-3003	Sequence 3003, App
c 157	14.2	71.0	35	6	US-10-027-632-53376	Sequence 53376, A	c 230	13.6	68.0	50	7	US-10-602-837-2	Sequence 2, Appl
c 158	14.2	71.0	35	6	US-10-314-578-771	Sequence 771, App	c 231	13.6	68.0	50	7	US-10-602-837-24	Sequence 24, Appl
c 159	14.2	71.0	35	7	US-10-239-176-8	Sequence 8, Appl	c 232	13.4	67.0	19	9	US-10-739-904-61	Sequence 61, Appl
c 160	14.2	71.0	35	8	US-10-831-778-771	Sequence 771, App	c 233	13.4	67.0	21	9	US-10-617-070-428	Sequence 428, App
c 161	14.2	71.0	37	6	US-10-405-158-1	Sequence 1, Appl	c 234	13.4	67.0	21	9	US-10-956-507-428	Sequence 428, App
c 162	14.2	71.0	37	6	US-10-405-158-4	Sequence 4, Appl	c 235	13.4	67.0	35	8	US-10-412-137-3	Sequence 3, Appl
c 163	14.2	71.0	38	8	US-10-795-667-124	Sequence 124, App	c 236	13.4	67.0	35	8	US-10-723-947-3	Sequence 3, Appl
c 164	14.2	71.0	40	7	US-10-797-333A-52	Sequence 52, Appl	c 237	13.4	67.0	36	7	US-10-332-542-15	Sequence 15, Appl
c 165	14.2	71.0	40	7	US-10-661-088-21	Sequence 21, Appl	c 238	13.4	67.0	41	7	US-10-035-833A-68	Sequence 68, Appl
c 166	14.2	71.0	40	7	US-10-661-088-22	Sequence 22, Appl	c 239	13.4	67.0	41	7	US-10-035-833A-2047	Sequence 2047, App
c 167	14.2	71.0	40	7	US-10-661-087-21	Sequence 21, Appl	c 240	13.4	67.0	41	7	US-10-035-833A-2675	Sequence 2675, App
c 168	14.2	71.0	40	7	US-10-661-097-22	Sequence 22, Appl	c 241	13.4	67.0	41	7	US-10-035-833A-5344	Sequence 5344, App
c 169	14.2	71.0	40	7	US-10-661-355-21	Sequence 21, Appl	c 242	13.4	67.0	41	7	US-10-035-833A-6296	Sequence 6296, App

```
C 243 13.4 67.0 41 7 US-10-035-833A-7304
C 244 13.4 67.0 47 6 US-10-349-143-523
C 245 13.4 67.0 48 5 US-10-006-593-114
C 246 13.4 67.0 48 6 US-10-307-724-114
C 247 13.4 67.0 48 8 US-10-737-290-114
C 248 13.4 67.0 48 8 US-10-412-137-2
C 249 13.4 67.0 49 8 US-10-723-947-2
C 250 13.4 67.0 50 6 US-10-131-827-1882
C 251 13.2 66.0 18 3 US-09-904-744-3
C 252 13.2 66.0 18 3 US-09-949-305B-2
C 253 13.2 66.0 18 6 US-10-352-704-24
C 254 13.2 66.0 18 8 US-10-849-072-22
C 255 13.2 66.0 18 8 US-10-849-072-24
C 256 13.2 66.0 18 8 US-10-473-126-1085
C 257 13.2 66.0 18 8 US-10-473-126-1086
C 258 13.2 66.0 18 9 US-10-984-919-38
C 259 13.2 66.0 19 3 US-09-932-300-31
C 260 13.2 66.0 19 3 US-09-776-479-559
C 261 13.2 66.0 19 3 US-09-776-479-559
C 262 13.2 66.0 19 5 US-10-112-653-536
C 263 13.2 66.0 19 5 US-10-017-995-559
C 264 13.2 66.0 19 6 US-10-356-625-117
C 265 13.2 66.0 19 6 US-10-314-578-559
C 266 13.2 66.0 19 7 US-10-433-258-90
C 267 13.2 66.0 19 8 US-10-831-778-559
C 268 13.2 66.0 21 3 US-09-932-300-23
C 269 13.2 66.0 21 3 US-09-918-889-26
C 270 13.2 66.0 22 3 US-09-919-042-26
C 271 13.2 66.0 22 8 US-10-840-455-34
C 272 13.2 66.0 23 9 US-10-708-204-3759
C 273 13.2 66.0 24 3 US-09-894-799-22
C 274 13.2 66.0 24 7 US-10-648-984-22
C 275 13.2 66.0 25 5 US-10-972-135A-14
C 276 13.2 66.0 25 9 US-10-010-476-57
C 277 13.2 66.0 25 9 US-10-956-157-135641
C 278 13.2 66.0 25 9 US-10-956-157-176142
C 279 13.2 66.0 25 9 US-10-956-157-214942
C 280 13.2 66.0 25 9 US-10-956-157-267177
C 281 13.2 66.0 25 10 US-11-036-317-155963
C 282 13.2 66.0 25 10 US-11-036-317-156507
C 283 13.2 66.0 25 10 US-11-036-317-158662
C 284 13.2 66.0 25 10 US-11-036-317-166862
C 285 13.2 66.0 25 10 US-11-036-317-198478
C 286 13.2 66.0 25 10 US-11-036-317-228006
C 287 13.2 66.0 25 10 US-11-036-317-250515
C 288 13.2 66.0 25 10 US-11-036-317-267219
C 289 13.2 66.0 25 10 US-11-036-317-356771
C 290 13.2 66.0 25 10 US-11-036-317-362045
C 291 13.2 66.0 25 10 US-11-060-756-133786
C 292 13.2 66.0 25 10 US-11-060-756-183495
C 293 13.2 66.0 25 10 US-11-060-756-201310
C 294 13.2 66.0 25 10 US-11-060-756-240365
C 295 13.2 66.0 25 10 US-11-060-756-248970
C 296 13.2 66.0 25 10 US-11-060-756-249389
C 297 13.2 66.0 25 10 US-11-060-756-279353
C 298 13.2 66.0 25 10 US-11-060-756-291543
C 299 13.2 66.0 26 8 US-10-466-894-1770
C 300 13.2 66.0 27 9 US-10-931-077-26
```

## ALIGNMENTS

```
RESULT 1
US-09-776-479-906
; Sequence 906, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; Treatment of Asthma and Allergy
```

```
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 906
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-906
```

```
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20
| | | | | | | | | | | | | | | | | |
Db 1 AGGGAGGGAGGGAGGGG 20
```

```
RESULT 2
US-09-776-479-906
; Sequence 906, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 906
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-906
```

```
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 AGGGAGGGAGGGAGGGG 20
| | | | | | | | | | | | | | | | | |
Db 1 AGGGAGGGAGGGAGGGG 20
```

```
RESULT 3
US-10-112-653-875
; Sequence 875, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
```

; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 875  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-112-653-875

Query Match 100.0%; Score 20; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGGGAGGGGAGGGAGGGG 20

RESULT 4  
US-10-017-995-906  
; Sequence 906, Application US/10017995  
; Publication No. US20030055014A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
; FILE REFERENCE: C1037/7025 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/017,995  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,534  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 906  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-017-995-906

Query Match 100.0%; Score 20; DB 5; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGGGAGGGGAGGGAGGGG 20

RESULT 5  
US-10-314-578-906  
; Sequence 906, Application US/10314578  
; Publication No. US20030212026A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schetter, Christian  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
; FILE REFERENCE: C1039/7035 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/314,578  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 60/156,113  
; PRIOR FILING DATE: 1999-09-25  
; PRIOR APPLICATION NUMBER: US 60/156,135  
; PRIOR FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: US 60/227,436  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 1145  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 906  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-314-578-906

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGGGAGGGGAGGGAGGGG 20

RESULT 6  
US-10-831-778-906  
; Sequence 906, Application US/10831778  
; Publication No. US20040235774A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/831,778  
; CURRENT FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 906  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-831-778-906

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGGGAGGGGAGGGAGGGG 20

RESULT 7  
US-10-010-920-43  
; Sequence 43, Application US/10010920  
; Publication No. US20030027165A1  
; GENERAL INFORMATION:  
; APPLICANT: Saus, Juan  
; TITLE OF INVENTION: Alternatively spliced polk nucleotide and amino acid sequences  
; FILE REFERENCE: 98,723-E3  
; CURRENT APPLICATION NUMBER: US/10/010,920  
; CURRENT FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/254,649  
; PRIOR FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer ON-TATaDel  
US-10-010-920-43

Query Match 87.0%; Score 17.4; DB 5; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



```
US-08-781-986A-2153/c
; Sequence 2153, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781.986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: P8248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-2153

Query Match      82.0%; Score 16.4; DB 2; Length 50;
Best Local Similarity 89.5%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20
   ||||| ||||| ||||| |||||
Db 28 GGGGGGGGGGGGGAGGGG 10

RESULT 13
US-10-329-624-2153/c
; Sequence 2153, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
```

```
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329.624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956.171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: P8248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2153:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2153:
US-10-329-624-2153

Query Match      82.0%; Score 16.4; DB 7; Length 50;
Best Local Similarity 89.5%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20
   ||||| ||||| ||||| |||||
Db 28 GGGGGGGGGGGGGAGGGG 10

RESULT 14
US-09-263-959-923
; Sequence 923, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 923:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
```



```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-923

Query Match          79.0%; Score 15.8; DB 3; Length 19;
Best Local Similarity 89.5%; Pred. No. 9.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 1 GGGGCGGGGAGGGCGGGG 19

RESULT 15
US-10-010-476-38
; Sequence 38, Application US/10010476
; Publication No. US20030114402A1
; GENERAL INFORMATION:
; APPLICANT: Reich, No. US20030114402Albert O.
; FLYNN, James
; TITLE OF INVENTION: MODULATORS OF DNA CYTOSINE-5
; METHYLTRANSFERASE AND METHODS FOR USE THEREOF
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010,476
; FILING DATE: 07-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/485,071
; FILING DATE: 12-Jun-1998
; APPLICATION NUMBER: 60/057,411
; FILING DATE: 29-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Canady, Karen S
; REGISTRATION NUMBER: 39,927
; REFERENCE/DOCKET NUMBER: 30794.30W001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-010-476-38

Query Match          79.0%; Score 15.8; DB 5; Length 26;
Best Local Similarity 89.5%; Pred. No. 8.4e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 2 GGGGTGGGAGCGGAGGGG 20

RESULT 16
US-10-407-449-41
```

```
; Sequence 41, Application US/10407449
; Publication No. US20040005601A1
; GENERAL INFORMATION:
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Hurley, Laurence
; APPLICANT: Farrell, Thomas
; APPLICANT: Grand, Cory
; APPLICANT: Bears, David
; TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLIX DNA
; FILE REFERENCE: 53223-20004.00
; CURRENT APPLICATION NUMBER: US/10/407,449
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/404,966
; PRIOR FILING DATE: 2002-08-04
; PRIOR APPLICATION NUMBER: US 60/370,358
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: Unknown
; PRIOR FILING DATE: 2003-03-20
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Generalized quadruplex structure for RET
US-10-407-449-41

Query Match          76.0%; Score 15.2; DB 6; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 1 AGGGCGGGGCGGGCGGGG 20

RESULT 17
US-10-407-449-44
; Sequence 44, Application US/10407449
; Publication No. US20040005601A1
; GENERAL INFORMATION:
; APPLICANT: Siddiqui-Jain, Adam
; APPLICANT: Hurley, Laurence
; APPLICANT: Farrell, Thomas
; APPLICANT: Grand, Cory
; APPLICANT: Bears, David
; TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLIX DNA
; FILE REFERENCE: 53223-20004.00
; CURRENT APPLICATION NUMBER: US/10/407,449
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/404,966
; PRIOR FILING DATE: 2002-08-04
; PRIOR APPLICATION NUMBER: US 60/370,358
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: Unknown
; PRIOR FILING DATE: 2003-03-20
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of the TMPyP4-induced photocleavage site
US-10-407-449-44

Query Match          76.0%; Score 15.2; DB 6; Length 22;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGGAGGGG 20
    ||||| ||||| ||||| |||||
```

Db 1 AGGGCGGGCGGGCGGGG 20

## RESULT 18

US-10-820-487-5  
; Sequence 5, Application US/10820487  
; Publication No. US20050004160A1  
; GENERAL INFORMATION:  
; APPLICANT: WHITTEN, Jeffrey P.  
; APPLICANT: SCHWABE, Michael  
; APPLICANT: MORAN, Terrance  
; TITLE OF INVENTION: HETEROCYCLIC SUBSTITUTED  
; TITLE OF INVENTION: 1,4-DIHYDRO-4-OXO-1,8-NAPHTHYRIDINE ANALOGS  
; FILE REFERENCE: 532232001200  
; CURRENT APPLICATION NUMBER: US/10/820,487  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/461,205  
; PRIOR FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US 60/519,569  
; PRIOR FILING DATE: 2003-11-12  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-820-487-5

Query Match 76.0%; Score 15.2; DB 8; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.4e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20

Db 1 AGGGCGGGCGGGCGGGG 20

## RESULT 19

US-10-903-975-5  
; Sequence 5, Application US/10903975  
; Publication No. US20050085468A1  
; GENERAL INFORMATION:  
; APPLICANT: WHITTEN, Jeffrey P.  
; APPLICANT: SCHWABE, Michael  
; APPLICANT: SIDDIQUI-JAIN, Adam  
; APPLICANT: MORAN, Terrance  
; TITLE OF INVENTION: SUBSTITUTED QUINOBENZOXAZINE ANALOGS  
; FILE REFERENCE: 532232001120  
; CURRENT APPLICATION NUMBER: US/10/903,975  
; CURRENT FILING DATE: 2004-07-30  
; PRIOR APPLICATION NUMBER: US 10/821,243  
; PRIOR FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/461,271  
; PRIOR FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: US 60/463,171  
; PRIOR FILING DATE: 2003-04-15  
; PRIOR APPLICATION NUMBER: US 60/519,535  
; PRIOR FILING DATE: 2003-11-12  
; PRIOR APPLICATION NUMBER: US 60/532,727  
; PRIOR FILING DATE: 2003-12-23  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-903-975-5

Query Match 76.0%; Score 15.2; DB 9; Length 22;  
Best Local Similarity 85.0%; Pred. No. 1.4e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20

Db 1 AGGGCGGGCGGGCGGGG 20

## RESULT 20

US-10-407-449-43  
; Sequence 43, Application US/10407449  
; Publication No. US20040005601A1  
; GENERAL INFORMATION:  
; APPLICANT: Siddiqui-Jain, Adam  
; APPLICANT: Hurley, Laurence  
; APPLICANT: Farrell, Thomas  
; APPLICANT: Grand, Cory  
; APPLICANT: Bearss, David  
; TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLEX DNA  
; FILE REFERENCE: 53223-20004.00  
; CURRENT APPLICATION NUMBER: US/10/407,449  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US 60/404,966  
; PRIOR FILING DATE: 2002-08-04  
; PRIOR APPLICATION NUMBER: US 60/370,358  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: Unknown  
; PRIOR FILING DATE: 2003-03-20  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: RET quadruplex-forming nucleotide sequence  
US-10-407-449-43

Query Match 76.0%; Score 15.2; DB 6; Length 24;  
Best Local Similarity 85.0%; Pred. No. 1.4e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20

Db 1 AGGGCGGGCGGGCGGGG 20

## RESULT 21

US-10-931-077-28/c  
; Sequence 28, Application US/10931077  
; Publication No. US20050204432A1  
; GENERAL INFORMATION:  
; APPLICANT: Pioneer Hi-Bred International, Inc.  
; APPLICANT: Multani, Dilbag  
; APPLICANT: Niu, Xiaomu  
; APPLICANT: Tones, Dwight T  
; APPLICANT: Wang, Haiyin  
; APPLICANT: Xu, Deping  
; TITLE OF INVENTION: BR2 AND DW3 PROMOTERS AND METHODS OF USE  
; FILE REFERENCE: 035718/281933  
; CURRENT APPLICATION NUMBER: US/10/931,077  
; CURRENT FILING DATE: 2004-08-31  
; PRIOR APPLICATION NUMBER: 60/499,580  
; PRIOR FILING DATE: 2003-09-02  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 28  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-10-931-077-28

Query Match 76.0%; Score 15.2; DB 9; Length 27;  
Best Local Similarity 85.0%; Pred. No. 1.4e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20

Db 26 AGGGAGGAGGAGGAGGGGG 7  
||||| ||||| ||||| |||||

RESULT 22  
US-10-239-176-13/c  
; Sequence 13, Application US/10239176  
; Publication No. US20040086856A1  
; GENERAL INFORMATION:  
; APPLICANT: TAKAHASHI, MASAYOSHI  
; APPLICANT: OKADA, JUN  
; APPLICANT: HASHIMOTO, KOJI  
; TITLE OF INVENTION: NUCLEIC ACID PROBE-IMMOBILIZED SUBSTRATE AND METHOD OF  
; TITLE OF INVENTION: DETECTING THE PRESENCE OF TARGET NUCLEIC ACID BY USING THE SAME  
; FILE REFERENCE: 228763US0SRDPT  
; CURRENT APPLICATION NUMBER: US/10/239,176  
; CURRENT FILING DATE: 2003-03-19  
; PRIOR APPLICATION NUMBER: PCT/JPO2/08670  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: JP 2002-218644  
; PRIOR FILING DATE: 2002-07-26  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 35  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic DNA  
US-10-239-176-13

Query Match 76.0%; Score 15.2; DB 7; Length 35;  
Best Local Similarity 85.0%; Pred. No. 1.2e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGAGGAGGAGGGGG 20  
||||| ||||| ||||| |||||  
Db 22 AGGGGGGGGGGGGGGGGG 3

RESULT 23  
US-10-239-176-3/c  
; Sequence 3, Application US/10239176  
; Publication No. US20040086856A1  
; GENERAL INFORMATION:  
; APPLICANT: TAKAHASHI, MASAYOSHI  
; APPLICANT: OKADA, JUN  
; APPLICANT: HASHIMOTO, KOJI  
; TITLE OF INVENTION: NUCLEIC ACID PROBE-IMMOBILIZED SUBSTRATE AND METHOD OF  
; TITLE OF INVENTION: DETECTING THE PRESENCE OF TARGET NUCLEIC ACID BY USING THE SAME  
; FILE REFERENCE: 228763US0SRDPT  
; CURRENT APPLICATION NUMBER: US/10/239,176  
; CURRENT FILING DATE: 2003-03-19  
; PRIOR APPLICATION NUMBER: PCT/JPO2/08670  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: JP 2002-218644  
; PRIOR FILING DATE: 2002-07-26  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic DNA  
US-10-239-176-3

Query Match 76.0%; Score 15.2; DB 7; Length 39;  
Best Local Similarity 85.0%; Pred. No. 1.2e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGAGGAGGAGGGGG 20  
||||| ||||| ||||| |||||

Db 21 AGGGGGGGGGGGGGGGGGGG 2

RESULT 24  
US-10-239-176-4/c  
; Sequence 4, Application US/10239176  
; Publication No. US20040086856A1  
; GENERAL INFORMATION:  
; APPLICANT: TAKAHASHI, MASAYOSHI  
; APPLICANT: OKADA, JUN  
; APPLICANT: HASHIMOTO, KOJI  
; TITLE OF INVENTION: NUCLEIC ACID PROBE-IMMOBILIZED SUBSTRATE AND METHOD OF  
; TITLE OF INVENTION: DETECTING THE PRESENCE OF TARGET NUCLEIC ACID BY USING THE SAME  
; FILE REFERENCE: 228763US0SRDPT  
; CURRENT APPLICATION NUMBER: US/10/239,176  
; CURRENT FILING DATE: 2003-03-19  
; PRIOR APPLICATION NUMBER: PCT/JPO2/08670  
; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: JP 2002-218644  
; PRIOR FILING DATE: 2002-07-26  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic DNA  
US-10-239-176-4

Query Match 76.0%; Score 15.2; DB 7; Length 48;  
Best Local Similarity 85.0%; Pred. No. 1.1e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGGAGGAGGAGGAGGGGG 20  
||||| ||||| ||||| |||||  
Db 30 AGGGGGGGGGGGGGGGGG 11

RESULT 25  
US-09-263-959-443/c  
; Sequence 443, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McWaters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 443:

;  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-09-263-959-443

Query Match 75.0%; Score 15; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.9e+04;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GAGGGGAGGGGAGGG 19  
Db 15 GAGGGGAGGGGAGGG 1

## RESULT 26

US-10-035-833A-1181  
; Sequence 1181, Application US/10035833A  
; Publication No. US20040072156A1  
; GENERAL INFORMATION:  
; APPLICANT: Nakamura, Yuho  
; APPLICANT: Sekine, Akihiro  
; APPLICANT: Iida, Aritoshi  
; APPLICANT: Saito, Osamu  
; TITLE OF INVENTION: Detection of Genetic Polymorphisms  
; FILE REFERENCE: FORS-06904  
; CURRENT APPLICATION NUMBER: US/10/035,833A  
; CURRENT FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 7669  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1181  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-035-833A-1181

Query Match 75.0%; Score 15; DB 7; Length 41;  
Best Local Similarity 88.2%; Pred. No. 1.4e+04;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGAGGGGAGGGAGGGG 20  
Db 10 GGAAGGGAGGGAGGGG 26

## RESULT 27

US-10-035-833A-5376  
; Sequence 5376, Application US/10035833A  
; Publication No. US20040072156A1  
; GENERAL INFORMATION:  
; APPLICANT: Nakamura, Yuho  
; APPLICANT: Sekine, Akihiro  
; APPLICANT: Iida, Aritoshi  
; APPLICANT: Saito, Osamu  
; TITLE OF INVENTION: Detection of Genetic Polymorphisms  
; FILE REFERENCE: FORS-06904  
; CURRENT APPLICATION NUMBER: US/10/035,833A  
; CURRENT FILING DATE: 2001-12-27  
; NUMBER OF SEQ ID NOS: 7669  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5376  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-035-833A-5376

Query Match 75.0%; Score 15; DB 7; Length 41;  
Best Local Similarity 88.2%; Pred. No. 1.4e+04;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GGAGGGGAGGGAGGGG 20  
||| |||||:|||||

Db 10 GGAAGGGAGGGAGGGG 26

## RESULT 28

US-10-010-476-55  
; Sequence 55, Application US/10010476  
; Publication No. US20030114402A1  
; GENERAL INFORMATION:  
; APPLICANT: Reich, No. US20030114402Albert O.  
; Flynm, James  
; TITLE OF INVENTION: MODULATORS OF DNA CYTOSINE-5  
; METHYLTRANSFERASE AND METHODS FOR USE THEREOF  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 11150 Santa Monica Boulevard, Suite 400  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/010,476  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/485,071  
; FILING DATE: 12-Jun-1998  
; APPLICATION NUMBER: 60/057,411  
; FILING DATE: 29-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Canady, Karen S  
; REGISTRATION NUMBER: 39,927  
; REFERENCE/DOCKET NUMBER: 30794.30WO01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 310 445-1140  
; TELEFAX: 310 445-9031  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:  
US-10-010-476-55

Query Match 74.0%; Score 14.8; DB 5; Length 26;  
Best Local Similarity 88.9%; Pred. No. 1.9e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGGAGGGGAGGGAGGGG 20  
Db 3 GGGGGGGAGGGAGGGG 20

## RESULT 29

US-10-010-476-107  
; Sequence 107, Application US/10010476  
; Publication No. US20030114402A1  
; GENERAL INFORMATION:  
; APPLICANT: Reich, No. US20030114402Albert O.  
; Flynm, James  
; TITLE OF INVENTION: MODULATORS OF DNA CYTOSINE-5  
; METHYLTRANSFERASE AND METHODS FOR USE THEREOF  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt  
; STREET: 11150 Santa Monica Boulevard, Suite 400  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/010,476  
; FILING DATE: 07-Dec-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/485,071  
; FILING DATE: 12-Jun-1998  
; APPLICATION NUMBER: 60/057,411  
; FILING DATE: 29-AUG-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Canady, Karen S  
; REGISTRATION NUMBER: 39,927  
; REFERENCE/DOCKET NUMBER: 30794.30WO01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 310 445-1140  
; TELEFAX: 310 445-9031  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 55:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:  
US-10-010-476-55

Query Match 74.0%; Score 14.8; DB 5; Length 26;  
Best Local Similarity 88.9%; Pred. No. 1.9e+04;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GGAGGGGAGGGAGGGG 20  
||| |||||:|||||

```

, CITY: Los Angeles
, STATE: CA
, COUNTRY: USA
, ZIP: 90025
, COMPUTER READABLE FORM:
, MEDIUM TYPE: diskette
, COMPUTER: IBM Compatible
, OPERATING SYSTEM: DOS
, SOFTWARE: FastSEQ for Windows Version 2.0
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/10/010,476
, FILING DATE: 07-Dec-2001
, CLASSIFICATION: <unknown>
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US/09/485,071
, FILING DATE: 12-Jun-1998
, APPLICATION NUMBER: 60/057,411
, FILING DATE: 29-AUG-1997
, ATTORNEY/AGENT INFORMATION:
, NAME: Canady, Karen S
, REGISTRATION NUMBER: 39,927
, REFERENCE/DOCKET NUMBER: 30794.30W001
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 310 445-1140
, TELEFAX: 310 445-9031
, TELEX: <Unknown>
, INFORMATION FOR SEQ ID NO: 107:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 26 base pairs
, TYPE: nucleic acid
, TOPOLOGY: double
, STRANDEDNESS: linear
, SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-10-010-476-107

```

Query Match	74.0%;	Score 14.8;	DB 5;	Length 26;
Best Local Similarity	88.9%;	Pred. No. 1.9e+04;		
Matches 16;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	3	GGGAGGGGAGGGGAGGGG	20	
Db	3	GGGAGGGGAGGGGAGGGG	20	

```

RESULT 30
US-10-224-683-93
; Sequence 93, Application US/10224683
; Publication No. US20030162192A1
; GENERAL INFORMATION:
; APPLICANT: Sotos, John
; APPLICANT: Rienhoff, Jr., Hugh
; APPLICANT: Guida, Marco
; APPLICANT: Curran, Mark
; TITLE OF INVENTION: Polymorphisms Associated with Ion-Channel Disease
; FILE REFERENCE: 4389-33
; CURRENT APPLICATION NUMBER: US/10/224,683
; CURRENT FILING DATE: 2002-01-06
; PRIOR APPLICATION NUMBER: 60/314,331
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/378,521
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-224-683-93

```

```

Qy      2  GCGGAGGGGAGGGGAGG 19
      | | | | | | | | | |
Db      3  GAGGAGGGGAGGGCAGG 20

RESULT 31
US-10-942-561A-93
; Sequence 93. Application US/10942561A
; Publication No. US20050089905A1
; GENERAL INFORMATION:
; APPLICANT: Sotos, John
; APPLICANT: Rienhoff, Jr., Hugh
; APPLICANT: Guida, Marco
; APPLICANT: Curran, Mark
; TITLE OF INVENTION: Polymorphisms AS
; FILE REFERENCE: DNA-33US2
; CURRENT APPLICATION NUMBER: US/10/94
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 10/224,683
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/314,331
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/378,521
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-942-561A-93

```

```

RESULT 32
US-10-035-833A-6318/c
; Sequence 6318, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7689
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6318
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: c is present or absent.
US-10-035-833A-6318

```

```

Query Match      74.0%; Score 14.8; DB 7; Length 41;
Best Local Similarity 88.9%; Pred. No. 1.6e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2  GGGGAGGGGAGGGGAGGG 19
        |||||
Db      31  GGGCGGGGAGGGGGGGG 14

```



Best Local Similarity 93.8%; Pred. No. 2.3e+04; Mismatches 0; Gaps 0; Indels 1;

Qy 5 GAGGGGAGGGGAGGGG 20  
Db 23 GTGGGGAGGGGAGGGG 38

## RESULT 37

US-10-617-070-432  
; Sequence 432, Application US/10617070  
; Publication No. US20040096874A1  
; GENERAL INFORMATION:  
; APPLICANT: Neville, Matt  
; APPLICANT: de Arruda Indig, Monika  
; APPLICANT: Cao, Feng  
; APPLICANT: Oldenburg, Mary C.  
; APPLICANT: Koelbl, Jim C.  
; APPLICANT: Aizenstein, Brian D.  
; APPLICANT: Davey, Keith  
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes  
; FILE REFERENCE: FORS-08195  
; CURRENT APPLICATION NUMBER: US/10/617,070  
; CURRENT FILING DATE: 2003-07-10  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 10/411,954  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 60/371,819  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 529  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 432  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; US-10-617-070-432

Query Match 72.0%; Score 14.4; DB 7; Length 39;  
Best Local Similarity 93.8%; Pred. No. 2.3e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GAGGGGAGGGGAGGGG 20  
Db 23 GTGGGGAGGGGAGGGG 38

## RESULT 38

US-10-956-507-431  
; Sequence 431, Application US/10956507  
; Publication No. US20050196771A1  
; GENERAL INFORMATION:  
; APPLICANT: Neville, Matt  
; APPLICANT: de Arruda Indig, Monika  
; APPLICANT: Cao, Feng  
; APPLICANT: Oldenburg, Mary C.  
; APPLICANT: Koelbl, Jim C.  
; APPLICANT: Aizenstein, Brian D.  
; APPLICANT: Davey, Keith  
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes  
; FILE REFERENCE: FORS-08195  
; CURRENT APPLICATION NUMBER: US/10/956,507  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: US/10/617,070  
; PRIOR FILING DATE: 2003-07-10  
; PRIOR APPLICATION NUMBER: 10/411,954  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 60/371,819  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 529  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 431  
; LENGTH: 39

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; US-10-956-507-431

Query Match 72.0%; Score 14.4; DB 9; Length 39;  
Best Local Similarity 93.8%; Pred. No. 2.3e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GAGGGGAGGGGAGGGG 20  
Db 23 GTGGGGAGGGGAGGGG 38

## RESULT 39

US-10-956-507-432  
; Sequence 432, Application US/10956507  
; Publication No. US20050196771A1  
; GENERAL INFORMATION:  
; APPLICANT: Neville, Matt  
; APPLICANT: de Arruda Indig, Monika  
; APPLICANT: Cao, Feng  
; APPLICANT: Oldenburg, Mary C.  
; APPLICANT: Koelbl, Jim C.  
; APPLICANT: Aizenstein, Brian D.  
; APPLICANT: Davey, Keith  
; TITLE OF INVENTION: Characterization of CYP2D6 Genotypes  
; FILE REFERENCE: FORS-08195  
; CURRENT APPLICATION NUMBER: US/10/956,507  
; CURRENT FILING DATE: 2004-10-01  
; PRIOR APPLICATION NUMBER: US/10/617,070  
; PRIOR FILING DATE: 2003-07-10  
; PRIOR APPLICATION NUMBER: 10/411,954  
; PRIOR FILING DATE: 2003-04-11  
; PRIOR APPLICATION NUMBER: 60/371,819  
; PRIOR FILING DATE: 2002-04-11  
; NUMBER OF SEQ ID NOS: 529  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 432  
; LENGTH: 39  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; US-10-956-507-432

Query Match 72.0%; Score 14.4; DB 9; Length 39;  
Best Local Similarity 93.8%; Pred. No. 2.3e+04;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GAGGGGAGGGGAGGGG 20  
Db 23 GTGGGGAGGGGAGGGG 38

## RESULT 40

US-09-916-369A-2/c  
; Sequence 2, Application US/09916369A  
; Publication No. US20020058802A1  
; GENERAL INFORMATION:  
; APPLICANT: Dellinger, Douglas J  
; APPLICANT: Perboost, Michael GM  
; APPLICANT: Caruthers, Marvin H  
; APPLICANT: Betley, Jason R  
; TITLE OF INVENTION: Synthesis of Polynucleotides Using Combined Oxidation/Deprotection  
; FILE REFERENCE: 10003869-1  
; CURRENT APPLICATION NUMBER: US/09/916,369A  
; CURRENT FILING DATE: 2001-07-21  
; PRIOR APPLICATION NUMBER: US 09/627,249  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 9

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-09-916-369A-2

Query Match          71.0%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  20 GGGGGGGGGGGGGGGGGG 20

RESULT 41
US-09-800-266A-133
; Sequence 133, Application US/09800266A
; Patent No. US20020156033A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids and
; TITLE OF INVENTION: Cancer Medicament Combination Therapy for the Treatment of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: C10377/7017 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/800,266A
; PRIOR FILING DATE: 2001-03-05
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 133
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-800-266A-133

Query Match          71.0%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  1 GGGGGGGGGGGGGGGGGG 19

RESULT 42
US-09-895-007A-133
; Sequence 133, Application US/09895007A
; Patent No. US20020165178A1
; GENERAL INFORMATION:
; APPLICANT: Schetter, Christian
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS FOR THE
; FILE REFERENCE: C1041/7014 (AWS)
; CURRENT APPLICATION NUMBER: US/09/895,007A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/214,369
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 133
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
US-09-895-007A-133

; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-895-007A-133

Query Match          71.0%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  1 GGGGGGGGGGGGGGGGGG 19

RESULT 43
US-09-920-313-133
; Sequence 133, Application US/09920313
; Publication No. US20020198165A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Nucleic Acids for the Prevention and
; TITLE OF INVENTION: Treatment of Gastric Ulcers
; FILE REFERENCE: C10377/7019 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/920,313
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 60/222,248
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 133
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-920-313-133

Query Match          71.0%; Score 14.2; DB 3; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 GGGGAGGGGAGGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db  1 GGGGGGGGGGGGGGGGGG 19

RESULT 44
US-09-888-326-168/c
; Sequence 168, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 168
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-168
```



Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGAGGGAGGG 20  
Db 20 GGGGGGGGGGGGGGGG 2

**RESULT 45**

```

US-09-888-326-169/c
; Sequence 169, Application US/09888326
; Publication NO. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 169
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-169

```

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels

Qy 2 GGGAGGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||  
Db 20 GGGGGGGGGGGGGGGGGG 2

RESULT 46

```

US-09-888-326-429
; Sequence 429, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Call Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 429
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-429

```

Query Match	71.0%;	Score 14.2;	DB 3;	Length 20;
Best Local Similarity	84.2%;	Pred. No. 3.4e+04;		
Matches 16: Conservative	0;	Mismatches 3	Indels	

Qy 2 GCGAGCGGAGCGGAGCGG 20  
||| ||| ||| ||| ||| ||| |||  
pb 1 GCGGCGCGCGCGCGCGCGG 19

## RESULT 47

```

US-09-888-326-430
; Sequence 430, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 430
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-430

```

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels

Qy 2 GGGAGGGAGGGAGGG 20  
||| ||| ||| ||| |||  
pb 1 GGGGGGGGGGGGGGGG 19

RESULT 48

```

US-09-776-479-257/c
; Sequence 257, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 257
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-257

```

Query Match	71.0%;	Score 14.2;	DB 3;	Length 20;
Best Local Similarity	84.2%;	Pred. No. 3.4e+04;		

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | |  
Db 20 GGGGGGGGGGGGGGGGG 2

RESULT 49  
US-09-776-479-530/c  
; Sequence 530, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 530  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-530

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | |  
Db 20 GGGGGGGGGGGGGGGGG 2

RESULT 50  
US-09-776-479-531  
; Sequence 531, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 531  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-531

Query Match 71.0%; Score 14.2; DB 3; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.4e+04;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGGAGGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | |  
Db 1 GGGGGGGGGGGGGGGGG 19

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2006, 02:03:53 ; Search time 186.446 Seconds  
(without alignments)  
98.157 Million cell updates/sec

Title: US-09-669-187a-906

Perfect score: 20

Sequence: 1 agggaggaggaggaggagg 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6247088 seqs, 457523669 residues

Total number of hits satisfying chosen parameters: 11812030

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications NA New:\*

1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*

2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*

3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*

4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*

5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*

6: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*

7: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*

8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*

12: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	11	US-11-127-654-875
2	20	100.0	26	7	US-10-310-914A-1295111
3	19	95.0	19	7	US-10-310-914A-7761511
4	19	95.0	19	7	US-10-310-914A-7761512
5	19	95.0	20	7	US-10-310-914A-739686
6	19	95.0	20	7	US-10-310-914A-1162719
7	19	95.0	21	7	US-10-310-914A-1162726
8	19	95.0	21	7	US-10-310-914A-1162727
9	19	95.0	21	7	US-10-310-914A-1295143
10	19	95.0	23	7	US-10-310-914A-1295148
11	19	95.0	23	7	US-10-310-914A-1295149
12	19	95.0	26	7	US-10-310-914A-739676
13	19	95.0	27	7	US-10-310-914A-1162700
14	19	95.0	28	7	US-10-310-914A-1162700
15	18.4	92.0	20	7	US-10-310-914A-1155402
16	18.4	92.0	24	7	US-10-310-914A-162906
17	18.4	92.0	24	7	US-10-310-914A-162961
18	18.4	92.0	24	7	US-10-310-914A-162974
19	18.4	92.0	28	7	US-10-310-914A-282266
20	18	90.0	19	7	US-10-310-914A-906589
21	18	90.0	22	7	US-10-310-914A-1295146
Sequence 875, App					
Sequence 1295111,					
Sequence 776151,					
Sequence 776152,					
Sequence 739686,					
Sequence 1162719,					
Sequence 1162726,					
Sequence 1295143,					
Sequence 1295144,					
Sequence 1295148,					
Sequence 1295149,					
Sequence 739676,					
Sequence 1162700,					
Sequence 1155402,					
Sequence 162906,					
Sequence 162961,					
Sequence 162974,					
Sequence 282266,					
Sequence 906589,					
Sequence 1295146,					

US-10-310-914A-739675	7	90.0	23	7	Sequence 739675,
US-10-310-914A-1047386	23	90.0	23	7	Sequence 1047386,
US-10-310-914A-100302	7	87.0	19	7	Sequence 100302,
US-10-310-914A-148888	24	87.0	19	7	Sequence 148888,
US-10-310-914A-162912	19	87.0	19	7	Sequence 162912,
US-10-310-914A-386824	26	87.0	19	7	Sequence 386824,
US-10-310-914A-386825	27	87.0	19	7	Sequence 386825,
US-10-310-914A-386850	19	87.0	19	7	Sequence 386850,
US-10-310-914A-288225	28	87.0	19	7	Sequence 288225,
US-10-310-914A-588532	30	87.0	20	7	Sequence 588532,
US-10-310-914A-628864	31	87.0	20	7	Sequence 628864,
US-10-310-914A-1155411	32	87.0	20	7	Sequence 1155411,
US-10-310-914A-100342	20	87.0	20	7	Sequence 100342,
US-10-310-914A-288226	21	87.0	21	7	Sequence 288226,
US-10-310-914A-288227	35	87.0	21	7	Sequence 288227,
US-10-310-914A-386839	21	87.0	21	7	Sequence 386839,
US-10-310-914A-386841	21	87.0	21	7	Sequence 386841,
US-10-310-914A-386851	37	87.0	21	7	Sequence 386851,
US-10-310-914A-659280	39	87.0	21	7	Sequence 659280,
US-10-310-914A-1345469	40	87.0	21	7	Sequence 1345469,
US-10-310-914A-282307	17	87.0	21	7	Sequence 282307,
US-10-310-914A-386862	42	87.0	22	7	Sequence 386862,
US-10-310-914A-560684	22	87.0	22	7	Sequence 560684,
US-10-310-914A-628966	44	87.0	22	7	Sequence 628966,
US-10-310-914A-659284	45	87.0	22	7	Sequence 659284,
US-10-310-914A-1345363	46	87.0	22	7	Sequence 1345363,
US-10-310-914A-100318	47	87.0	22	7	Sequence 100318,
US-10-310-914A-162972	48	87.0	22	7	Sequence 162972,
US-10-310-914A-386823	49	87.0	23	7	Sequence 386823,
US-10-310-914A-386848	50	87.0	23	7	Sequence 386848,
US-10-310-914A-386852	51	87.0	23	7	Sequence 386852,
US-10-310-914A-628968	52	87.0	23	7	Sequence 628968,
US-10-310-914A-148889	53	87.0	23	7	Sequence 148889,
US-10-310-914A-162908	54	87.0	24	7	Sequence 162908,
US-10-310-914A-162973	55	87.0	24	7	Sequence 162973,
US-10-310-914A-271752	56	87.0	24	7	Sequence 271752,
US-10-310-914A-912847	57	87.0	24	7	Sequence 912847,
US-10-310-914A-271805	58	87.0	24	7	Sequence 271805,
US-10-310-914A-288142	59	87.0	26	7	Sequence 288142,
US-10-310-914A-659221	60	87.0	26	7	Sequence 659221,
US-10-310-914A-386820	61	87.0	27	7	Sequence 386820,
US-10-310-914A-386821	62	87.0	18	7	Sequence 386821,
US-10-310-914A-351503	63	85.0	18	7	Sequence 351503,
US-10-310-914A-351511	64	85.0	17	7	Sequence 351511,
US-10-310-914A-386821	65	85.0	19	7	Sequence 386821,
US-10-310-914A-590218	66	85.0	17	7	Sequence 590218,
US-10-310-914A-398994	67	85.0	19	7	Sequence 398994,
US-10-310-914A-1047383	68	85.0	21	7	Sequence 1047383,
US-10-310-914A-386822	69	85.0	21	7	Sequence 386822,
US-10-310-914A-776181	70	85.0	22	7	Sequence 776181,
US-10-310-914A-1162723	71	85.0	22	7	Sequence 1162723,
US-10-310-914A-351503	72	85.0	23	7	Sequence 351503,
US-10-310-914A-84063	73	85.0	26	7	Sequence 84063, A
US-10-310-914A-673446	74	84.0	20	7	Sequence 673446,
US-10-310-914A-668894	75	84.0	20	7	Sequence 668894,
US-10-310-914A-84145	76	84.0	21	7	Sequence 84145, A
US-10-310-914A-391177	77	84.0	22	7	Sequence 391177,
US-10-310-914A-774655	78	84.0	22	7	Sequence 774655,
US-10-310-914A-1037972	79	84.0	22	7	Sequence 1037972,
US-10-310-914A-100280	80	84.0	22	7	Sequence 100280,
US-10-310-914A-162907	81	84.0	23	7	Sequence 162907,
US-10-310-914A-1185315	82	84.0	23	7	Sequence 1185315,
US-10-310-914A-219652	83	84.0	23	7	Sequence 219652,
US-10-310-914A-1283210	84	84.0	24	7	Sequence 1283210,
US-10-310-914A-84064	85	84.0	26	7	Sequence 84064, A
US-10-310-914A-100304	86	84.0	26	7	Sequence 100304,
US-10-310-914A-303168	87	82.0	18	7	Sequence 303168,
US-10-310-914A-386849	88	82.0	18	7	Sequence 386849,
US-10-310-914A-560683	89	82.0	16.4	7	Sequence 560683,
US-10-310-914A-590293	90	82.0	18	7	Sequence 590293,
US-10-310-914A-1283209	91	82.0	16.4	7	Sequence 1283209,
US-10-310-914A-433666	92	82.0	16.4	7	Sequence 433666,
US-10-310-914A-959340	93	82.0	16.4	7	Sequence 959340,

c 95	16.4	82.0	19	7	US-10-310-914A-1162720	Sequence 1162720,	168	15.8	79.0	21	7	US-10-310-914A-678373	Sequence 678373,
c 96	16.4	82.0	19	7	US-10-310-914A-1162721	Sequence 1162721,	169	15.8	79.0	21	7	US-10-310-914A-845519	Sequence 845519,
c 97	16.4	82.0	20	7	US-10-310-914A-172750	Sequence 172750,	170	15.8	79.0	21	7	US-10-310-914A-1227157	Sequence 1227157,
c 98	16.4	82.0	20	7	US-10-310-914A-271793	Sequence 271793,	c 171	15.8	79.0	21	7	US-10-310-914A-1371973	Sequence 1371973,
c 99	16.4	82.0	20	7	US-10-310-914A-282308	Sequence 282308,	172	15.8	79.0	22	7	US-10-310-914A-130734	Sequence 130734,
c 100	16.4	82.0	20	7	US-10-310-914A-628863	Sequence 628863,	173	15.8	79.0	22	7	US-10-310-914A-130795	Sequence 130795,
c 101	16.4	82.0	20	7	US-10-310-914A-1240445	Sequence 1240445,	174	15.8	79.0	22	7	US-10-310-914A-369359	Sequence 369359,
c 102	16.4	82.0	21	7	US-10-310-914A-100306	Sequence 100306,	175	15.8	79.0	22	7	US-10-310-914A-390269	Sequence 390269,
c 103	16.4	82.0	21	7	US-10-310-914A-496762	Sequence 496762,	176	15.8	79.0	22	7	US-10-310-914A-391201	Sequence 391201,
c 104	16.4	82.0	21	7	US-10-310-914A-560700	Sequence 560700,	177	15.8	79.0	22	7	US-10-310-914A-955344	Sequence 955344,
c 105	16.4	82.0	21	7	US-10-310-914A-732268	Sequence 732268,	c 178	15.8	79.0	22	7	US-10-310-914A-1185318	Sequence 1185318,
c 106	16.4	82.0	21	7	US-10-310-914A-758538	Sequence 758538,	179	15.8	79.0	23	7	US-10-310-914A-130713	Sequence 130713,
c 107	16.4	82.0	21	7	US-10-310-914A-1240416	Sequence 1240416,	180	15.8	79.0	23	7	US-10-310-914A-327849	Sequence 327849,
c 108	16.4	82.0	21	7	US-10-310-914A-1283269	Sequence 1283269,	181	15.8	79.0	23	7	US-10-310-914A-390256	Sequence 390256,
c 109	16.4	82.0	21	7	US-10-310-914A-1302766	Sequence 1302766,	182	15.8	79.0	23	7	US-10-310-914A-391202	Sequence 391202,
c 110	16.4	82.0	22	7	US-10-310-914A-810508	Sequence 810508,	c 183	15.8	79.0	23	7	US-10-310-914A-424313	Sequence 424313,
c 111	16.4	82.0	22	7	US-10-310-914A-898815	Sequence 898815,	184	15.8	79.0	23	7	US-10-310-914A-659288	Sequence 659288,
c 112	16.4	82.0	22	7	US-10-310-914A-988521	Sequence 988521,	185	15.8	79.0	23	7	US-10-310-914A-702282	Sequence 702282,
c 113	16.4	82.0	22	7	US-10-310-914A-1240527	Sequence 1240527,	186	15.8	79.0	23	7	US-10-310-914A-728892	Sequence 728892,
c 114	16.4	82.0	23	7	US-10-310-914A-59881	Sequence 59881, A	c 187	15.8	79.0	23	7	US-10-310-914A-1066133	Sequence 1066133,
c 115	16.4	82.0	23	7	US-10-310-914A-433723	Sequence 433723,	188	15.8	79.0	24	7	US-10-310-914A-271796	Sequence 271796,
c 116	16.4	82.0	23	7	US-10-310-914A-595326	Sequence 595326,	189	15.8	79.0	24	7	US-10-310-914A-281031	Sequence 281031,
c 117	16.4	82.0	24	7	US-10-310-914A-59876	Sequence 59876, A	190	15.8	79.0	24	7	US-10-310-914A-281091	Sequence 281091,
c 118	16.4	82.0	24	7	US-10-310-914A-590304	Sequence 590304,	191	15.8	79.0	25	7	US-10-310-914A-879624	Sequence 879624,
c 119	16.4	82.0	24	7	US-10-310-914A-689570	Sequence 689570,	c 192	15.8	79.0	25	7	US-10-310-914A-121551	Sequence 121551,
c 120	16.4	82.0	24	7	US-10-310-914A-732087	Sequence 732087,	193	15.8	79.0	25	7	US-10-310-914A-298907	Sequence 298907,
c 121	16.4	82.0	25	7	US-10-310-914A-659207	Sequence 659207,	194	15.8	79.0	25	11	US-11-121-849-23512	Sequence 23512, A
c 122	16.4	82.0	25	7	US-10-310-914A-826277	Sequence 826277,	195	15.8	79.0	25	11	US-11-121-849-38847	Sequence 38847, A
c 123	16.4	82.0	25	7	US-10-310-914A-912851	Sequence 912851,	196	15.8	79.0	26	7	US-10-310-914A-137621	Sequence 137621,
c 124	16.4	82.0	25	7	US-10-310-914A-271802	Sequence 271802,	197	15.8	79.0	26	7	US-10-310-914A-137639	Sequence 137639,
c 125	16.4	82.0	27	7	US-10-310-914A-433727	Sequence 433727,	c 198	15.8	79.0	26	7	US-10-310-914A-168667	Sequence 168667,
c 126	16.4	82.0	27	7	US-10-310-914A-612116	Sequence 612116,	199	15.8	79.0	27	7	US-10-310-914A-678220	Sequence 678220,
c 127	16	80.0	18	7	US-10-310-914A-612117	Sequence 612117,	c 200	15.8	79.0	27	7	US-10-310-914A-840062	Sequence 840062,
c 128	16	80.0	18	7	US-10-310-914A-1047392	Sequence 1047392,	c 201	15.8	79.0	27	11	US-11-177-000-20	Sequence 20, Appl
c 129	16	80.0	19	7	US-10-310-914A-271757	Sequence 271757,	202	15.8	79.0	27	11	US-11-177-000-21	Sequence 21, Appl
c 130	16	80.0	19	7	US-10-310-914A-1047384	Sequence 1047384,	c 203	15.8	79.0	31	7	US-10-310-914A-1066057	Sequence 1066057,
c 131	16	80.0	19	7	US-10-310-914A-1047387	Sequence 1047387,	204	15.4	77.0	18	7	US-10-310-914A-282309	Sequence 282309,
c 132	16	80.0	20	7	US-10-310-914A-612127	Sequence 612127,	c 205	15.4	77.0	18	7	US-10-310-914A-496354	Sequence 496354,
c 133	16	80.0	21	7	US-10-310-914A-612134	Sequence 612134,	206	15.4	77.0	18	7	US-10-310-914A-551203	Sequence 551203,
c 134	16	80.0	21	7	US-10-310-914A-1047382	Sequence 1047382,	207	15.4	77.0	18	7	US-10-310-914A-758543	Sequence 758543,
c 135	15.8	79.0	19	7	US-10-310-914A-162959	Sequence 162959,	208	15.4	77.0	18	7	US-10-310-914A-959337	Sequence 959337,
c 136	15.8	79.0	19	7	US-10-310-914A-325657	Sequence 325657,	209	15.4	77.0	19	7	US-10-310-914A-227821	Sequence 227821,
c 137	15.8	79.0	19	7	US-10-310-914A-673482	Sequence 673482,	210	15.4	77.0	19	7	US-10-310-914A-229386	Sequence 229386,
c 138	15.8	79.0	19	7	US-10-310-914A-689749	Sequence 689749,	211	15.4	77.0	19	7	US-10-310-914A-229387	Sequence 229387,
c 139	15.8	79.0	19	7	US-10-310-914A-774654	Sequence 774654,	212	15.4	77.0	19	7	US-10-310-914A-261343	Sequence 261343,
c 140	15.8	79.0	19	7	US-10-310-914A-840061	Sequence 840061,	213	15.4	77.0	19	7	US-10-310-914A-278047	Sequence 278047,
c 141	15.8	79.0	19	7	US-10-310-914A-1302929	Sequence 1302929,	214	15.4	77.0	19	7	US-10-310-914A-298911	Sequence 298911,
c 142	15.8	79.0	20	7	US-10-310-914A-90712	Sequence 90712, A	c 215	15.4	77.0	19	7	US-10-310-914A-443852	Sequence 443852,
c 143	15.8	79.0	20	7	US-10-310-914A-130775	Sequence 130775,	216	15.4	77.0	19	7	US-10-310-914A-490785	Sequence 490785,
c 144	15.8	79.0	20	7	US-10-310-914A-137638	Sequence 137638,	217	15.4	77.0	19	7	US-10-310-914A-732307	Sequence 732307,
c 145	15.8	79.0	20	7	US-10-310-914A-148912	Sequence 148912,	218	15.4	77.0	19	7	US-10-310-914A-758544	Sequence 758544,
c 146	15.8	79.0	20	7	US-10-310-914A-162960	Sequence 162960,	c 219	15.4	77.0	19	7	US-10-310-914A-1289847	Sequence 1289847,
c 147	15.8	79.0	20	7	US-10-310-914A-168717	Sequence 168717,	220	15.4	77.0	19	7	US-10-310-914A-1289818	Sequence 1289818,
c 148	15.8	79.0	20	7	US-10-310-914A-287572	Sequence 287572,	c 221	15.4	77.0	19	7	US-10-310-914A-1305555	Sequence 1305555,
c 149	15.8	79.0	20	7	US-10-310-914A-391200	Sequence 391200,	222	15.4	77.0	20	7	US-10-310-914A-375633	Sequence 375633,
c 150	15.8	79.0	20	7	US-10-310-914A-761167	Sequence 761167,	223	15.4	77.0	20	7	US-10-310-914A-391173	Sequence 391173,
c 151	15.8	79.0	20	7	US-10-310-914A-774755	Sequence 774755,	224	15.4	77.0	20	7	US-10-310-914A-500346	Sequence 500346,
c 152	15.8	79.0	20	7	US-10-310-914A-845518	Sequence 845518,	225	15.4	77.0	20	7	US-10-310-914A-560704	Sequence 560704,
c 153	15.8	79.0	20	7	US-10-310-914A-879479	Sequence 879479,	c 226	15.4	77.0	20	7	US-10-310-914A-758567	Sequence 758567,
c 154	15.8	79.0	20	7	US-10-310-914A-939253	Sequence 939253,	227	15.4	77.0	20	7	US-10-310-914A-1289907	Sequence 1289907,
c 155	15.8	79.0	20	7	US-10-310-914A-1037971	Sequence 1037971,	c 228	15.4	77.0	21	7	US-10-310-914A-257955	Sequence 257955,
c 156	15.8	79.0	21	7	US-10-310-914A-65142	Sequence 65142, A	229	15.4	77.0	21	7	US-10-310-914A-282326	Sequence 282326,
c 157	15.8	79.0	21	7	US-10-310-914A-121502	Sequence 121502,	230	15.4	77.0	21	7	US-10-310-914A-351069	Sequence 351069,
c 158	15.8	79.0	21	7	US-10-310-914A-130712	Sequence 130712,	231	15.4	77.0	21	7	US-10-310-914A-443853	Sequence 443853,
c 159	15.8	79.0	21	7	US-10-310-914A-130794	Sequence 130794,	232	15.4	77.0	21	7	US-10-310-914A-465230	Sequence 465230,
c 160	15.8	79.0	21	7	US-10-310-914A-271794	Sequence 271794,	233	15.4	77.0	21	7	US-10-310-914A-785950	Sequence 785950,
c 161	15.8	79.0	21	7	US-10-310-914A-271795	Sequence 271795,	c 234	15.4	77.0	21	7	US-10-310-914A-792149	Sequence 792149,
c 162	15.8	79.0	21	7	US-10-310-914A-329858	Sequence 329858,	235	15.4	77.0	22	7	US-10-310-914A-148935	Sequence 148935,
c 163	15.8	79.0	21	7	US-10-310-914A-386842	Sequence 386842,	c 236	15.4	77.0	22	7	US-10-310-914A-172788	Sequence 172788,
c 164	15.8	79.0	21	7	US-10-310-914A-390315	Sequence 390315,	237	15.4	77.0	22	7	US-10-310-914A-455481	Sequence 455481,
c 165	15.8	79.0	21	7	US-10-310-914A-390316	Sequence 390316,	c 238	15.4	77.0	22	7	US-10-310-914A-1065863	Sequence 1065863,
c 166	15.8	79.0	21	7	US-10-310-914A-390317	Sequence 390317,	c 239	15.4	77.0	23	7	US-10-310-914A-258008	Sequence 258008,
c 167	15.8	79.0	21	7	US-10-310-914A-659279	Sequence 659279,	240	15.4	77.0	23	7	US-10-310-914A-278058	Sequence 278058,

241 15.4 77.0 23 7 US-10-310-914A-375554  
c 242 15.4 77.0 24 7 US-10-310-914A-172751  
243 15.4 77.0 24 7 US-10-310-914A-282262  
c 244 15.4 77.0 24 7 US-10-310-914A-356072  
c 245 15.4 77.0 24 7 US-10-310-914A-455464  
c 246 15.4 77.0 24 7 US-10-310-914A-455466  
247 15.4 77.0 24 7 US-10-310-914A-861182  
248 15.4 77.0 24 7 US-10-310-914A-1302921  
c 249 15.4 77.0 25 7 US-10-310-914A-273461  
c 250 15.4 77.0 26 7 US-10-310-914A-172752  
c 251 15.4 77.0 26 7 US-10-310-914A-172758  
c 252 15.4 77.0 26 7 US-10-310-914A-465225  
c 253 15.4 77.0 26 7 US-10-310-914A-1162712  
254 15.4 77.0 28 7 US-10-310-914A-1156363  
c 255 15.4 77.0 29 7 US-10-310-914A-490746  
c 256 15.2 76.0 20 7 US-10-310-914A-253916  
c 257 15.2 76.0 20 7 US-10-310-914A-362674  
c 258 15.2 76.0 20 7 US-10-310-914A-1072829  
c 259 15.2 76.0 21 7 US-10-310-914A-121454  
c 260 15.2 76.0 21 7 US-10-310-914A-138032  
261 15.2 76.0 21 7 US-10-310-914A-220594  
262 15.2 76.0 21 7 US-10-310-914A-253917  
263 15.2 76.0 21 7 US-10-310-914A-313487  
264 15.2 76.0 21 7 US-10-310-914A-939225  
c 265 15.2 76.0 21 7 US-10-310-914A-995316  
c 266 15.2 76.0 21 7 US-10-310-914A-1185247  
c 267 15.2 76.0 21 7 US-10-310-914A-1194774  
268 15.2 76.0 22 7 US-10-310-914A-131311  
269 15.2 76.0 22 7 US-10-310-914A-348780  
270 15.2 76.0 22 7 US-10-310-914A-391284  
271 15.2 76.0 22 8 US-11-106-909-5  
272 15.2 76.0 23 7 US-10-310-914A-288141  
c 273 15.2 76.0 23 7 US-10-310-914A-367876  
c 274 15.2 76.0 23 7 US-10-310-914A-497156  
275 15.2 76.0 23 7 US-10-310-914A-678353  
276 15.2 76.0 23 7 US-10-310-914A-718705  
277 15.2 76.0 23 7 US-10-310-914A-767802  
278 15.2 76.0 23 7 US-10-310-914A-840057  
279 15.2 76.0 23 7 US-10-310-914A-993088  
280 15.2 76.0 24 7 US-10-310-914A-63005  
281 15.2 76.0 24 7 US-10-310-914A-80883  
c 282 15.2 76.0 24 7 US-10-310-914A-172569  
283 15.2 76.0 24 7 US-10-310-914A-203029  
c 284 15.2 76.0 24 7 US-10-310-914A-239883  
285 15.2 76.0 24 7 US-10-310-914A-253942  
286 15.2 76.0 24 7 US-10-310-914A-285672  
c 287 15.2 76.0 24 7 US-10-310-914A-443940  
c 288 15.2 76.0 24 7 US-10-310-914A-571568  
c 289 15.2 76.0 24 7 US-10-310-914A-710243  
290 15.2 76.0 24 7 US-10-310-914A-969660  
291 15.2 76.0 24 7 US-10-310-914A-993073  
c 292 15.2 76.0 25 7 US-10-310-914A-367906  
c 293 15.2 76.0 25 7 US-10-310-914A-367909  
294 15.2 76.0 25 7 US-10-310-914A-682082  
295 15.2 76.0 25 7 US-10-310-914A-840058  
c 296 15.2 76.0 25 7 US-10-310-914A-845336  
297 15.2 76.0 25 11 US-11-121-849-23511  
298 15.2 76.0 26 7 US-10-310-914A-76617  
299 15.2 76.0 26 7 US-10-310-914A-348779  
c 300 15.2 76.0 26 7 US-10-310-914A-444004

ALIGNMENTS

RESULT 1  
US-11-127-654-875  
; Sequence 875, Application US/11127654  
; Publication No. US20050250726A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC

Sequence 375554,  
Sequence 172751,  
Sequence 282262,  
Sequence 356072,  
Sequence 455464,  
Sequence 455466,  
Sequence 861182,  
Sequence 1302921,  
Sequence 273461,  
Sequence 172752,  
Sequence 172758,  
Sequence 465225,  
Sequence 1162712,  
Sequence 1156363,  
Sequence 490746,  
Sequence 253916,  
Sequence 362674,  
Sequence 1072829,  
Sequence 121454,  
Sequence 138032,  
Sequence 220594,  
Sequence 253917,  
Sequence 313487,  
Sequence 939225,  
Sequence 995316,  
Sequence 1185247,  
Sequence 1194774,  
Sequence 131311,  
Sequence 348780,  
Sequence 391284,  
Sequence 5, Appli  
Sequence 288141,  
Sequence 367876,  
Sequence 497156,  
Sequence 678353,  
Sequence 718705,  
Sequence 767802,  
Sequence 840057,  
Sequence 993088,  
Sequence 63005, A  
Sequence 80883, A  
Sequence 172569,  
Sequence 203029,  
Sequence 239883,  
Sequence 253942,  
Sequence 285672,  
Sequence 443940,  
Sequence 571568,  
Sequence 710243,  
Sequence 969660,  
Sequence 993073,  
Sequence 367906,  
Sequence 367909,  
Sequence 682082,  
Sequence 840058,  
Sequence 845336,  
Sequence 76617, A  
Sequence 348779,  
Sequence 444004,

; TITLE OF INVENTION: INFLAMMATORY DISEASES  
; FILE REFERENCE: C1039.70060US01  
; CURRENT APPLICATION NUMBER: US/11/127,654  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US 10/112,653  
; PRIOR FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 875  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide  
US-11-127-654-875  
  
Query Match 100.0%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 AGGGAGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGGGAGGGAGGGAGGGG 20  
  
RESULT 2  
US-10-310-914A-1295111  
; Sequence 1295111, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1295111  
; LENGTH: 26  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1295111  
  
Query Match 100.0%; Score 20; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 AGGGAGGGAGGGAGGGG 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 AGGGAGGGAGGGAGGGG 20  
  
RESULT 3  
US-10-310-914A-776151/c  
; Sequence 776151, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuza  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 776151  
; LENGTH: 19  
; TYPE: RNA

```
; ORGANISM: Human
US-10-310-914A-776151

Query Match          95.0%; Score 19; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20
   |||||
Db 19 GGGGAGGGGAGGGAGGGG 1

RESULT 4
US-10-310-914A-776152/c
; Sequence 776152, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 776152
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-776152

Query Match          95.0%; Score 19; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20
   |||||
Db 19 GGGGAGGGGAGGGAGGGG 1

RESULT 5
US-10-310-914A-739686
; Sequence 739686, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 739686
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-739686

Query Match          95.0%; Score 19; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20
   |||||
Db 1 GGGGAGGGGAGGGAGGGG 19

RESULT 6
US-10-310-914A-1162719/c
; Sequence 1162719, Application US/10310914A
```

```
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1162719
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1162719

Query Match          95.0%; Score 19; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20
   |||||
Db 19 GGGGAGGGGAGGGAGGGG 1

RESULT 7
US-10-310-914A-1162726/c
; Sequence 1162726, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1162726
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1162726

Query Match          95.0%; Score 19; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20
   |||||
Db 21 GGGGAGGGGAGGGAGGGG 3

RESULT 8
US-10-310-914A-1295143
; Sequence 1295143, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1295143
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
```

## US-10-310-914A-1295143

Query Match 95.0%; Score 19; DB 7; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 19  
|||||

Db 3 AGGGAGGGAGGGAGGGG 21  
|||||

## RESULT 9

US-10-310-914A-1295144  
; Sequence 1295144, Application US/10310914A  
; Publication No. US2006000322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1295144  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human

## US-10-310-914A-1295144

Query Match 95.0%; Score 19; DB 7; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 19  
|||||

Db 3 AGGGAGGGAGGGAGGGG 21  
|||||

## RESULT 10

US-10-310-914A-1295148  
; Sequence 1295148, Application US/10310914A  
; Publication No. US2006000322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1295148  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human

## US-10-310-914A-1295148

Query Match 95.0%; Score 19; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 19  
|||||

Db 5 AGGGAGGGAGGGAGGGG 23  
|||||

## RESULT 11

US-10-310-914A-1295149  
; Sequence 1295149, Application US/10310914A  
; Publication No. US2006000322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1295149  
; LENGTH: 23  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1295149

Query Match 95.0%; Score 19; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 19  
|||||

Db 5 AGGGAGGGAGGGAGGGG 23  
|||||

## RESULT 12

US-10-310-914A-739676  
; Sequence 739676, Application US/10310914A  
; Publication No. US2006000322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 739676  
; LENGTH: 26  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-739676

Query Match 95.0%; Score 19; DB 7; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGAGGGAGGGAGGGG 20  
|||||

Db 6 GGGAGGGAGGGAGGGG 24  
|||||

## RESULT 13

US-10-310-914A-1162727/c  
; Sequence 1162727, Application US/10310914A  
; Publication No. US2006000322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1162727  
; LENGTH: 27  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1162727

```

Query Match          95.0%; Score 19; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 GGGGAGGGAGGGAGGGG 20
    |||||
Db  21 GGGGAGGGAGGGAGGGG 3

RESULT 14
US-10-310-914A-1162700/c
; Sequence 1162700, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1162700
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1162700

Query Match          95.0%; Score 19; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 GGGGAGGGAGGGAGGGG 20
    |||||
Db  25 GGGGAGGGAGGGAGGGG 7

RESULT 15
US-10-310-914A-1155402
; Sequence 1155402, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1155402
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1155402

Query Match          92.0%; Score 18.4; DB 7; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 AGGGAGGGAGGGAGGGG 20
    |||||
Db  1 AGGGAGGGAGGGAGGGG 20

RESULT 16
US-10-310-914A-162906
; Sequence 162906, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162906
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-162906

Query Match          92.0%; Score 18.4; DB 7; Length 24;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 AGGGAGGGAGGGAGGGG 20
    |||||
Db  3 AGGGAGGGAGGGAGGGG 22

RESULT 17
US-10-310-914A-162961
; Sequence 162961, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162961
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-162961

Query Match          92.0%; Score 18.4; DB 7; Length 24;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 AGGGAGGGAGGGAGGGG 20
    |||||
Db  5 AGGGAGGGAGGGAGGGG 24

RESULT 18
US-10-310-914A-162974
; Sequence 162974, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162974
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-162974

```



```
Query Match          92.0%; Score 18.4; DB 7; Length 24;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 5 AGGGAGGGAGGGAGGGG 24
    ||||| ||||| ||||| |||||

RESULT 19
US-10-310-914A-282266
; Sequence 282266, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 282266
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-282266

Query Match          92.0%; Score 18.4; DB 7; Length 28;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGAGGGAGGGAGGGG 20
    ||||| ||||| ||||| |||||
Db 7 AGGGAGGGAGGGAGGGG 26
    ||||| ||||| ||||| |||||

RESULT 20
US-10-310-914A-906589
; Sequence 906589, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 906589
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-906589

Query Match          90.0%; Score 18; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 19
    ||||| ||||| ||||| |||||
Db 2 GGGGAGGGAGGGAGGGG 19
    ||||| ||||| ||||| |||||

RESULT 21
US-10-310-914A-1295146
; Sequence 1295146, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
```

```
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1295146
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1295146

Query Match          90.0%; Score 18; DB 7; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 19
    ||||| ||||| ||||| |||||
Db 5 GGGGAGGGAGGGAGGGG 22
    ||||| ||||| ||||| |||||

RESULT 22
US-10-310-914A-739675
; Sequence 739675, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 739675
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-739675

Query Match          90.0%; Score 18; DB 7; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGGAGGGAGGGAGGGG 19
    ||||| ||||| ||||| |||||
Db 6 GGGGAGGGAGGGAGGGG 23
    ||||| ||||| ||||| |||||

RESULT 23
US-10-310-914A-1047386
; Sequence 1047386, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1047386
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1047386

Query Match          90.0%; Score 18; DB 7; Length 23;
```

```
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162912
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-162912

Query Match      87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGAGGGGAGGGAGGGG 20
    |||||
Db 2 GGGAGGGGAGGGAGGGG 19

RESULT 24
US-10-310-914A-100302/c
; Sequence 100302, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 100302
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-100302

Query Match      87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGAGGGGAGGGAGGGG 20
    |||||
Db 19 GGGGTGGGAGGGAGGGG 1

RESULT 25
US-10-310-914A-148888
; Sequence 148888, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 148888
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-148888

Query Match      87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGAGGGGAGGGAGGGG 20
    |||||
Db 1 GGGGUGGGAGGGAGGGG 19

RESULT 26
US-10-310-914A-162912
; Sequence 162912, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
```

```
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162912
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-162912

Query Match      87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGAGGGAGGGAGGGG 19
    |||||
Db 1 AGGGAGGGAGGGAGGGG 19

RESULT 27
US-10-310-914A-386824
; Sequence 386824, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386824
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386824

Query Match      87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGAGGGAGGGAGGGG 19
    |||||
Db 1 AGGGAGGGAGGGAGGGG 19

RESULT 28
US-10-310-914A-386825
; Sequence 386825, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386825
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386825

Query Match      87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGAGGGAGGGAGGGG 19
    |||||
Db 1 AGGGAGGGAGGGAGGGG 19
```

```
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGAGGG 19
|||||
Db 1 AGGGGAGGGGAGGGAGGG 19
|||||

RESULT 29
US-10-310-914A-386850
; Sequence 386850, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 386850
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-386850

Query Match 87.0%; Score 17.4; DB 7; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20
|||||
Db 1 GGGGAGGGGAGGGAGGGG 19
|||||

RESULT 30
US-10-310-914A-288225
; Sequence 288225, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 288225
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-288225

Query Match 87.0%; Score 17.4; DB 7; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20
|||||
Db 1 GGGGAGGGGAGGGAGGGG 19
|||||

RESULT 31
US-10-310-914A-588532
; Sequence 588532, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
```

```
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 588532
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-588532

Query Match 87.0%; Score 17.4; DB 7; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGAGGGG 20
|||||
Db 1 GGGGAGGGGAGGGAGGGG 19
|||||

RESULT 32
US-10-310-914A-628864
; Sequence 628864, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 628864
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-628864

Query Match 87.0%; Score 17.4; DB 7; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGAGGG 19
|||||
Db 2 AGGGGAGGGGAGGGAGGG 20
|||||

RESULT 33
US-10-310-914A-1155411
; Sequence 1155411, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1155411
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1155411

Query Match 87.0%; Score 17.4; DB 7; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 2 GGGGAGGGGAGGGAGGGG 20  
Db 1 GGGGAGUGGAGGGAGGGG 19

RESULT 34  
US-10-310-914A-100342/c  
; Sequence 100342, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 100342  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-100342

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20  
Db 20 GGGGAGGGGAGGGGAAGGG 2

RESULT 35  
US-10-310-914A-288226  
; Sequence 288226, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 288226  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-288226

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20  
Db 1 GGGGAGGGGAGGGAGCGG 19

RESULT 36  
US-10-310-914A-288227  
; Sequence 288227, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof

; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 288227  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-288227

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGGAGGGGAGGGAGGGG 20  
Db 1 GGGGAGGGGAGGGAGCGG 19

RESULT 37  
US-10-310-914A-386839  
; Sequence 386839, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386839  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386839

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGGAGGGAGGGG 19  
Db 2 AAGGGAGGGGAGGGAGGGG 20

RESULT 38  
US-10-310-914A-386841  
; Sequence 386841, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 386841  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-386841

Query Match 87.0%; Score 17.4; DB 7; Length 21;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

; APPLICANT: BENWICH, ISAAC
; APPLICANT: Shiler, Kvuazt
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01

```

Qy 1 AGGGAGGGAGGGAGGG 19

Db 4 AGGGGAGGGAGGGAGGG 22  
||||| ||||| ||||| |||||

## RESULT 44

US-10-310-914A-560684  
; Sequence 560684, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 560684  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-560684

Query Match 87.0%; Score 17.4; DB 7; Length 22;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGAGGGAGGG 19  
||||| ||||| ||||| |||||

Db 1 AGGGGUGGGAGGGAGGG 19  
||||| ||||| ||||| |||||

## RESULT 45

US-10-310-914A-628966  
; Sequence 628966, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 628966  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-628966

Query Match 87.0%; Score 17.4; DB 7; Length 22;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGAGGGAGGG 19  
||||| ||||| ||||| |||||

Db 4 AGGGGAGGGAGGGAGGG 22  
||||| ||||| ||||| |||||

## RESULT 46

US-10-310-914A-659284  
; Sequence 659284, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 659284  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-659284

Query Match 87.0%; Score 17.4; DB 7; Length 22;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGGGAGGGAGGGAGGG 19  
||||| ||||| ||||| |||||

Db 4 AGGGGAGGGAGGGAGGG 22  
||||| ||||| ||||| |||||

## RESULT 47

US-10-310-914A-1345363/c  
; Sequence 1345363, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1345363  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1345363

Query Match 87.0%; Score 17.4; DB 7; Length 22;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGGAGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||

Db 20 GGGGAGGGAGGGAGGGG 2  
||||| ||||| ||||| |||||

## RESULT 48

US-10-310-914A-1345365/c  
; Sequence 1345365, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1345365  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1345365

Query Match 87.0%; Score 17.4; DB 7; Length 22;  
Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGGAGGGAGGGAGGGG 20  
||||| ||||| ||||| |||||

Db 19 GGGGAGGGGACGGGGGGGG 1

RESULT 49

US-10-310-914A-100318/c  
 ; Sequence 100318, Application US/10310914A  
 ; Publication No. US20060003322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shiler, Kvuzat  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; TITLE OF INVENTION: uses thereof  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310.914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 100318  
 ; LENGTH: 23  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-100318

Query Match 87.0%; Score 17.4; DB 7; Length 23;  
 Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGGAGGGGAGGGGGGGG 20

Db 22 GGGGAGGGGAGGGGAAGGG 4

RESULT 50

US-10-310-914A-162972  
 ; Sequence 162972, Application US/10310914A  
 ; Publication No. US20060003322A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bentwich, Isaac  
 ; APPLICANT: Shiler, Kvuzat  
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
 ; TITLE OF INVENTION: uses thereof  
 ; FILE REFERENCE: 06087.0200.CPUS01  
 ; CURRENT APPLICATION NUMBER: US/10/310.914A  
 ; CURRENT FILING DATE: 2002-12-06  
 ; NUMBER OF SEQ ID NOS: 1388402  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 162972  
 ; LENGTH: 23  
 ; TYPE: RNA  
 ; ORGANISM: Human  
 US-10-310-914A-162972

Query Match 87.0%; Score 17.4; DB 7; Length 23;  
 Best Local Similarity 94.7%; Pred. No. 4.6e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGGGGAGGGGAGGGGAGGG 19

Db 5 AGGGGAGGGGAGGGGAGGG 23

Search completed: February 16, 2006, 02:53:09  
 Job time : 189.446 secs

**THIS PAGE BLANK (USPTO)**